Phenotype and Genotype Object Model (PAGE-OM)

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Preface

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- CORBAservices

- CORBAfacilities
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1 Scope

PAGE-OM provides a timely, robust, and useful data model, sufficiently developed and tested to justify formal registration and deployment to the many and various communities engaged in genotype-phenotype data handling.

2 Conformance

The normative parts of this specification are:

- Platform independent model (Chapter 7), expressed in the attached XML file created according to XMI format rules, v2.1, using program Enterprise Architect (http://www.sparxsystems.com/), version 7.5.847, UML version 2.1.
- Platform specific model (Chapter 8), representing an XML-based data exchange format, defined by an XML Schema definition.

Any implementation using or producing data exchange format defined by the Platform specific model defined by this specification is considered complying with this specification.

Any platform specific model that is derived from the platform independent model defined by this specification is also considered compliant.

If there is any inconsistency, or discrepancy between generality and specificity, between the platform independent and platform specific model, the platform specific model has precedence.

The normative parts are expressed in the accompanying files in a document whose number is given in Annex A (or elsewhere in this document). Parts of these files may also appear in the explanatory text of this document. If they do and if there are some differences or discrepancies, the content of the normative accompanying files has precedence.

Regarding the use of ontology, it is not normative to use the ones listed in Chapter 7's "Ontology" section, but it is highly suggested. The reason why this specification is not stricter about it is the reflection of the fact that ontology is a moving target in the bio-community and insisting on using only specific ones, may harm the usability of this specification.

3 Normative References

There are no normative references associated with this specification.

4 Terms and Definitions

BQS	Bibliographic Query Service
CDS	Coding sequence
DNA	Deoxyribonucleic acid
GO	Gene Ontology
HUGO	Human Genome Organisation
ICIS	International Crop Information System
LD	linkage disequilibrium
LSID	Life Sciences Identifier
PCR	Polymerase chain reaction
RNA	Ribonucleic acid
SNP	Single Nucleotide Polymorphism

5 Supporting Organizations

The following organizations have been involved in the process of developing, prototyping, financing this project, and/or reviewing this specification. The authors thank them for participating and giving their valuable input.

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- Stanford University, USA
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- Tokyo Metropolitan Institute of Gerontology, Japan
- UNISYS, USA
- University College London
- University of Bergen, Norway
- University of Leicester, UK
- Yale University, USA

5.1 Acknowledgements

The authors of this document wish to express their appreciation to those listed below (in non-significant order) for their contributions of ideas and experience. Ultimately, the ideas expressed in this document are those of the authors and do not necessarily reflect the views or ideas of these individuals, nor does the inclusion of their names imply an endorsement of the final product.

Kimitoshi Naito, Akihiko Konagaya, Albert V. Smith, Anthony J. Brookes, David Fredman, Debasis Dash, Haseena Rajeevan, Heikki Lehväslaiho, Hideaki Sugawara, Hiroshi Mizushima, Juha Muilu, Jun Nakaya, Katsushi Tokunaga, KeiHoi Cheung, Kenshi Hayashi, Mark Woon, Masako Kuroda, Masashi Tanaka, Martin Senger, Matthew Darlison, Takeshi Tomiki, Toshio Kojima, Yasumasa Shigemoto, Yoshiji Yamada.

6 Introduction

Modern biology is striving to understand what factors generate inter-individual differences in structure, development, or behavior within a species. Genetic factors ('genotypes') are undoubtedly of key importance in this equation, as are environmental conditions and even stochastic events, and much research is being done to elucidate how these things impact a range of normal and disease 'phenotypes' (i.e., the characteristics that can be observed). Progress in this area will ultimately lead to improved and increasingly personalized medical care, more productive agricultural and farming systems, and better solutions for environmental monitoring and control.

Many organisms are being explored and utilized with regards to deciphering genotype-phenotype relationships. On the genetic level, it is now possible to determine DNA sequences at extremely high-throughput, thereby revealing normal and pathogenic variation in and around genes, across individuals. On the level of the phenotype, an almost unlimited number of things could be influenced by genetic variants, and increasingly precise and standardized assays are being devised to measure and assess such things.

Both genetic and phenotype datasets need to be managed and combined to elucidate genotype-phenotype relationships. The genetic datasets have so far mostly comprised assays of specific sites of variation (creating 'genotypes'), which have recently been growing exponentially due to technical advances. A subsequent new era is emerging wherein large DNA stretches (and perhaps complete genetic complements) are being fully (re)sequenced in relevant individuals. Phenotype datasets, both in human and non-human model organisms, are also being scaled up via the investigation of thousands or tens of thousands of individuals. Indeed, study integration is a major feature of current research; for example, existing Genome-wide Association (GWA) data done on various different studies are being merged in the ENAGE (http://www.euengage.org/) program leading to a potential GWA resource of 80,000 samples. As a result of this rapid progress in the modes of both genetic and phenotype analysis, the amount of genotype-phenotype data being generated is increasing at an exponential rate. The potential for converting this raw 'data' into useful 'knowledge' is therefore immense, but achieving this effectively will require distinct studies to be inter-related, cross-validated, and compared. In short, there is now an urgent need to ensure that genotype-phenotype investigations are supported by technologies that make them interoperable. Key to achieving this is a robust reference model for these types of data, via which all relevant domain knowledge can be effectively integrated and disseminated. That is precisely the motivation behind building the Phenotype And GEnotype Object Model (PAGE-OM).

Anticipated user communities for PAGE-OM include biomedical researchers, clinicians, people involved in teaching and training such groups, and information technologists working in support of these domains.

Given the modern data production systems now at their disposal, biomedical researchers are constantly facing challenges of genotype-phenotype data management (e.g., storage, retrieval, tracking, reformatting, merging) and this directly impacts their ability to effectively analyze, share, and report their various datasets. Clinicians - for whom genotype-phenotype relationships are only one of many things to be considered - require streamlined and standardized access to explanations about DNA sequence alternatives and how and in which situations they may impact their clinical work. All of these needs will be helped by the development of PAGE-OM, which specifies the rational and functional segmentation of genotype-phenotype information into sub-components that are operationally distinct (the high-level objects in the model) and lays out the natural inter-relationships between these components. Once biomedical researchers and clinicians come to be familiar with these logical components and their relationships, it will be far easier for both groups to process and make sense of genotype-phenotype information, both within their own fields and in the important task of communicating between their domains of work. For this reason, it is also highly desirable that teachers of their two professions become familiar with the object modeling concepts, in order that they may suitably educate the researchers and doctors of the future.

Information technologists working in the biomedical fields will, more than any other group, benefit from understanding PAGE-OM in depth. These individuals have the job of providing the universe of databases, data pipelines, analysis tools, search functionalities, and exchange protocols in which genotype-phenotype information will exist and be processed for exploitation. In the absence of any data model for genotype-phenotype information, these workers would each have to devise their own data model. Not only would this constant re-invention of the wheel be highly wasteful of manpower, it is also likely that many of the solutions they come up with would be suboptimal - given the limited experience that any one IT individual or IT team would usually have. Instead, PAGE-OM has been designed and piloted by a consortium of expert participants from nearly 50 Institutions engaged in many diverse genotype-phenotype projects.

The PAGE-OM therefore provides a first-version common language, well-documented entity list, and carefully considered array of entity- relationships that IT workers can take directly off the shelf, with confidence that it should need nothing more than small adjustments or additions to serve their own specific needs. Additionally, as more and more IT groups adopt PAGE-OM and base their systems upon it, those systems naturally will become more and more similar and able to intercommunicate. This is an absolute necessity if the totality of genotype-phenotype information is ever to be merged into a single virtual corpus, for holistic and optimal utilization.

To enable PAGE-OM to achieve its goals, it is structured as several high level concepts that can be used independently on the conceptual level (but not necessarily when using a modeling tool). Examples of these concepts are: Marker, Assay, Sample, Genotype, Frequency, Phenotype, and Experiment. For example: A company providing DNA analysis kits might only need to use the Marker and Assay parts of this model. A genome variation database might use solely the Marker component, or perhaps the Assay, Sample, Genotype, and Frequency entities as well listing variant findings in population groups. A project involved in collecting and examining clinical samples might use only Sample and Phenotype parts, and if that team subsequently undertook DNA analysis it could extend their data systems by incorporating some or all of the remaining concepts in order to fully describe whatever genotype-phenotype relationships they might discover. Such flexibility is a necessary and innate characteristic of PAGE-OM, and that extends into the way we have matched the design principles and various classes of the model to those of other data standards initiates that cover other domains of biomedical research.

In conclusion, we believe PAGE-OM provides a timely, robust, and useful data model, sufficiently developed and tested to justify formal registration and deployment to the many and various communities engaged in genotype-phenotype data handling.

7 Platform Independent Model

The platform independent model is expressed as a UML model, UML version 2.1. The normative is its XMI representation, attached in the “Accompanying files” as the file PIM/ PAGE-OM_uml_2. 1_xmi_2. 1 .xml. The XMI was generated by the tool Enterprise Architect (http://www.sparxsystems.com/), version 7.5.847, including the EA specific extensions.

The XMI representing the platform independent model includes, because of the technical reasons and because of lacking package names, also the classes of the SNP specification (that are used by this specification).

The basic data types (e.g., string or dateTime) are those inspired by the data types from the XML Schema (XML Schema Part 2: Datatypes - http://www.w3.org/TR/xmlschema-2/), where their exact descriptions can be found.

The full details with class and attributes description are attached in a generated file PIM/PAGE-OM.rtf. This file can be used interchangeably with the XMI file because both were generated from a model created by the Enterprise Architect tool - whose main file is also attached as file PIM/PAGE-OM.EAP. Note, however, that the latter file may have some EA specific expressions and extensions that are not normative for this specification.

For convenience, the whole PAGE-OM specification can be seen at http://www.pageom.org/models/omg/v_1.0/.

7.1 Model Diagrams

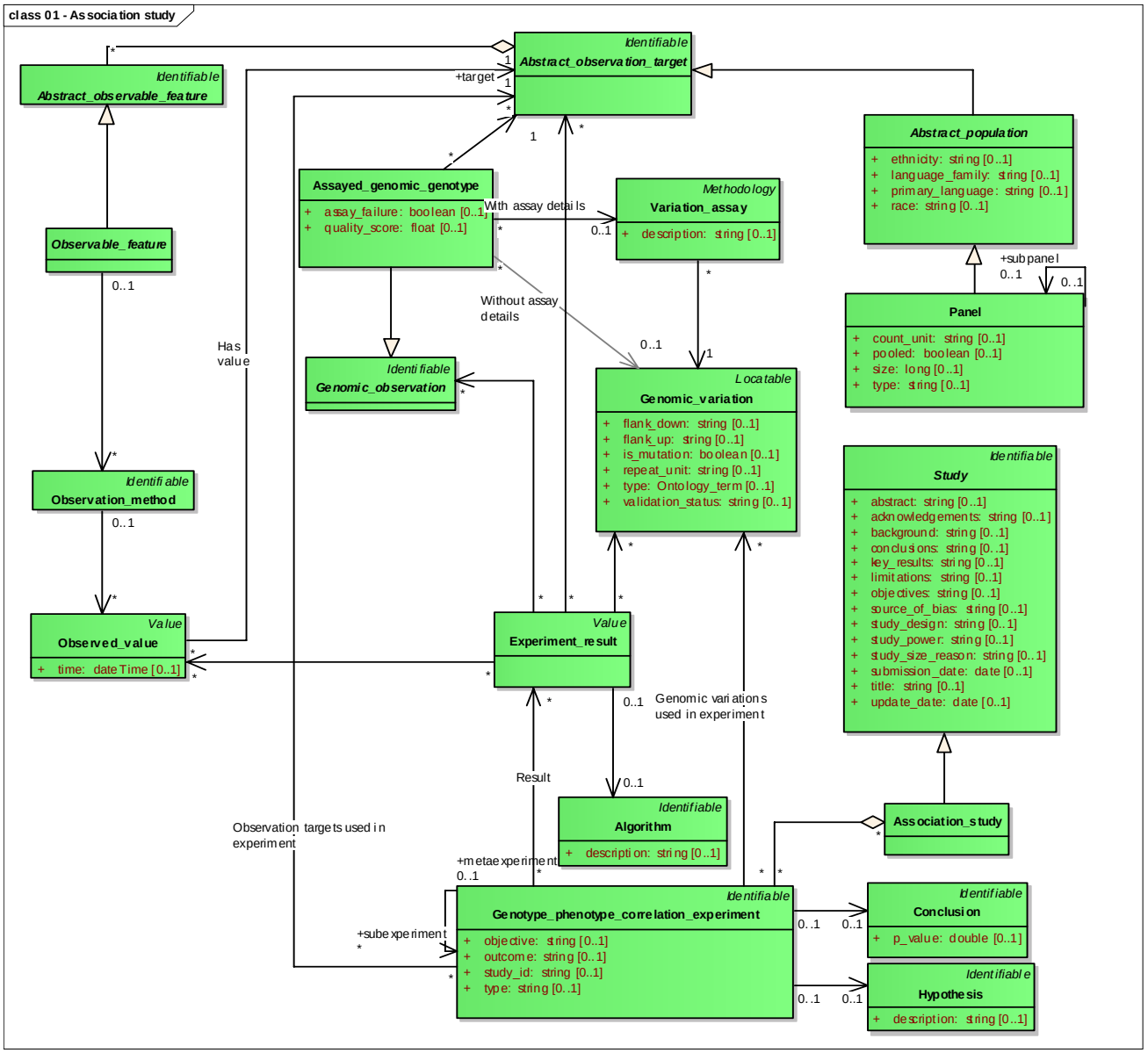

Figure 7.1 - Association study

Association study is the only kind of study specified in this model. Its parent, Study, can be used as an extension point to add new study types. Association studies are composed from a set of experiments (Genotype_phenotype_correlation_experiment) done over observation targets (Panel, Molecular_sample, Individual). These experiments lead to a set of results (Experiment_result) documented by genomic observations and observed phenotype values.

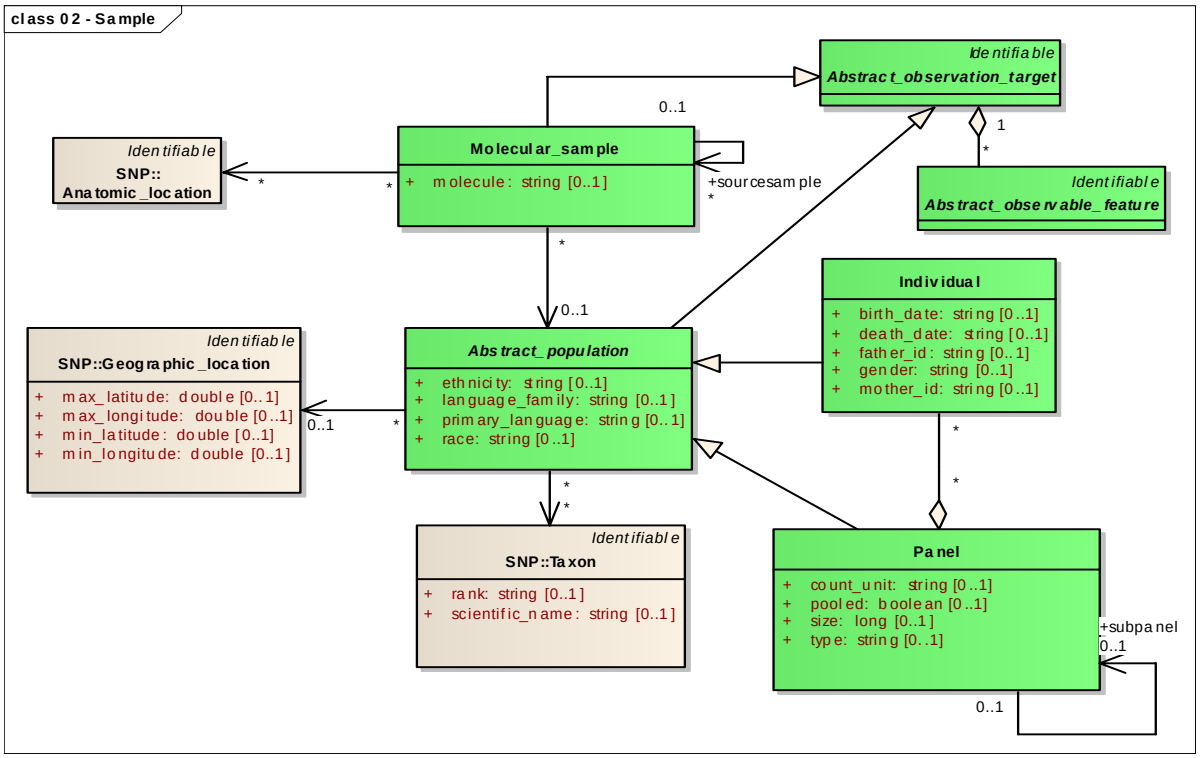

Figure 7.2 - Sample

An individual (Individual) interacts with the rest of the model by giving one or more samples (Molecular_samples) from different tissues. Mixed samples and more complicated sample organizations are modeled by allowing Molecular_samples and Panels to be composed of multiples of themselves. In these cases it is common that individuals cannot be identified.

An individual (Individual) has parent IDs as attributes. This information makes it possible to reconstruct pedigrees when needed. A taxon identifies the taxonomic group, typically species, the individual, or the population sample belongs to. Further, they can be placed on a geographic map (Geographic_location).

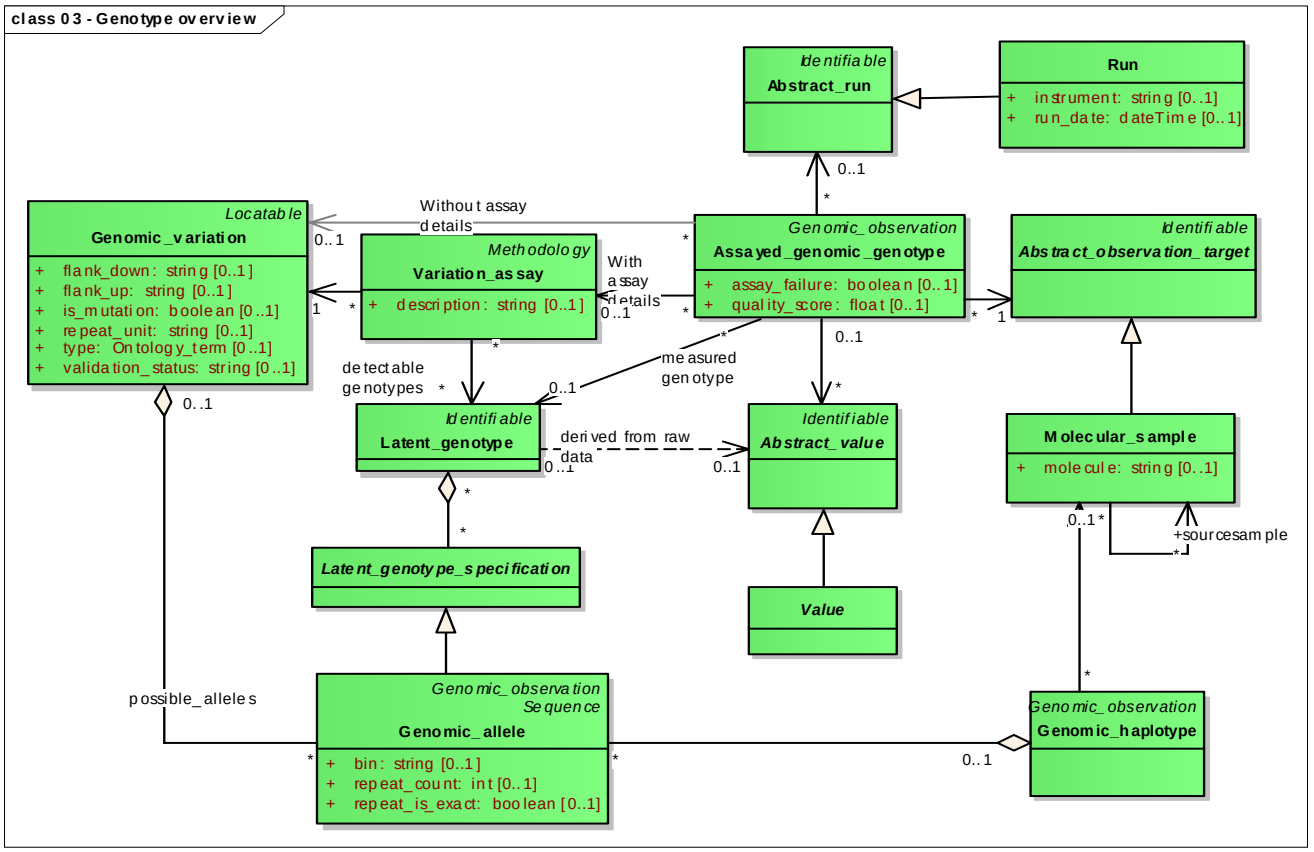

Figure 7.3 - Genotype overview

Genotypes (Assayed_genomic_genotype) produced over markers (Genomic_variation) and samples (Abstract_ovservation_target) under specific experimental conditions (Run). Latent_genotype has a set of alleles (Genomic_allele) depending on ploidy level.

Genotyping assay can detect different genotypes from different individuals. One genotype is measured from one individual at given marker site. Genotypes may be stored with or without assay information (Variation assay is PCR (Polymerase Chain Reaction) assay designed for the variation site).

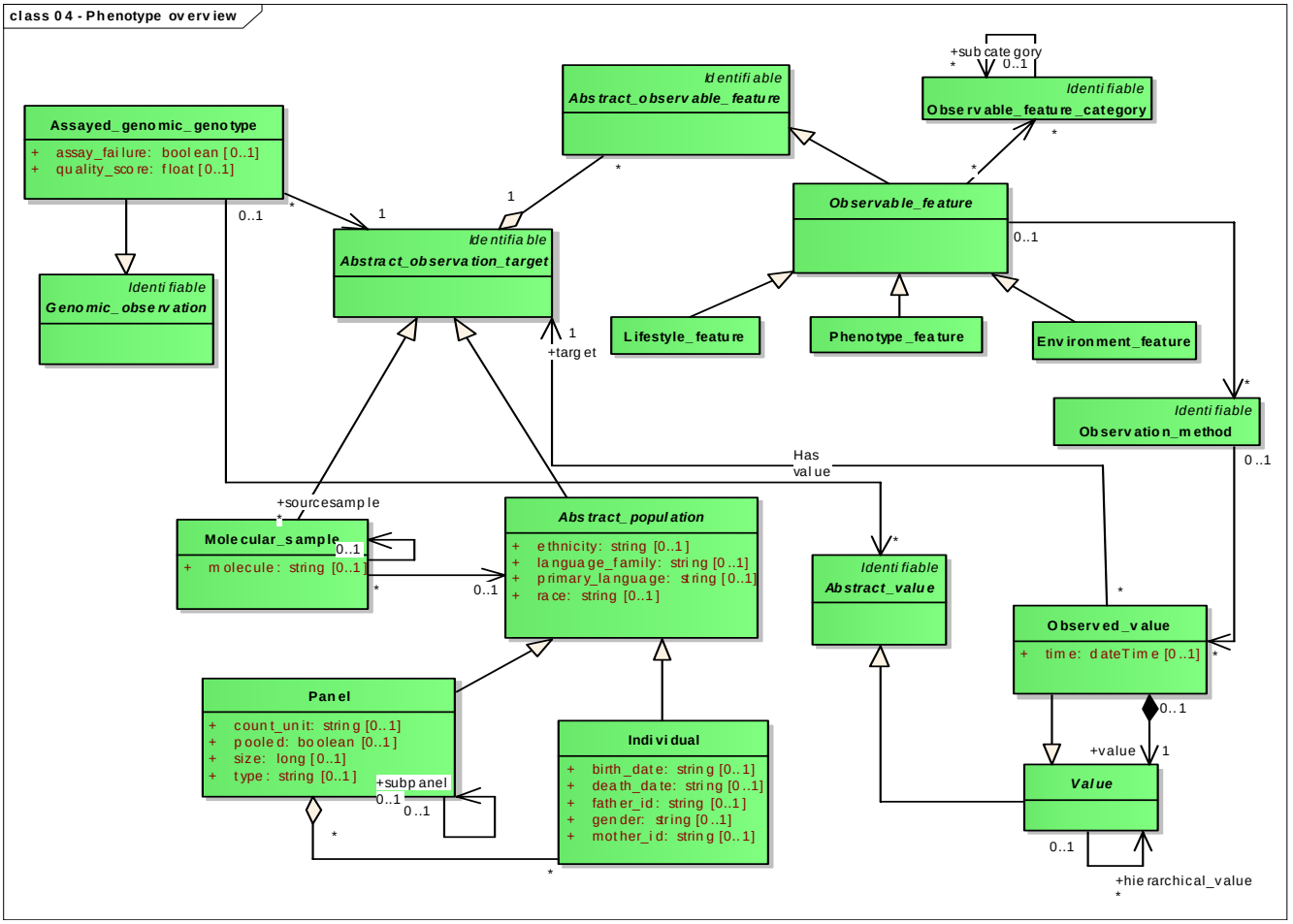

Figure 7.4 - Phenotype overview

Phenotype, environment, and life style features are special cases of observable features from which observations can be made using specific observation methods. These observations lead to observed values obtained at a specific time from observation target. Values can be also derived or categorized values (for example, high cholesterol level) in which case supporting values can be obtained from associated values, implemented using a recursion in the value model.

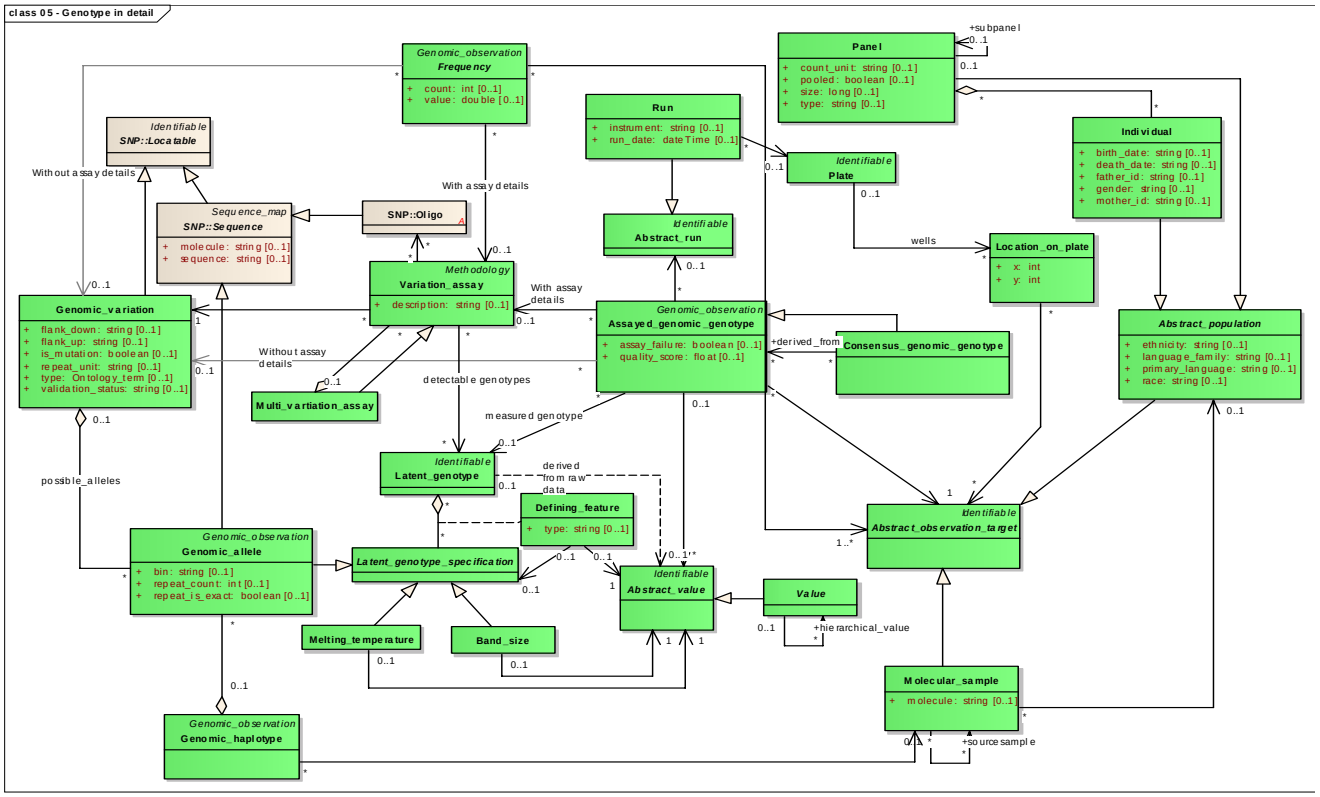

Figure 7.5 - Genotype in detail

An assay (Variation_assay) is applied to a sample (Molecular_sample) to get a genotype (Assayed_genomic_genotype). One or more Assayed_genomic_genotype are used to reach a consensus (Consensus_genomic_genotype). The assays commonly use oligo primers to detect allelic variations (Genomic_alleles in Genomic_variation).

Assay can have reference to possible detectable latent genotype (combination of alleles depending on ploidy). One of these combinations can be detected in single genotype measurement (Assayed_genomic_genotype) done using the specific assay.

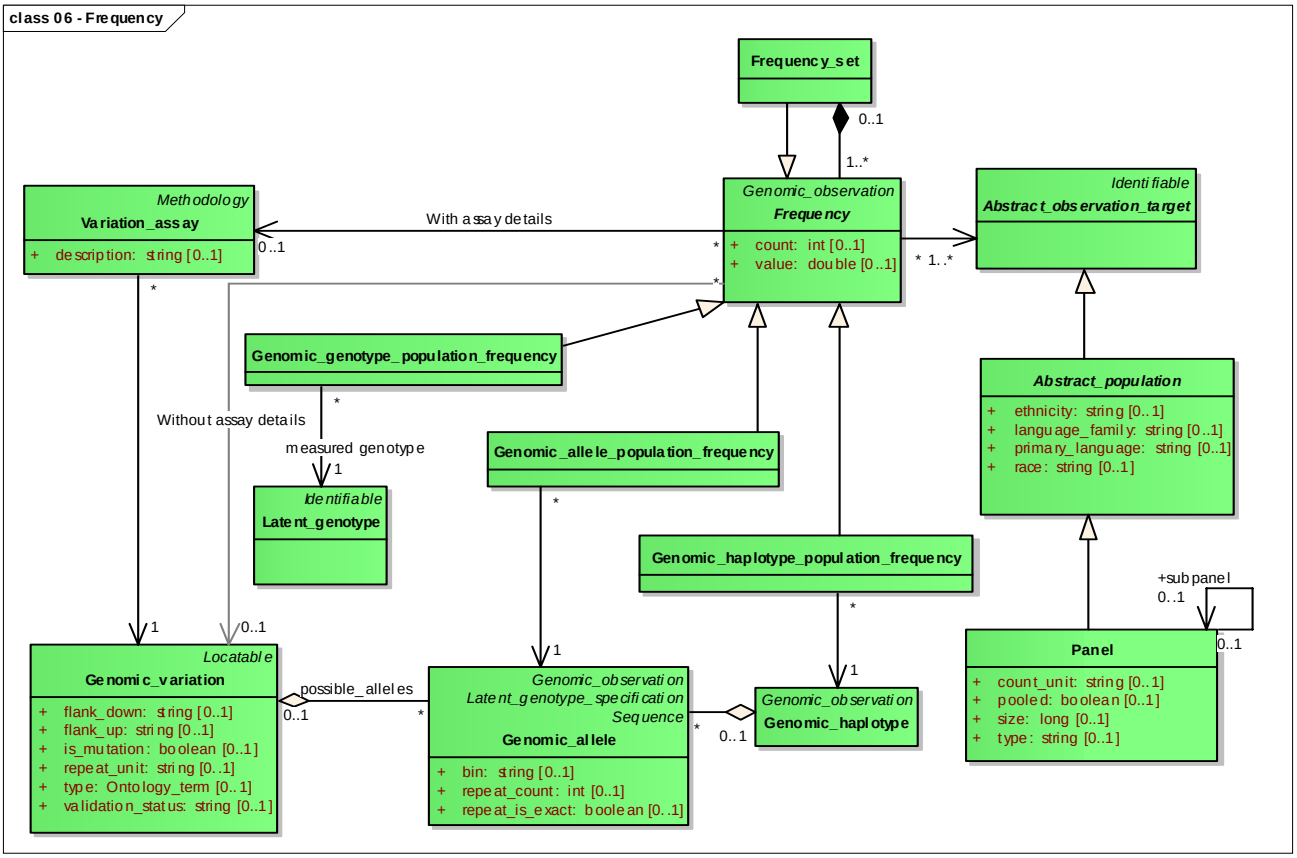

Figure 7.6 - Frequency

Alleles (Genomic_alleles), genotypes (Latent_genotype), and haplotypes (Genomic_haplotype) can have measured frequencies in population samples (Panels). In addition, heterozygosity (Heterozygosity) is a measure of observed variability of a polymorphic site (Genomic_variation) in a sub-population (Panel).

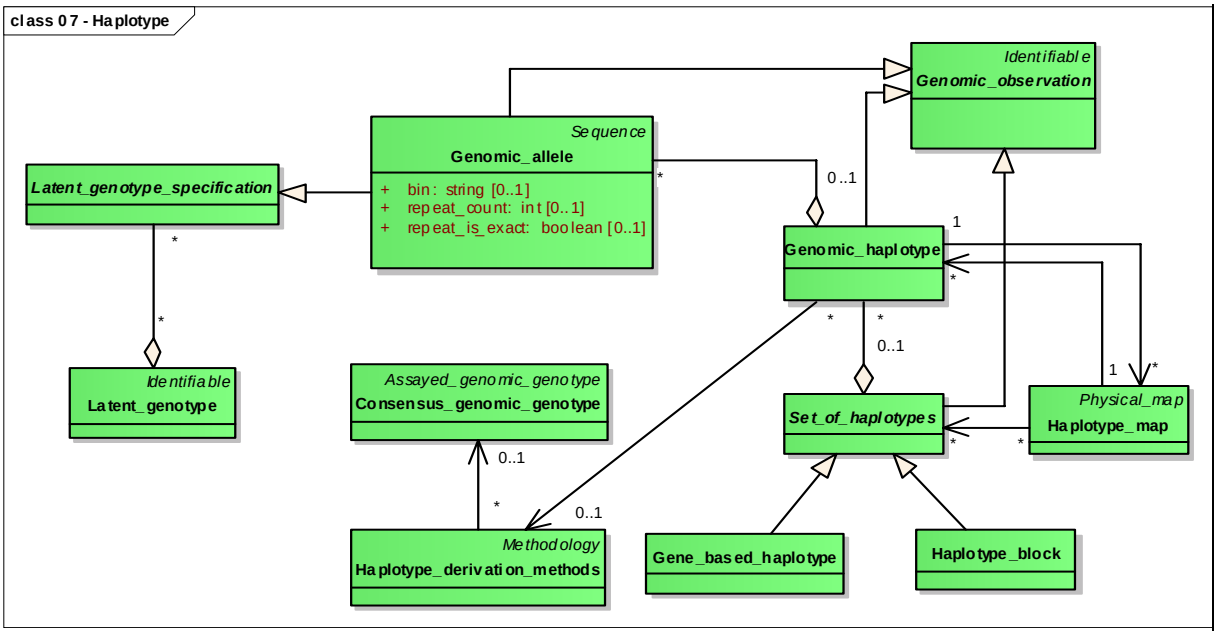

Figure 7.7 - Haplotype

Haplotype (Genomic_haplotype) is a set of polymorphisms (Genomic alleles) on a single chromosome (chromatid). Haplotypes may be grouped into sets like haplotype blocks (Haplotype_block) separated by recombination regions and gene based haplotype (Gene_based_haplotype), which combines sets of haplotypes on same gene structure.

Depending on an assay used, a genotype (Consensus_genomic_genotype) may contain information about the phase of the detected Genomic_alleles. Alternatively, various additional methods (Haplotype_derivation_methods) can be used to measure or calculate haplotypes (Genomic_haplotypes) from the genotype data. The aim of many haplotype studies is to find haplotypes within a given sequence region that define most of the variation in populations (Set_of_haplotypes). Haplotype blocks (Haplotype_blocks) are clusters determined by linkage disequilibrium-based methods. The other common way to define clusters is to use the sequence region of the gene (Gene_based_haplotype).

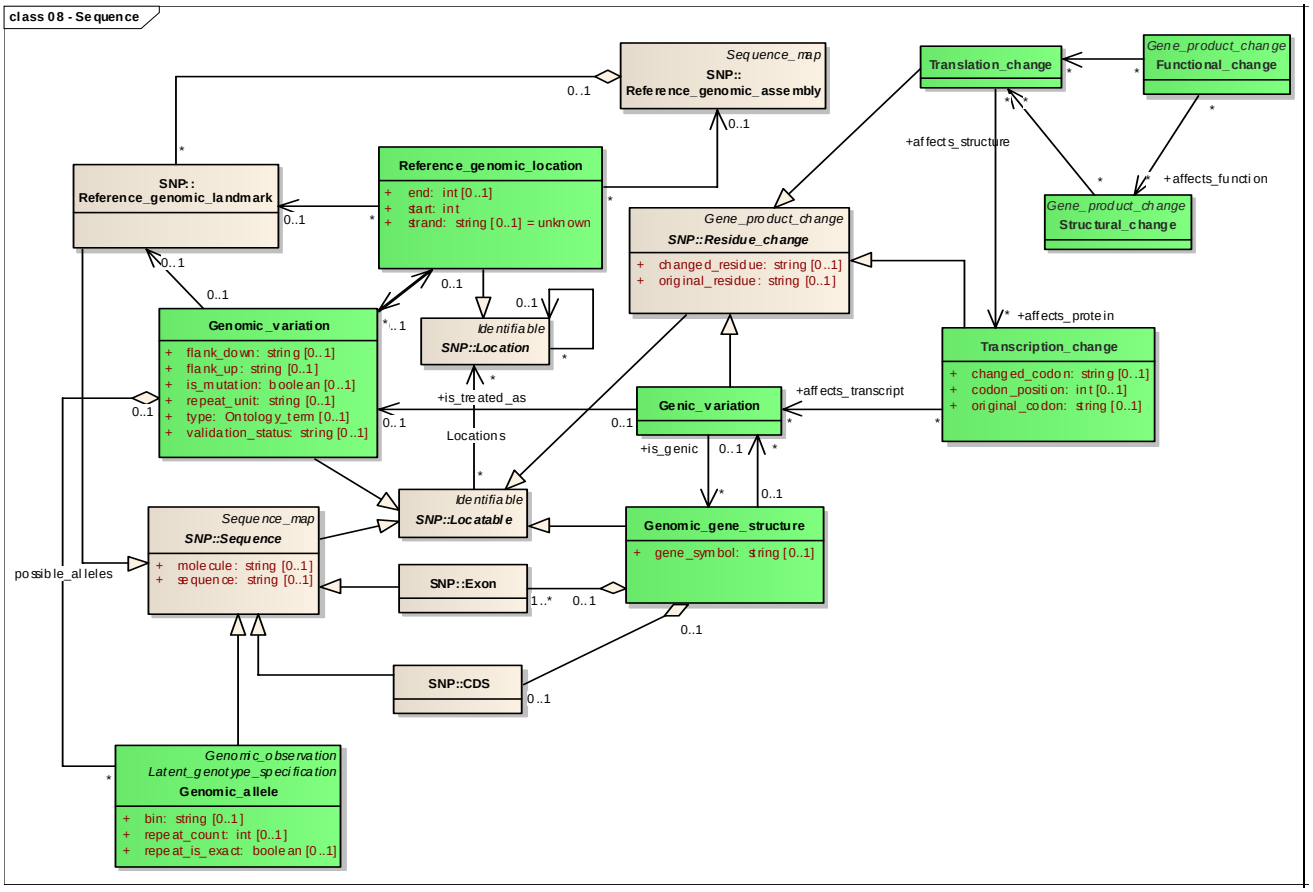

Figure 7.8 - Sequence

All sequences inherit from a generic Sequence class. All sequences (Sequence) and sequence features (e.g., Genomic_variation) can be located within a genomic sequence (Reference_genomic_sequence). This is modeled by common inheritance from an abstract superclass Locatable that can have several locations (Genomic_reference_location).

A Reference_genomic_landmark is any accessioned sequence within Reference_genomic_assembly. The model allows for multiple assemblies. Any location within a landmark and therefore in an assembly is called Reference_genomic_location. Any variable site in an assembly is a Genomic_polymorphism. The variable sequences within Genomic_variations are called Genomic_alleles.

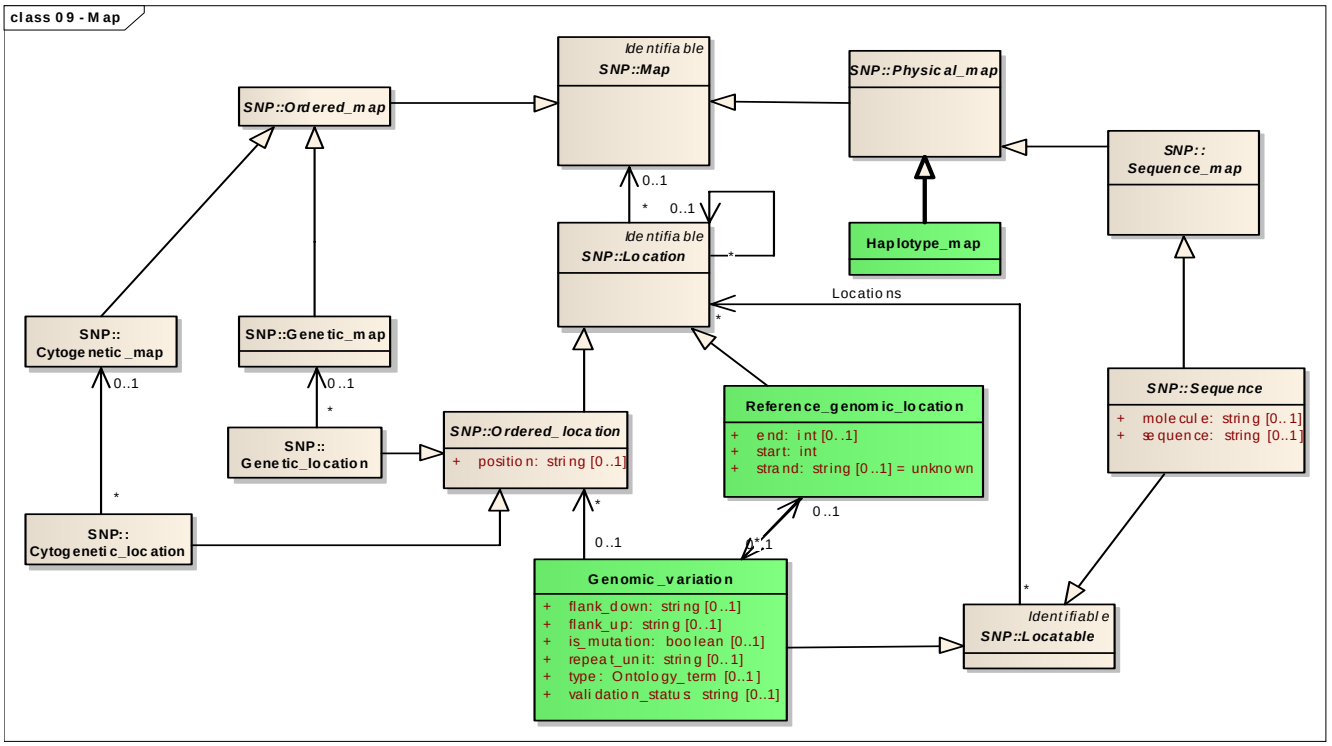

Figure 7.9 - Map

A map organizes genomic features and assigns them locations. The primary maps (Physical_map, Sequence_map) that have additive sequence residue count distances between markers, are separated here from secondary maps (Ordered_map) which at best can only deal with non-metric distances. For each map (Map) type there is a corresponding location (Location). Hence a marker (Genetic_variation) can have several locations (Reference_genomic_location) in sequences (Reference_genomic_landmark) and additionally can be located within a band (Cytogenetic_location) in a species-specific karyotype (Cytogenetic_map) as well as in (Genetic_location) several genetic maps (Genetic_map), e.g., in maps based on male and female recombination frequencies. Genomic assembly (Reference_genomic_assembly) is a physical sequence map that is a combination of genomic sequence (Reference_genomic_landmark). Feature locations can also be expressed in chromosomal locations in an assembly (Reference_genomic_location_in_assembly).

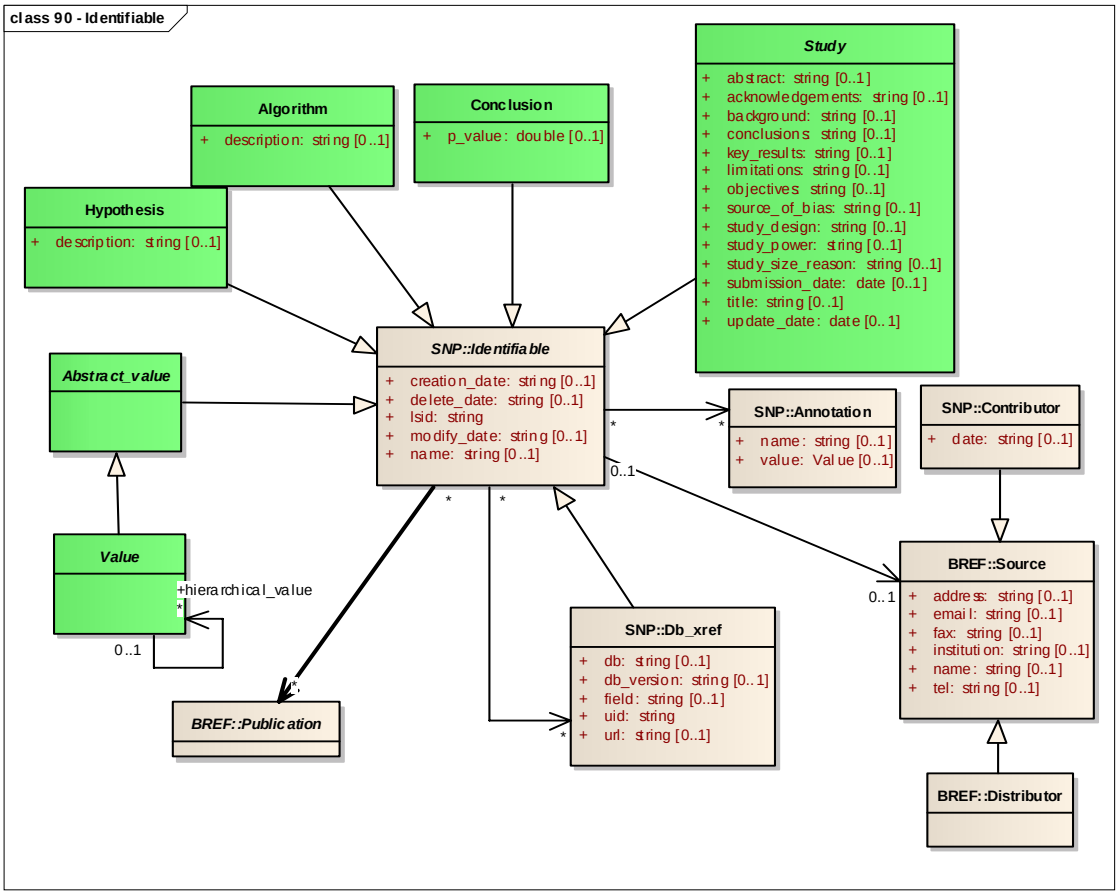

Figure 7.10 - Identifiable

All classes in the model inherit from Identifiable. In this way, their instances are uniquely identifiable. Any Identifiable instance must use its “lsid attribute.” For this attribute, it is recommended to use the OMG Life Sciences Identifier specification. All classes in the model can be linked with annotation (Annotation) and database cross-reference (Db_xref). Special kinds of cross references are Source for source of data, Distributor for the original database of the data, and Contributor for tracking editorial changes to data.

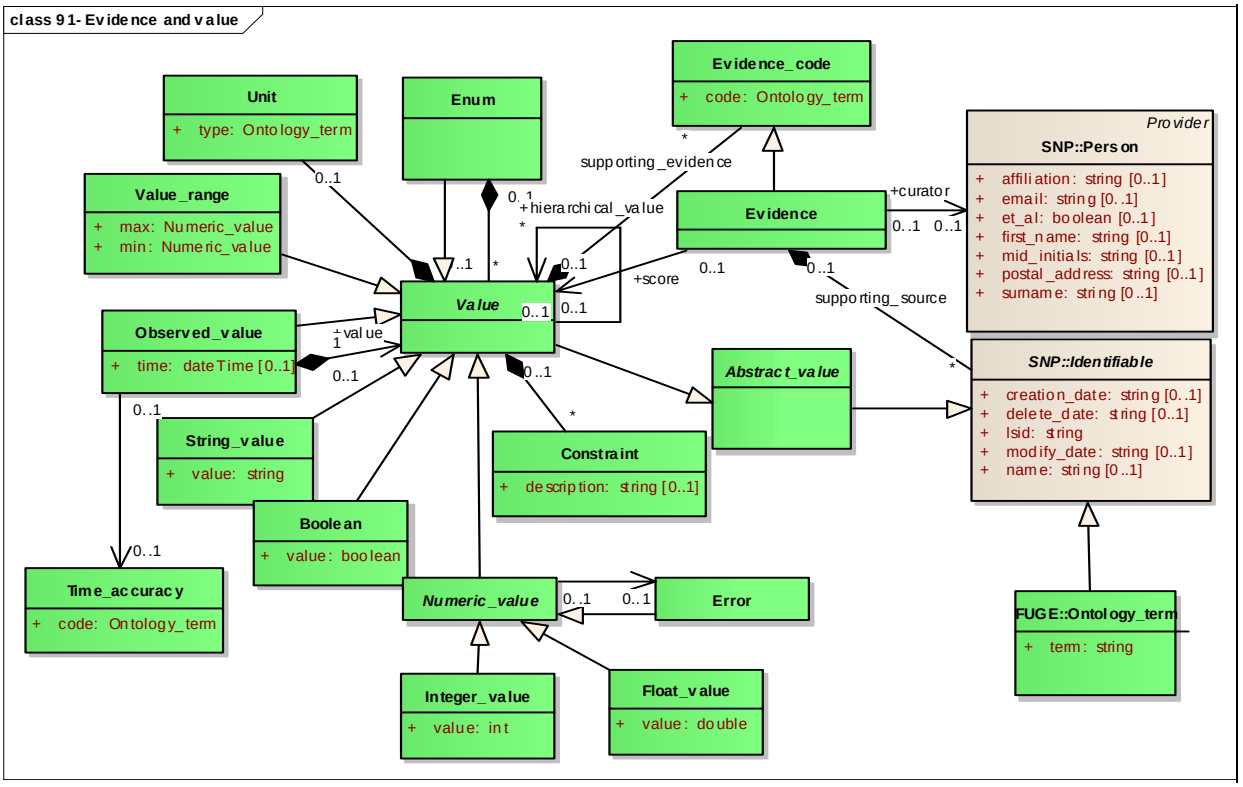

Figure 7.11 - Evidence and Value

Core (“simple”) string, arithmetic data types, and object references are modeled here in the Value model. The model is based on concept developed in Generation Challenge Program: http://pantheon.generationcp.org/demeter/Values.html Model Documentation.

7.2 Detailed Model Documentation

Note – Those cardinalities that are not explicitly given in PIM should be interpreted as “0..1.”

7.2.1 Model Documentation

7.2.1.1 PAGE-OM

Package: Model

Document:

PAGE-OM model (Brookes) captures information related to genotype and phenotype observations and their relationships. The core conceptual domain is experiment part (See Figure 7.1), which brings in data from phenotype (Figure 7.4) and genotype domains (Figure 7.3, Figure 7.5, and Figure 7.6) along with experimental result information that elucidates how genetic variations influence phenotypic variation.

7.2.1.2 Abstract_observable_feature

Type: **Class_Identifiable**

Package: **PAGE-OM**

Document:

An extension point for other kinds of observable features.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Observable_feature	 Abstract_observable_feature
Aggregation Target, for example sample or individual.	Card. Role Name	* Abstract_observable_feature	1 Abstract_observation_target
Generalization	Card. Role Name	 Abstract_observable_feature	 Identifiable

7.2.1.3 Abstract_observation_target

Type: **Class_Identifiable**

Package: **PAGE-OM**

Document:

It is an abstract class for all entities from which one can make genotype or phenotype measurements or observations. It deals with entities capable of being observed.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Molecular_sample	 Abstract_observation_target
Association Observation target (e.g., sample) from which genotype is measured.	Card. Role Name	* Assayed_genomic_genotype	1 Abstract_observation_target
Aggregation Target, for example sample or individual.	Card. Role Name	* Abstract_observable_feature	1 Abstract_observation_target
Generalization	Card. Role Name	 Abstract_population	 Abstract_observation_target
Association Observation target, sample, on well location.	Card. Role Name	* Location_on_plate	* Abstract_observation_target
Association Target from which frequency is measured.	Card. Role Name	* Frequency	1..* Abstract_observation_target
Association *Has value* Observed values (of observable features) measured on the target	Card. Role Name	* Observed_value	1 target Abstract_observation_target
Association Panel (set of samples or study subjects) over which experiment was done.	Card. Role Name	* Experiment_result	* Abstract_observation_target
Association *Observation targets used in experiment*	Card. Role Name	* Genotype_phenotype_correlation_experiment	* Abstract_observation_target
Generalization	Card. Role Name	 Abstract_observation_target	 Identifiable

7.2.1.4 Abstract_population

Type: **Class _ Abstract_observation_target**

Package: **PAGE-OM**

Document:

An interbreeding set of individuals, from whom a Panel is drawn. (Population in SNP). Extends Abstract_observation_target, which is abstract class for all entities from which one can make genotype or phenotype measurements or observations.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Abstract_population	Abstract_observation_target
Association Source of sample. For example individual or panel (pool of individuals).	Card. Role Name	* Molecular_sample	0..1 Abstract_population
Association Geographic location of individual or group of individuals (panel).	Card. Role Name	* Abstract_population	0..1 Geographic_location
Association Taxonomic name (e.g., species) of individual or population.	Card. Role Name	* Abstract_population	* Taxon
Generalization	Card. Role Name	Individual	Abstract_population
Generalization	Card. Role Name	Panel	Abstract_population

Attributes:

Attribute	Lower bound	Notes
ethnicity	0	Additional ethnic category of the population sample or “mixed.”
language_family	0	Language family name or code, e.g., as in Ethnologue.
primary_language	0	Language spoken (name or code), e.g., as in Ethnologue.
race	0	Broad ethnic category of the population sample or “mixed.”

7.2.1.5 Abstract_run

Type: **Class _ Identifiable**

Package: **PAGE-OM**

Document:

An extension point for other kinds of runs.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Abstract_run	 Identifiable
Association Provides information on experimental conditions (run of experiment).	Card. Role Name	* Assayed_genomic_genotype	0..1 Abstract_run
Generalization	Card. Role Name	 Run	 Abstract_run

7.2.1.6 Abstract_value

Type: **Class _ Identifiable**

Package: **PAGE-OM**

Document:

An extension point for kinds of values.

Connections:

Connector		Source	Target
Association Raw data values used in allele calling.	Card. Role Name	0..1 Defining_feature	1 Abstract_value
Generalization	Card. Role Name	 Value	 Abstract_value
Generalization	Card. Role Name	 Abstract_value	 Identifiable
Dependency *derived from raw data* Latent genotypes do depend on actual measured values (raw data).	Card. Role Name	0..1 Latent_genotype	0..1 Abstract_value
Association Raw data. Actual measured values like intensities.	Card. Role Name	0..1 Assayed_genomic_genotype	* Abstract_value
Association Value of melting temperature.	Card. Role Name	0..1 Melting_temperature	1 Abstract_value
Association Value of band-size.	Card. Role Name	0..1 Band_size	1 Abstract_value

7.2.1.7 Algorithm

Type: **Class _ Identifiable**

Package: **PAGE-OM**

Document:

Step-by-step procedure for solving a problem.

Connections:

Connector		Source	Target
Association	Card. Role Name	0..1 Page	* Algorithm
Association Algorithm used to obtain the result.	Card. Role Name	0..1 Experiment_result	0..1 Algorithm
Generalization	Card. Role Name	 Algorithm	 Identifiable

Attributes:

Attribute	Lower bound	Notes
description	0	Description of algorithm

7.2.1.8 Assayed_genomic_genotype

Type: **Class _ Genomic_observation**

Package: **PAGE-OM**

Document:

The result of applying a variation assay to an individual, to reveal one or more of the genomic alleles carried by that individual. This term applies to the observed data rather than to the inferred state of the individual. Thus the same individual might have several different genotypes at the same site, where the variation might be due to differing assays, experimental error, dominant systems, missing data, and so forth. *Synonym: Measurement*.

Connections:

Connector		Source	Target
Association Observation target (e.g., sample) from which genotype is measured.	Card. Role Name	* Assayed_genomic_genotype	1 Abstract_observation_target
Association Provides information on experimental conditions (run of experiment).	Card. Role Name	* Assayed_genomic_genotype	0..1 Abstract_run
Association *measured genotype*	Card. Role Name	* Assayed_genomic_genotype	0..1 Latent_genotype
Association *Without assay details* Used when assay level information is not known or is not important. There can be more than one genotype per genomic variation, done over different samples.	Card. Role Name	* Assayed_genomic_genotype	0..1 Genomic_variation
Association *With assay details* Used when assay level information is needed. Specific variation assay designed for genomic site (locus).	Card. Role Name	* Assayed_genomic_genotype	0..1 Variation_assay
Association Source genotypes from which consensus is derived from.	Card. Role Name	* Consensus_genomic_genotype	* derived_from Assayed_genomic_genotype
Association	Card. Role Name	0..1 Page	* Assayed_genomic_genotype
Generalization	Card. Role Name	 Consensus_genomic_genotype	 Assayed_genomic_genotype
Association Raw data. Actual measured values like intensities.	Card. Role Name	0..1 Assayed_genomic_genotype	* Abstract_value
Generalization	Card. Role Name	 Assayed_genomic_genotype	 Genomic_observation

Attributes:

Attribute	Lower bound	Notes
assay_failure	0	Failure of assay. Value is true if assay has failed.
quality_score	0	Quality score of measurement. Depends on the instrument.

7.2.1.9 Association_study

Type: **Class _ Study**

Package: **PAGE-OM**

Document:

Association study is core concept of the specification. It captures relationships between phenotypes and genotypes. It is an examination of genetic variation across the genome, designed to identify genetic associations with observable phenotypes. Association studies are results of correlation experiments.

Connections:

Connector		Source	Target
Association	Card. Role Name	0..1 Page	* Association_study
Aggregation Correlation experiments that are part (or used in) study.	Card. Role Name	* Genotype_phenotype_correlation_experiment	* Association_study
Generalization	Card. Role Name	 Association_study	 Study

7.2.1.10 Band_size

Type: **Class _ Latent_genotype_specification**

Package: **PAGE-OM**

Document:

DNA fragment length estimated from gel electrophoresis.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Band_size	 Latent_genotype_specification
Association	Card. Role Name	0..1 Page	* Band_size
Association Value of band-size.	Card. Role Name	0..1 Band_size	1 Abstract_value

7.2.1.11 Boolean

Type: **Class _ Value**

Package: **PAGE-OM**

Document:

Value of type boolean

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Boolean	 Value

Attributes:

Attribute	Lower bound	Notes
value	1	Boolean value

7.2.1.12 Conclusion

Type: **Class _ Identifiable**

Package: **PAGE-OM**

Document:

A reasoned judgment of an experiment.

Connections:

Connector		Source	Target
Association Conclusion of experiment	Card. Role Name	0..1 Genotype_phenotype_correlation_experiment	0..1 Conclusion
Association	Card. Role Name	0..1 Page	* Conclusion
Generalization	Card. Role Name	 Conclusion	 Identifiable

Attributes:

Attribute	Lower bound	Notes
p_value	0	Probability value

7.2.1.13 Consensus_genomic_genotype

Type: **Class _ Assayed_genomic_genotype**

Package: **PAGE-OM**

Document:

This class represents consensus from several experiments providing genotypes of the same sample on the same site.

Connections:

Connector		Source	Target
Association Consensus genotypes used to derive the haplotype.	Card. Role Name	* Haplotype_derivation_methods	0..1 Consensus_genomic_genotype
Association The consensus genotype whose frequency is given.	Card. Role Name	* Genomic_genotype_population_frequency	0..1 Consensus_genomic_genotype
Association Source genotypes from which consensus is derived from.	Card. Role Name	* Consensus_genomic_genotype	* derived_from Assayed_genomic_genotype
Generalization	Card. Role Name	 Consensus_genomic_genotype	 Assayed_genomic_genotype

7.2.1.14 Constraint

Type: **Class**

Package: **PAGE-OM**

Document:

The contents of a Value can be limited by Constraints. Different types of Constraints allow various ways to limit or validate one or more Value instances. The Constraint superclass only stores a string description of the Constraint. The actual full semantics of a constraint are specified in various subclasses described below.

But there are no subclasses in the PAGE-OM - because they are out of scope of PAGE-OM.

Connections:

Connector		Source	Target
Aggregation Constraints	Card. Role Name	* Constraint	0..1 Value

Attributes:

Attribute	Lower bound	Notes
description	0	Description

7.2.1.15 Defining_feature

Type: **AssociationClass**

Package: **PAGE-OM**

Document:

Is an association class that has list of values, which are used in defining the instance of Latent_genotype_specifications (for example, intensity values used in allele calling). The class captures information how alleles are called (observed) from raw measurement values like intensity values.

Connections:

Connector		Source	Target
Association Raw data values used in allele calling.	Card. Role Name	0..1 Defining_feature	1 Abstract_value
Association Gives information on allele calling.	Card. Role Name	0..1 Defining_feature	0..1 Latent_genotype_specification

Attributes:

Attribute	Lower bound	Notes
type	0	Type of feature

7.2.1.16 Enum

Type: **Class _ _Value**

Package: **PAGE-OM**

Document:

Enumeration contains list of Values.

Connections:

Connector		Source	Target
Aggregation	Card. Role Name	* Value	0..1 Enum
Generalization	Card. Role Name	 Enum	 Value

7.2.1.17 Environment_feature

Type: **Class _ _Observable_feature**

Package: **PAGE-OM**

Document:

Circumstances, objects, or conditions by which one is surrounded.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Environment_feature	 Observable_feature
Association	Card. Role Name	0..1 Page	* Environment_feature

7.2.1.18 Error

Type: **Class _ _Numeric_value**

Package: **PAGE-OM**

Document:

Error value is numeric value of accuracy. Quality score

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Error	 Numeric_value
Association Error of numeric value.	Card. Role Name	0..1 Numeric_value	0..1 Error

7.2.1.19 Evidence

Type: **Class _ Evidence_code**

Package: **PAGE-OM**

Document:

Evidence indicates reliability of a feature or simply documents its authoritative origin.

Connections:

Connector		Source	Target
Aggregation *supporting_source* Supporting evidences: Citations, studies, ontology terms, etc.	Card. Role Name	* Identifiable	0..1 Evidence
Association Score of evidence (e.g., p-value).	Card. Role Name	0..1 Evidence	0..1 score *score of value* Value
Association	Card. Role Name	0..1 Page	* Evidence

Connector		Source	Target
Generalization	Card. Role Name	 Evidence	 Evidence_code
Association Curator of evidence	Card. Role Name	0..1 Evidence	0..1 curator *Curator of evidence* Person

7.2.1.20 Evidence_code

Type: **Class**

Package: **PAGE-OM**

Document:

Evidence can be an EvidenceCode (which is a controlled vocabulary term such as a GO evidence code or ICIS Method code) but can be a more fully documented Evidence object (inheriting from EvidenceCode) generally curated by a specified person, a curator modeled as a Contact.

Its strength is expressed by the score (which is usually a numeric value between 0 and 1, but also other types of Value are allowed (e.g., an ontology term value).

The core of an evidence is its supporting source that can be anything (because it is identified by a SimpleIdentifier). Usual evidence sources are BiblioReferences, Studies, and OntologyTerms. Reference (generationcp - http://pantheon.generationcp.org/demeter/Features.html).

Connections:

Connector		Source	Target
Aggregation *supporting_evidence* Values supporting the evidence.	Card. Role Name	* Evidence_code	0..1 Value
Generalization	Card. Role Name	 Evidence	 Evidence_code

Attributes:

Attribute	Lower bound	Notes
code	1	Evidence code as specified using ontology term.

7.2.1.21 Experiment_result

Type: **Class _ Value**

Package: **PAGE-OM**

Document:

The experiment result (for example, a single p-value) gathers correlation between genomic observation and phenotypic observed values. A correlation experiment can consist of more than one experiment result.

Connections:

Connector		Source	Target
Association	Card. Role Name	0..1 Page	* Experiment_result
Association *Result* Experiments results that are part of the correlation experiment.	Card. Role Name	* Genotype_phenotype_correlation_experiment	* Experiment_result
Association Algorithm used to obtain the result.	Card. Role Name	0..1 Experiment_result	0..1 Algorithm
Generalization	Card. Role Name	 Experiment_result	 Value
Association Panel (set of samples or study subjects) over which experiment was done.	Card. Role Name	* Experiment_result	* Abstract_observation_target

Connector		Source	Target
Association Combination of Genomic_observations determined for each Observation_target. For example, actual genotypes over Molecular_samples.	Card. Role Name	* Experiment_result	* Genomic_observation
Association Combination of Observable_values determined for each Observation_target. For example, phenotype in GWA studies.	Card. Role Name	* Experiment_result	* Observed_value
Association Combination of Genomic_variations studied for each Observation_target. For example, marker dimension in GWA studies.	Card. Role Name	* Experiment_result	* Genomic_variation

7.2.1.22 Float_value

Type: **Class _ Numeric_value**

Package: **PAGE-OM**

Document:

Value of type float

Connections

Connector		Source	Target
Generalization	Card. Role Name	 Float_value	 Numeric_value

Attributes:

Attribute	Lower bound	Notes
value	1	Value

7.2.1.23 Frequency

Type: **Class _ Genomic_observation**

Package: **PAGE-OM**

Document:

Abstract class for frequencies, expressed in percentages. Alleles (Genomic_alleles), genotypes (Consensus_genomic_genotype), and haplotypes (Genomic_haplotype) can have measured frequencies in population samples (Panels). In addition, heterozygosity (Heterozygosity) is a measure of observed variability of a polymorphic site (Genomic_variation) in a sub-population (Panel).

Connections:

Connector		Source	Target
Generalization Frequency of heterozygote alleles.	Card. Role Name	 Heterozygosity	 Frequency
Association Target from which frequency is measured.	Card. Role Name	* Frequency	1..* Abstract_observation_target
Generalization	Card. Role Name	 Frequency	 Genomic_observation
Association *Without assay details* Genomic variation site (for example, marker).	Card. Role Name	* Frequency	0..1 Genomic_variation

Connector		Source	Target
Association *With assay details* Assay designed for the variation site. Association is used when assay level information is needed. (Optional with the "direct" association from Frequency to Genomic_variation).	Card. Role Name	* Frequency	0..1 Variation_assay
Generalization	Card. Role Name	 Frequency_set	 Frequency
Aggregation Set of frequencies.	Card. Role Name	1..* Frequency	0..1 Frequency_set
Generalization	Card. Role Name	 Genomic_allele_population_frequency	 Frequency
Generalization	Card. Role Name	 Genomic_haplotype_population_frequency	 Frequency
Generalization	Card. Role Name	 Genomic_genotype_population_frequency	 Frequency

Attributes:

Attribute	Lower bound	Notes
count	0	Total number
value	0	Value of frequency (%)

7.2.1.24 Frequency_set

Type: **Class _ Frequency**

Package: **PAGE-OM**

Document:

Set of frequencies

Connections:

Connector		Source	Target
Association	Card. Role Name	0..1 Page	* Frequency_set
Generalization	Card. Role Name	 Frequency_set	 Frequency
Aggregation Set of frequencies.	Card. Role Name	1..* Frequency	0..1 Frequency_set

7.2.1.25 Functional_change

Type: **Class _ Gene_product_change**

Package: **PAGE-OM**

Document:

Change in the function of the final gene product.

Connections:

Connector		Source	Target
Association Translation that affects function of protein.	Card. Role Name	* Functional_change	* Translation_change
Association Structural change that has impact on function of protein.	Card. Role Name	* Functional_change	* affects_function Structural_change
Association	Card. Role Name	0..1 Page	* Functional_change
Generalization	Card. Role Name	 Functional_change	 Gene_product_change

7.2.1.26 Gene_based_haplotype

Type: **Class _ Set of haplotypes**

Package: **PAGE-OM**

Document:

Collection of variable nucleotides (Genomic_alleles in Genomic_variations) that define a gene. In older usage synonym locus.

Connections:

Connector		Source	Target
Association	Card. Role Name	0..1 Page	* Gene_based_haplotype
Generalization	Card. Role Name	 Gene_based_haplotype	 Set_of_haplotypes

7.2.1.27 Genic_variation

Type: **Class _ Residue_change**

Package: **PAGE-OM**

Document:

Genomic variation with location in genic coordinates. Synonym: mutation (when change from a common allele affects phenotype).

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Genic_variation	 Residue_change
Association Genioc variation that has impact on gene structure.	Card. Role Name	0..1 Genomic_gene_structure	* Genic_variation
Association Genomic variation site of the genic variation.	Card. Role Name	0..1 Genic_variation	0..1 is_treated_as Genomic_variation
Association Genic variation that influences on the transcript change.	Card. Role Name	* Transcription_change	* affects_transcript Genic_variation
Association Genomic structure(s) that are associated to the genic variation.	Card. Role Name	0..1 is_genic Genic_variation	* Genomic_gene_structure
Association	Card. Role Name	0..1 Page	* Genic_variation

7.2.1.28 Genomic_allele

Type: **Class _ Genomic_observation, Latent_genotype_specification, Sequence**

Package: **PAGE-OM**

Document:

One of several alternative DNA sequences of a Reference_genomic_location as it appears in the population of organisms. Synonym: variant, allele.

Connections:

Connector		Source	Target
Association Alleles that are part of the haplotype (i.e., are on same phase).	Card. Role Name	* Genomic_allele	0..1 Genomic_haplotype
Generalization	Card. Role Name	 Genomic_reference_allele	 Genomic_allele
Aggregation *possible_alleles* The relationship gives information on possible sequence variations attached to the locus (as defined by flanking sequences).	Card. Role Name	* Genomic_allele	0..1 Genomic_variation
Generalization	Card. Role Name	 Genomic_allele	 Latent_genotype_specification
Generalization	Card. Role Name	 Genomic_allele	 Sequence

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Genomic_allele	Genomic_observation
Association The DNA sequence of a genomic variation as it appears in the public database.	Card. Role Name	0..1 one_of Genomic_reference_allele	0..1 Genomic_allele
Association	Card. Role Name	0..1 Page	* Genomic_allele
Association Allele whose frequency is reported.	Card. Role Name	* Genomic_allele_population_frequency	1 Genomic_allele

Attributes:

Attribute	Lower bound	Notes
bin	0	Size class for microsatellite alleles when exact size cannot be determined. Semantic name.
repeat_count	0	If the Genomic_variation type is ‘microsatellite,’ get number of repeat units as value, e.g., 7.
repeat_is_exact	0	The Genomic_variation type is ‘microsatellite’ and gets value true if the allele region consists of repeat units only.

7.2.1.29 Genomic_allele_population_frequency

Type: **Class _ Frequency**

Package: **PAGE-OM**

Document:

The frequency with which a particular Genomic_allele is seen in a particular Panel. This frequency can be measured from pooled samples. Synonyms: Genomic_allele_panel_frequency, allele_frequency.

Connections:

Connector		Source	Target
Association	Card. Role Name	0..1 Page	* Genomic_allele_population_frequency
Association Allele whose frequency is reported.	Card. Role Name	* Genomic_allele_population_frequency	1 Genomic_allele
Generalization	Card. Role Name	 Genomic_allele_population_frequency	 Frequency

7.2.1.30 Genomic_gene_structure

Type: **Class _ _Locatable**

Package: **PAGE-OM**

Document:

A structure of a gene expressed as location of the CDS and exons. Defines genic coordinate system from start of the CDS downstream.

Connections:

Connector		Source	Target
Association Coding region that is part of the gene structure.	Card. Role Name	0..1 CDS	0..1 Genomic_gene_structure
Association Exons that are part of gene structure.	Card. Role Name	1..* Exon	0..1 Genomic_gene_structure
Generalization	Card. Role Name	 Genomic_gene_structure	 Locatable

Connector		Source	Target
Association Genioc variation that has impact on gene structure.	Card. Role Name	0..1 Genomic_gene_structure	* Genic_variation
Association Genomic structure(s) that are associated to the genic variation.	Card. Role Name	0..1 is_genic Genic_variation	* Genomic_gene_structure
Association	Card. Role Name	0..1 Page	* Genomic_gene_structure

Attributes:

Attribute	Lower bound	Notes
gene_symbol	0	Gene symbol for the gene (e.g., approved by the HUGO nomenclature committee).

7.2.1.31 Genomic_genotype_population_frequency

Type: **Class _ Frequency**

Package: **PAGE-OM**

Document:

Frequency of a Consensus_genomic_genotype in a Panel.

Has many to one relationship to Latent_genotype (Consensus_genomic_genotype in SNP).

Connections:

Connector		Source	Target
Association *measured genotype*	Card. Role Name	* Genomic_genotype_population_frequency	1 Latent_genotype
Association The consensus genotype whose frequency is given.	Card. Role Name	* Genomic_genotype_population_frequency	0..1 Consensus_genomic_genotype
Association	Card. Role Name	0..1 Page	* Genomic_genotype_population_frequency
Generalization	Card. Role Name	 Genomic_genotype_population_frequency	 Frequency

7.2.1.32 Genomic_haplotype

Type: **Class _ Genomic_observation**

Package: **PAGE-OM**

Document:

A set of Genomic_alleles across an equal number of Genomic_variations in a single chromosome and in a single individual. The Genomic_haplotype is derived from a set of Consensus_genomic_genotype. For each Genomic_variation, the haplotype contains one and only one Genomic_allele. Furthermore, the Genomic_alleles are required to be in phase on the individual, meaning that they are located on the same contiguous strand of DNA. *Synonym: Haplotype.*

Connections:

Connector		Source	Target
Association Alleles that are part of the haplotype i.e., are on same phase.	Card. Role Name	* Genomic_allele	0..1 Genomic_haplotype
Association Provides information on haplotype derivation method.	Card. Role Name	* Genomic_haplotype	0..1 Haplotype_derivation_methods

Connector		Source	Target
Association Haplotype set	Card. Role Name	* Genomic_haplotype	0..1 Set_of_haplotypes
Generalization	Card. Role Name	 Genomic_haplotype	 Genomic_observation
Association Sample from which genomic haplotypes are measured.	Card. Role Name	* Genomic_haplotype	* Molecular_sample
Association Haplotypes that are part of the map.	Card. Role Name	1 Haplotype_map	* Genomic_haplotype
Association	Card. Role Name	0..1 Page	* Genomic_haplotype
Association Haplotype whose frequency is reported.	Card. Role Name	* Genomic_haplotype_population_frequency	1 Genomic_haplotype
Association Map of haplotype. Provides information on coordinate system.	Card. Role Name	1 Genomic_haplotype	* Haplotype_map

7.2.1.33 Genomic_haplotype_population_frequency

Type: **Class _ _Frequency**

Package: **PAGE-OM**

Document:

Frequency of a Genomic_haplotype in a Panel.

Connections:

Connector		Source	Target
Association	Card. Role Name	0..1 Page	* Genomic_haplotype_population_frequency
Association Haplotype whose frequency is reported.	Card. Role Name	* Genomic_haplotype_population_frequency	1 Genomic_haplotype
Generalization	Card. Role Name	 Genomic_haplotype_population_frequency	 Frequency

7.2.1.34 Genomic_observation

Type: **Class _ Identifiable**

Package: **PAGE-OM**

Document:

Genomic observation

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Genomic_haplotype	 Genomic_observation
Generalization	Card. Role Name	 Genomic_allele	 Genomic_observation
Generalization	Card. Role Name	 Frequency	 Genomic_observation

Connector		Source	Target
Association All genomic observations that were used in the experiment.	Card. Role Name	0..1 Genotype_phenotype_correlation_experiment	* Genomic_observation
Association Combination of Genomic_observations determined for each Observation_target. For example, actual genotypes over Molecular_samples.	Card. Role Name	* Experiment_result	* Genomic_observation
Generalization	Card. Role Name	 Genomic_observation	 Identifiable
Generalization	Card. Role Name	 Set_of_haplotypes	 Genomic_observation
Generalization	Card. Role Name	 Assayed_genomic_genotype	 Genomic_observation

7.2.1.35 Genomic_variation

Type: **Class _ Locatable**

Package: **PAGE-OM**

Document:

A variable site in a Reference_genomic_landmark sequence. Synonyms: polymorphic site, marker, (Genomic_polymorphism in SNP).

Connections:

Connector		Source	Target
Generalization Another genomic variation close enough to affect the primer design.	Card. Role Name	Neighbour_variation	Genomic_variation
Aggregation *possible_alleles* The relationship gives information on possible sequence variations attached to the locus (as defined by flanking sequences).	Card. Role Name	* Genomic_allele	0..1 Genomic_variation
Association Genomic variations that are associated to the location.	Card. Role Name	0..1 Reference_genomic_location	* Genomic_variation
Association Genomic landmark (part of sequence assembly).	Card. Role Name	0..1 Genomic_variation	0..1 Reference_genomic_landmark
Association Genomic variation site for which assay was designed.	Card. Role Name	* Variation_assay	1 Genomic_variation
Association Location on reference genome.	Card. Role Name	0..1 Genomic_variation	* Reference_genomic_location
Association Genomic variation site of the genic variation.	Card. Role Name	0..1 Genic_variation	0..1 is_treated_as Genomic_variation
Association Ordered location of variation (e.g., cytogenetic location).	Card. Role Name	* Ordered_location	0..1 Genomic_variation

Association *Without assay details* Used when assay level information is not known or is not important. There can be more than one genotype per genomic variation, done over different samples.	Card. Role Name	* Assayed_genomic_genotype	0..1 Genomic_variation
Association Variability of variation site.	Card. Role Name	0..1 Genomic_variation	* Heterozygosity
Association	Card. Role Name	0..1 Genomic_variation	* Neighbour_variation
Generalization	Card. Role Name	 Genomic_variation	 Locatable
Association	Card. Role Name	0..1 Page	* Genomic_variation
Association *Without assay details* Genomic variation site (for example, marker).	Card. Role Name	* Frequency	0..1 Genomic_variation
Association Combination of Genomic_variations studied for each Observation_target (for example, marker dimension in GWA studies).	Card. Role Name	* Experiment_result	* Genomic_variation
Association *Genomic variations used in experiment*	Card. Role Name	* Genotype_phenotype_correlation_experiment	* Genomic_variation

Attributes:

Attribute	Lower bound	Notes
flank_down	0	Downstream flanking sequence (at least 25 residues, if possible).
flank_up	0	Upstream flanking sequence (at least 25 residues, if possible).
is_mutation	0	Proven phenotype change causing mutation.
repeat_unit	0	If type is 'microsatellite,' gives the repeat unit, e.g., "CA."
type	0	The type of the polymorphism (e.g., SNP, microsatellite, indel, translocation,...).
validation_status	0	Validation status, e.g., "Proven," "Suspected."

7.2.1.36 Genotype_phenotype_correlation_experiment

Type: **Class _ Identifiable**

Package: **PAGE-OM**

Document:

Family or case control based association study experiment. Represents set of experiment sub-sections that would normally be listed in the results section in manuscripts.

Connections:

Connector		Source	Target
Association Experiments that are associated to meta experiment.	Card. Role Name	0..1 metaexperiment Genotype_phenotype_correlation_experiment	* subexperiment Genotype_phenotype_correlation_experiment
Association Conclusion of experiment	Card. Role Name	0..1 Genotype_phenotype_correlation_experiment	0..1 Conclusion
Association	Card. Role Name	0..1 Page	* Genotype_phenotype_correlation_experiment

Connector		Source	Target
Association *Result* Experiments results that are part of the correlation experiment.	Card. Role Name	* Genotype_phenotype_correlation_experiment	* Experiment_result
Aggregation Correlation experiments, which are part (or used in) study.	Card. Role Name	* Genotype_phenotype_correlation_experiment	* Association_study
Association All genomic observations that were used in the experiment.	Card. Role Name	0..1 Genotype_phenotype_correlation_experiment	* Genomic_observation
Association *Observation targets used in experiment*	Card. Role Name	* Genotype_phenotype_correlation_experiment	* Abstract_observation_target
Association Optional hypothesis of experiment	Card. Role Name	0..1 Genotype_phenotype_correlation_experiment	0..1 Hypothesis
Association *Genomic variations used in experiment*	Card. Role Name	* Genotype_phenotype_correlation_experiment	* Genomic_variation
Generalization	Card. Role Name	 Genotype_phenotype_correlation_experiment	 Identifiable

Attributes:

Attribute	Lower bound	Notes
objective	0	Objective of experiment
outcome	0	A free text description summarizing outcome of all experiment results in this correlation experiment.
study_id	0	Identifier of original study. Can be used in cases where experiment was originally done for different study.
type	0	Type of experiment

7.2.1.37 Haplotype_block

Type: **Class _ Set_of_haplotypes**

Package: **PAGE-OM**

Document:

Large (spanning a few kb to >100 kb) blocks of Genomic_alleles in linkage disequilibrium (LD) and a few haplotypes per block, separated by regions of recombination.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Haplotype_block	 Set_of_haplotypes
Association	Card. Role Name	0..1 Page	* Haplotype_block

7.2.1.38 Haplotype_derivation_methods

Type: **Class _ Methodology**

Package: **PAGE-OM**

Document:

Association class describing methods used to derive Genomic_haplotypes from Consensus_genomic_genotypes.

Connections:

Connector		Source	Target
Association Provides information on haplotype derivation method.	Card. Role Name	* Genomic_haplotype	0..1 Haplotype_derivation_methods
Association Consensus genotypes used to derive the haplotype.	Card. Role Name	* Haplotype_derivation_methods	0..1 Consensus_genomic_genotype
Association	Card. Role Name	0..1 Page	* Haplotype_derivation_methods
Generalization	Card. Role Name	 Haplotype_derivation_methods	 Methodology

7.2.1.39 Haplotype_map

Type: **Class _ Physical_map**

Package: **PAGE-OM**

Document:

Map of haplotypes. Features include: Block length distribution, measures of block variability, relative proportions of common haplotypes, block coverage of chromosomes and/or genome. LD and other values between haplotypes, markers, alleles.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Haplotype_map	 Physical_map
Association Set of haplotypes that are associated with the map.	Card. Role Name	* Haplotype_map	* Set_of_haplotypes

Connector		Source	Target
Association Haplotypes that are part of the map.	Card. Role Name	1 Haplotype_map	* Genomic_haplotype
Association	Card. Role Name	0..1 Page	* Haplotype_map
Association Map of haplotype. Provides information on coordinate system.	Card. Role Name	1 Genomic_haplotype	* Haplotype_map

7.2.1.40 Heterozygosity

Type: **Class _ Frequency**

Package: **PAGE-OM**

Document:

Heterozygosity (Heterozygosity) is a measure of observed variability of a polymorphic site (Genomic_variation) in a sub-population (Panel).

Connections:

Connector		Source	Target
Generalization Frequency of heterozygote alleles.	Card. Role Name	 Heterozygosity	 Frequency
Association Variability of variation site.	Card. Role Name	0..1 Genomic_variation	* Heterozygosity
Association	Card. Role Name	0..1 Page	* Heterozygosity

7.2.1.41 Hypothesis

Type: **Class _ Identifiable**

Package: **PAGE-OM**

Document:

Free text description of hypothesis of study.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Hypothesis	 Identifiable
Association	Card. Role Name	0..1 Page	* Hypothesis
Association Optional hypothesis of experiment	Card. Role Name	0..1 Genotype_phenotype_correlation_experiment	0..1 Hypothesis

Attributes:

Attribute	Lower bound	Notes
description	0	Description of hypothesis

7.2.1.42 Individual

Type: **Class _ Abstract_population**

Package: **PAGE-OM**

Document:

A single member of a species, where a species is an accessioned taxon defined by a public database, and the individual is accessioned in a public or private database. Synonym: “inbred strain” in homozygous lineages.

Connections:

Connector		Source	Target
Association Individuals that are part of the Panel.	Card. Role Name	* Individual	* Panel
Generalization	Card. Role Name	 Individual	 Abstract_population
Association	Card. Role Name	0..1 Page	* Individual

Attributes:

Attribute	Lower bound	Notes
birth_date	0	Date of birth of the individual. May be better abbreviated to birth year to protect the privacy of the individual.
death_date	0	Date of death of the individual. May be better abbreviated to plain year to protect the privacy of the individual.
father_id	0	Id of the father to allow building of pedigrees.
gender	0	Recommended values are ‘unknown,’ ‘male,’ and ‘female.’ Additional values can be used to denote unusual karyotypes.
mother_id	0	Id of the mother to allow building of pedigrees.

7.2.1.43 Integer_value

Type: **Class _ _Numeric_value**

Package: **PAGE-OM**

Document:

Value of type integer

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Integer_value	 Numeric_value

Attributes

Attribute	Lower bound	Notes
value	1	Integer value

7.2.1.44 Latent_genotype

Type: **Class__Identifiable**

Package: **PAGE-OM**

Document:

Potentially existing genotypes on specific site that could be observed by Variation_assays. Application of a Variation _assay on one Molecular_sample generates a single Latent_genotype, which has one or more Latent_genotype _specifications (this depends on ploidy level in case of Genomic_allele).

Latent_genotypes associated with one instance of a Variation_assay can have only one type of Latent_genotype_specifications, as defined by Defining_feature.

This class is a holder for one or many observable variation objects (Latent_genotype_specification). Latent_genotype is used to attach possible variations to measurements (Assayed_genomic_genotype), variation assays (Variation_assay), and marker loci (Genomic_variation).

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Latent_genotype	 Identifiable
AssociationClass (Generic) allleles that specify the genotype.	Card. Role Name	* Latent_genotype	* Latent_genotype_specification
Association *measured genotype*	Card. Role Name	* Assayed_genomic_genotype	0..1 Latent_genotype

Association *detectable genotypes* All genotypes that can be detected. Gives information on all measurable variations measurable (by this assay) on the variation site.	Card. Role Name	* Variation_assay	* Latent_genotype
Association *measured genotype*	Card. Role Name	* Genomic_genotype_population_frequency	1 Latent_genotype
Association	Card. Role Name	0..1 Page	* Latent_genotype
Dependency *derived from raw data* Latent genotypes do depend on actual measured values (raw data).	Card. Role Name	0..1 Latent_genotype	0..1 Abstract_value

7.2.1.45 Latent_genotype_specification

Type: **Class**

Package: **PAGE-OM**

Document:

Abstract super class of observable variation objects, like alleles, melting temperatures (Melting_temperature), band sizes (Band_size). The class is an extension point to other kinds of variations.

Connections:

Connector		Source	Target
AssociationClass (Generic) allleles that specify the genotype.	Card. Role Name	* Latent_genotype	* Latent_genotype_specification
Generalization	Card. Role Name	 Melting_temperature	 Latent_genotype_specification
Generalization	Card. Role Name	 Band_size	 Latent_genotype_specification
Generalization	Card. Role Name	 Genomic_allele	 Latent_genotype_specification
Association Gives information on allele calling.	Card. Role Name	0..1 Defining_feature	0..1 Latent_genotype_specification

7.2.1.46 Lifestyle_feature

Type: **Class _ Observable_feature**

Package: **PAGE-OM**

Document:

Way of life of an individual or panel.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Lifestyle_feature	 Observable_feature
Association	Card. Role Name	0..1 Page	* Lifestyle_feature

7.2.1.47 Location_on_plate

Type: **Class**

Package: **PAGE-OM**

Document:

X,Y plate_positions (wells). Numbering starts from one. Each well can contain one or more observation targets (molecular samples) prepared for measurement using one or more variation assays (e.g., assay multiplexing Assay_set). Note: These are optional laboratory specific details. (Sample and Assay information is in Assayed_genomic_genotype.)

Connections:

Connector		Source	Target
Association *wells* Well positions.	Card. Role Name	0..1 Plate	* Location_on_plate
Association Observation target, sample, on well location.	Card. Role Name	* Location_on_plate	* Abstract_observation_target
Association	Card. Role Name	0..1 Page	* Location_on_plate

Attributes:

Attribute	Lower bound	Notes
x	1	x coordinate of plate.
y	1	y coordinate of plate

7.2.1.48 Melting_temperature

Type: **Class _ Latent_genotype_specification**

Package: **PAGE-OM**

Document:

The temperature at which DNA goes from a double-stranded to a single-stranded state. Unit of temperature is Celsius.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Melting_temperature	 Latent_genotype_specification
Association	Card. Role Name	0..1 Page	* Melting_temperature
Association Value of melting temperature.	Card. Role Name	0..1 Melting_temperature	1 Abstract_value

7.2.1.49 Molecular_sample

Type: **Class _ _Abstract_observation_target**

Package: **PAGE-OM**

Document:

A sample from an Individual or from a Panel defining the molecule and tissue/cell used (Anatomic_locations) in the Variation_assay. Synonym: Sample of individual.

Connections:

Connector		Source	Target
Association Source of sample(s) from which sample is derived.	Card. Role Name	0..1 Molecular_sample	* sourcesample Molecular_sample
Generalization	Card. Role Name	 Molecular_sample	 Abstract_observation_target
Association Source of sample. For example individual or panel (pool of individuals).	Card. Role Name	* Molecular_sample	0..1 Abstract_population
Association Sample from which genomic haplotypes are measured.	Card. Role Name	* Genomic_haplotype	* Molecular_sample

Association Anatomic location from which sample was taken.	Card. Role Name	* Molecular_sample	* Anatomic_location
Association	Card. Role Name	0..1 Page	* Molecular_sample

Attributes:

Attribute	Lower bound	Notes
molecule	0	The molecule (RNA, DNA, protein) used in the assay.

7.2.1.50 Multi_variation_assay

Type: **Class _ _Variation_assay**

Package: **PAGE-OM**

Document:

Multi_variation_assay is a collection of assays that may be used simultaneously. Examples would be multiplex assays, micro-array based assays, or a panel of single-plex assays that share some common feature or purpose.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Multi_variation_assay	 Variation_assay
Aggregation Assays that are part of multivariation assay (for example, assay that can be applied on different variation sites).	Card. Role Name	* Variation_assay	0..1 Multi_variation_assay
Association	Card. Role Name	0..1 Page	* Multi_variation_assay

7.2.1.51 Neighbour_variation

Type: **Class _ Genomic_variation**

Package: **PAGE-OM**

Document:

Another Genomic_variation close enough to affect the primer design.

Connections:

Connector		Source	Target
Generalization Another genomic variation close enough to affect the primer design.	Card. Role Name	Neighbour_variation	Genomic_variation
Association	Card. Role Name	0..1 Genomic_variation	* Neighbour_variation
Association	Card. Role Name	0..1 Page	* Neighbour_variation

7.2.1.52 Numeric_value

Type: **Class _ Value**

Package: **PAGE-OM**

Document:

Numeric value

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Float_value	 Numeric_value
Generalization	Card. Role Name	 Integer_value	 Numeric_value
Generalization	Card. Role Name	 Error	 Numeric_value
Association Error of numeric value.	Card. Role Name	0..1 Numeric_value	0..1 Error
Generalization	Card. Role Name	 Numeric_value	 Value

7.2.1.53 Observable_feature

Type: **Class__Abstract_observable_feature**

Package: **PAGE-OM**

Document:

Measurable feature of observable (e.g., size of nose).

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Observable_feature	Abstract_observable_feature
Generalization	Card. Role Name	Environment_feature	Observable_feature
Association Optional generic categories that observable feature belongs to.	Card. Role Name	* Observable_feature	* Observable_feature_category
Association Observation method(s) used to measure the feature.	Card. Role Name	0..1 Observable_feature	* Observation_method
Generalization	Card. Role Name	Phenotype_feature	Observable_feature
Generalization	Card. Role Name	Lifestyle_feature	Observable_feature

7.2.1.54 Observable_feature_category

Type: **Class _ Identifiable**

Package: **PAGE-OM**

Document:

All features considered by this model can be categorized by using this class. The category should be expressed by an ontology term.

Connections:

Connector		Source	Target
Association	Card. Role Name	0..1 Observable_feature_category	* subcategory Observable_feature_category
Generalization	Card. Role Name	 Phenotype_disease_category	 Observable_feature_category
Association Optional generic categories that observable feature belongs to.	Card. Role Name	* Observable_feature	* Observable_feature_category
Association	Card. Role Name	0..1 Page	* Observable_feature_category
Generalization	Card. Role Name	 Observable_feature_category	 Identifiable

7.2.1.55 Observation_method

Type: **Class__Identifiable**

Package: **PAGE-OM**

Document:

Observable features can be measured by different methods. This class specifies which method has been used. For example, a method can be usage of a ruler or filling a questionnaire.

Connections:

Connector		Source	Target
Association Observation method(s) used to measure the feature.	Card. Role Name	0..1 Observable_feature	* Observation_method
Association	Card. Role Name	0..1 Page	* Observation_method
Association Values of measurements done by the method	Card. Role Name	0..1 Observation_method	* Observed_value
Generalization	Card. Role Name	 Observation_method	 Identifiable

7.2.1.56 Observed_value

Type: **Class _ Value**

Package: **PAGE-OM**

Document:

Observation done at specific point in time.

Connections:

Connector		Source	Target
Association Accuracy code for value.	Card. Role Name	0..1 Observed_value	0..1 Time_accuracy
Association	Card. Role Name	0..1 Page	* Observed_value
Association Actual value of observation.	Card. Role Name	0..1 Observed_value	1 value Value
Association *Has value* Observed values (of observable features) measured on the target.	Card. Role Name	* Observed_value	1 target Abstract_observation_target
Generalization	Card. Role Name	 Observed_value	 Value
Association Combination of Observable_values determined for each Observation_target (for example, phenotype in GWA studies).	Card. Role Name	* Experiment_result	* Observed_value
Association Values of measurements done by the method.	Card. Role Name	0..1 Observation_method	* Observed_value

Attributes:

Attribute	Lower bound	Notes
time	0	Time of observation

7.2.1.57 Page

Type: **Class**

Package: **PAGE-OM**

Document:

This class does not contain any scientific meaning. Its main purpose is to be the root element for the situations where this specification is used for data exchange formats (e.g., xml-schema). Therefore, it has optional direct associations to all important classes so that implementations can exchange only relevant data.

Connections:

Connector		Source	Target
Association	Card. Role Name	0..1 Page	* Algorithm
Association	Card. Role Name	0..1 Page	* Plate
Association	Card. Role Name	0..1 Page	* Genomic_genotype_population_frequency
Association	Card. Role Name	0..1 Page	* Melting_temperature
Association	Card. Role Name	0..1 Page	* Multi_variation_assay
Association	Card. Role Name	0..1 Page	* Observable_feature_category
Association	Card. Role Name	0..1 Page	* Observation_method
Association	Card. Role Name	0..1 Page	* Observed_value
Association	Card. Role Name	0..1 Page	* Phenotype_feature

Connector		Source	Target
Association	Card. Role Name	0..1 Page	* Lifestyle_feature
Association	Card. Role Name	0..1 Page	* Heterozygosity
Association	Card. Role Name	0..1 Page	* Frequency_set
Association	Card. Role Name	0..1 Page	* Run
Association	Card. Role Name	0..1 Page	* Assayed_genomic_genotype
Association	Card. Role Name	0..1 Page	* Functional_change
Association	Card. Role Name	0..1 Page	* Gene_based_haplotype
Association	Card. Role Name	0..1 Page	* Genic_variation
Association	Card. Role Name	0..1 Page	* Genomic_allele
Association	Card. Role Name	0..1 Page	* Genomic_allele_population_frequency
Association	Card. Role Name	0..1 Page	* Genotype_phenotype_correlation_experiment
Association	Card. Role Name	0..1 Page	* Band_size
Association	Card. Role Name	0..1 Page	* Location_on_plate

Association	Card. Role Name	0..1 Page	* Association_study
Association	Card. Role Name	0..1 Page	* Genomic_haplotype
Association	Card. Role Name	0..1 Page	* Conclusion
Association	Card. Role Name	0..1 Page	* Environment_feature
Association	Card. Role Name	0..1 Page	* Evidence
Association	Card. Role Name	0..1 Page	* Hypothesis
Association	Card. Role Name	0..1 Page	* Experiment_result
Association	Card. Role Name	0..1 Page	* Person
Association	Card. Role Name	0..1 Page	* Genomic_gene_structure
Association	Card. Role Name	0..1 Page	* Db_xref
Association	Card. Role Name	0..1 Page	* Exon
Association	Card. Role Name	0..1 Page	* Genetic_location
Association	Card. Role Name	0..1 Page	* Genetic_map
Association	Card. Role Name	0..1 Page	* Genomic_reference_allele

Association	Card. Role Name	0..1 Page	* Geographic_location
Association	Card. Role Name	0..1 Page	* Cytogenetic_location
Association	Card. Role Name	0..1 Page	* Organization
Association	Card. Role Name	0..1 Page	* Contributor
Association	Card. Role Name	0..1 Page	* Reference_genomic_assembly
Association	Card. Role Name	0..1 Page	* Reference_genomic_landmark
Association	Card. Role Name	0..1 Page	* Subject_descriptor
Association	Card. Role Name	0..1 Page	* Taxon
Association	Card. Role Name	0..1 Page	* Bibliographic_reference
Association	Card. Role Name	0..1 Page	* Bibref_description
Association	Card. Role Name	0..1 Page	* Journal
Association	Card. Role Name	0..1 Page	* Service
Association	Card. Role Name	0..1 Page	* Oligo
Association	Card. Role Name	0..1 Page	* Panel

Association	Card. Role Name	0..1 Page	* Genomic_haplotype_population_frequency
Association	Card. Role Name	0..1 Page	* Genomic_variation
Association	Card. Role Name	0..1 Page	* Haplotype_block
Association	Card. Role Name	0..1 Page	* Haplotype_derivation_methods
Association	Card. Role Name	0..1 Page	* Haplotype_map
Association	Card. Role Name	0..1 Page	* Individual
Association	Card. Role Name	0..1 Page	* Latent_genotype
Association	Card. Role Name	0..1 Page	* Cytogenetic_map
Association	Card. Role Name	0..1 Page	* Neighbour_variation
Association	Card. Role Name	0..1 Page	* Reference_genomic_location
Association	Card. Role Name	0..1 Page	* Structural_change
Association	Card. Role Name	0..1 Page	* Transcription_change
Association	Card. Role Name	0..1 Page	* Translation_change
Association	Card. Role Name	0..1 Page	* Variation_assay

Association	Card. Role Name	0..1 Page	* Anatomic_location
Association	Card. Role Name	0..1 Page	* Annotation
Association	Card. Role Name	0..1 Page	* CDS
Association	Card. Role Name	0..1 Page	* Molecular_sample
Association	Card. Role Name	0..1 Page	* Source

7.2.1.58 Panel

Type: **Class _ _Abstract_population**

Package: **PAGE-OM**

Document:

A set of samples from individuals drawn from the same species and used for genetic studies. A panel must be identifiable with a list of accessioned individuals, if possible. Panel can have subpanels. Synonym: SampleSet, Sample from population(s), “Plate” in Coriel sense.

Connections:

Connector		Source	Target
Association Individuals that are part of the Panel.	Card. Role Name	* Individual	* Panel
Association Panel can be made from subpanels.	Card. Role Name	0..1 Panel	0..1 subpanel Panel
Association	Card. Role Name	0..1 Page	* Panel
Generalization	Card. Role Name	 Panel	 Abstract_population

Attributes:

Attribute	Lower bound	Notes
count_unit	0	Values are ‘chromosome’ and ‘individual.’ Default is ‘individual.’
pooled	0	True if accessioned individuals are not available.
size	0	The size of the sample. Note that the count_unit field affects how this value is interpreted.
type	0	Optional identifier of the panel category (e.g., plate, family, population sample).

7.2.1.59 Phenotype_disease_category

Type: **Class _ Observable_feature_category**

Package: **PAGE-OM**

Document:

Specialized category of features representing diseases.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Phenotype_disease_category	Observable_feature_category

7.2.1.60 Phenotype_feature

Type: **Class _ Observable_feature**

Package: **PAGE-OM**

Document:

Observable part of the structure, function, or behavior of a living organism.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Phenotype_feature	 Observable_feature
Association	Card. Role Name	0..1 Page	* Phenotype_feature

7.2.1.61 Plate

Type: **Class _ Identifiable**

Package: **PAGE-OM**

Document:

A sample holder, for example a microtiter plate used in one or many runs, represented by instances of Run. Samples, represented by instances of Molecular_sample, are positioned on the plate using instances of Location_on_plate.

Connections:

Connector		Source	Target
Association *wells* Well positions.	Card. Role Name	0..1 Plate	* Location_on_plate
Generalization	Card. Role Name	 Plate	 Identifiable
Association Plate used in experiment run.	Card. Role Name	* Run	0..1 Plate
Association	Card. Role Name	0..1 Page	* Plate

7.2.1.62 Reference_genomic_location

Type: **Class _ Location**

Package: **PAGE-OM**

Document:

A location within a Reference_genomic_landmark. Attributes of the location are the Reference_genomic_assembly and/or the Reference_genomic_landmark, the start and end range and strand of the feature relative to the Reference_genomic_landmark.

Connections:

Connector		Source	Target
Association Landmark of the location. Identified region on assembly.	Card. Role Name	0..1 Reference_genomic_landmark	* Reference_genomic_location
Generalization	Card. Role Name	 Reference_genomic_location_in_assembly	 Reference_genomic_location
Generalization	Card. Role Name	 Reference_genomic_location	 Location
Association Reference assembly on which locations are defined (coordinate system).	Card. Role Name	0..1 Reference_genomic_assembly	* Reference_genomic_location
Association Genomic variations that are associated to the location.	Card. Role Name	0..1 Reference_genomic_location	* Genomic_variation
Association Location on reference genome.	Card. Role Name	0..1 Genomic_variation	* Reference_genomic_location
Association	Card. Role Name	0..1 Page	* Reference_genomic_location

Attributes:

Attribute	Lower bound	Notes
end	0	End of the location in the reference sequence.
start	1	Start of the location in the reference sequence.
strand unknown	0	Orientation of the feature in the reference sequence. One of ‘forward,’ ‘reverse,’ ‘unknown.’ Defaults to ‘unknown.’

7.2.1.63 Reference_genomic_location_in_assembly

Type: **Class__Reference_genomic_location**

Package: **PAGE-OM**

Document:

A location in one chromosome of a reference genomic assembly. Instead of the reference sequence being an accessioned sequence, it is a versioned assembly.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Reference_genomic_location_in_assembly	Reference_genomic_location

Attributes:

Attribute	Lower bound	Notes
chromosome_name	0	Name of the chromosome in the assembly.

7.2.1.64 Run

Type: **Class__Abstract_run**

Package: **PAGE-OM**

Document:

The class contains information on measurement of samples, done on a physical device connected to plate. This information includes time of execution, name of instrument, etc.

Connections:

Connector		Source	Target
Association Plate used in experiment run.	Card. Role Name	* Run	0..1 Plate
Association	Card. Role Name	0..1 Page	* Run
Generalization	Card. Role Name	 Run	 Abstract_run

Attributes:

Attribute	Lower bound	Notes
instrument	0	Name of the instrument
run_date	0	Date of run.

7.2.1.65 Set_of_haplotypes

Type: **Class _ _Genomic_observation**

Package: **PAGE-OM**

Document:

An extension point for collections of haplotypes.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Haplotype_block	Set_of_haplotypes
Association Haplotype set	Card. Role Name	* Genomic_haplotype	0..1 Set_of_haplotypes
Association Set of haplotypes that are associated with the map.	Card. Role Name	* Haplotype_map	* Set_of_haplotypes
Generalization	Card. Role Name	Gene_based_haplotype	Set_of_haplotypes
Generalization	Card. Role Name	Set_of_haplotypes	Genomic_observation

7.2.1.66 String_value

Type: **Class _ Value**

Package: **PAGE-OM**

Document:

Value of type string

Connections:

Connector		Source	Target
Generalization	Card. Role Name	String_value	Value

Attributes:

Attribute	Lower bound	Notes
value	1	Actual value

7.2.1.67 Structural_change

Type: **Class _ Gene_product_change**

Package: **PAGE-OM**

Document:

Change in the 3D structure of the polypeptide chain.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Structural_change	 Gene_product_change
Association Structural change that has impact on function of protein.	Card. Role Name	* Functional_change	* affects_function Structural_change
Association Translational change that leads to a structural change.	Card. Role Name	* Structural_change	* affects_structure Translation_change
Association	Card. Role Name	0..1 Page	* Structural_change

7.2.1.68 Study

Type: **Class _ Identifiable**

Package: **PAGE-OM**

Document:

An extension point for adding other kinds of studies in the future.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Association_study	 Study
Generalization	Card. Role Name	 Study	 Identifiable

Attributes:

Attribute	Lower bound	Notes
abstract	0	Abstract
acknowledgements	0	Acknowledgements
background	0	Background information
conclusions	0	Summarizing conclusion for all experiments in this study
key_results	0	Key findings
limitations	0	Limitations
objectives	0	Summarizing objective for all experiments in this study
source_of_bias	0	Possible source of bias
study_design	0	Study design
study_power	0	Power of study
study_size_reason	0	Reason for study size
submission_date	0	Submission date of study
title	0	Title of study
update_date	0	Date when study is updated

7.2.1.69 Time_accuracy

Type: **Class**

Package: **PAGE-OM**

Document:

Accuracy code contains information on incompleteness of time of measurement or information on reason why the time of measurement is unknown or incomplete.

Connections:

Connector		Source	Target
Association Accuracy code for value.	Card. Role Name	0..1 Observed_value	0..1 Time_accuracy

Attributes:

Attribute	Lower bound	Notes
code	1	Accuracy code as defined in specific ontology.

7.2.1.70 Transcription_change

Type: **Class _ Residue_change**

Package: **PAGE-OM**

Document:

Change in the quality or quantity of the mature RNA product.

Connections:

Connector		Source	Target
Association Transcription change that affects translation.	Card. Role Name	* Translation_change	* affects_protein Transcription_change
Association Genic variation that influences on the transcript change.	Card. Role Name	* Transcription_change	* affects_transcript Genic_variation
Association	Card. Role Name	0..1 Page	* Transcription_change
Generalization	Card. Role Name	 Transcription_change	 Residue_change

Attributes:

Attribute	Lower bound	Notes
changed_codon	0	The new codon in the transcript, if applicable.
codon_position	0	The first affected nucleotide in the codon. Values are: 1, 2 or 3.
original_codon	0	The affected codon in the transcript.

7.2.1.71 Translation_change

Type: **Class _ Residue_change**

Package: **PAGE-OM**

Document:

Change in the quality or quantity of (predicted) polypeptide chain (2D).

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Translation_change	Residue_change
Association Translation that affects function of protein.	Card. Role Name	* Functional_change	* Translation_change
Association Translational change that leads to a structural change.	Card. Role Name	* Structural_change	* affects_structure Translation_change
Association Transcription change that affects translation.	Card. Role Name	* Translation_change	* affects_protein Transcription_change
Association	Card. Role Name	0..1 Page	* Translation_change

7.2.1.72 Unit

Type: **Class**

Package: **PAGE-OM**

Document:

Unit of value. Unit is defined using ontology term.

Connections:

Connector		Source	Target
Aggregation Unit of value	Card. Role Name	0..1 Unit	0..1 Value

Attributes:

Attribute	Lower bound	Notes
type	1	Type of unit

7.2.1.73 Value

Type: **Class__Abstract_value**

Package: **PAGE-OM**

Document:

Abstract class. Extension point for Value implementations. Value model is based on concept developed in Generation Challenge Program: http://pantheon.generationcp.org/demeter/Values.html

Connections:

Connector		Source	Target
Aggregation *supporting_evidence* Values supporting the evidence.	Card. Role Name	* Evidence_code	0..1 Value
Generalization	Card. Role Name	 Value	 Abstract_value
Aggregation	Card. Role Name	* Value	0..1 Enum

Connector		Source	Target
Generalization	Card. Role Name	 Value_range	 Value
Generalization	Card. Role Name	 String_value	 Value
Generalization	Card. Role Name	 Boolean	 Value
Aggregation Constraints	Card. Role Name	* Constraint	0..1 Value
Association Score of evidence (e.g., p-value)	Card. Role Name	0..1 Evidence	0..1 score *score of value* Value
Association Actual value of observation	Card. Role Name	0..1 Observed_value	1 value Value
Generalization	Card. Role Name	 Experiment_result	 Value
Aggregation Unit of value	Card. Role Name	0..1 Unit	0..1 Value
Generalization	Card. Role Name	 Numeric_value	 Value
Generalization	Card. Role Name	 Observed_value	 Value

Generalization	Card. Role Name	Enum	Value
Association Value can be composed of inferred from other values.	Card. Role Name	0..1 Value	* hierarchical_value Value

7.2.1.74 Value_range

Type: **Class _ Value**

Package: **PAGE-OM**

Document:

Inclusive value range

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Value_range	Value

Attributes:

Attribute	Lower bound	Notes
max	1	maximum value
min	1	minimum value

7.2.1.75 Variation_assay

Type: **Class _ Methodology**

Package: **PAGE-OM**

Document:

An experimental lab protocol and set of reagents for detecting the Genomic_alleles of Genomic_variations carried by an individual or a panel of individuals. Synonym: Assay. Non instrument part of the experiment - same assay can be used in different instrument runs.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Multi_vartiation_assay	 Variation_assay
Generalization	Card. Role Name	 Variation_assay	 Methodology
Association *detectable genotypes* All genotypes that can be detected. Gives information on all measurable variations measurable (by this assay) on the variation site.	Card. Role Name	* Variation_assay	* Latent_genotype
Association Genomic variation site for which assay was designed.	Card. Role Name	* Variation_assay	1 Genomic_variation
Aggregation Assays that are part of multivariation assay (for example assay that can be applied on different variation sites).	Card. Role Name	* Variation_assay	0..1 Multi_vartiation_assay
Association PCR primers	Card. Role Name	* Variation_assay	* Oligo
Association *With assay details* Used when assay level information is needed. Specific variation assay designed for genomic site (locus).	Card. Role Name	* Assayed_genomic_genotype	0..1 Variation_assay

Association	Card. Role Name	0..1 Page	* Variation_assay
Association *With assay details* Assay designed for the variation site. Association is used when assay level information is needed. (Optional with the "direct" association from Frequency to Genomic_variation).	Card. Role Name	* Frequency	0..1 Variation_assay

Attributes:

Attribute	Lower bound	Notes
description	0	Free text description of the assay protocol.

7.2.1.76 FUGE

Package: PAGE-OM

Document:

FuGE (http://fuge.sourceforge.net/) is a model of the shared components in different functional genomics domains.

7.2.1.77 Ontology_source

Type: Class Identifiable

Package: FUGE

Document:

The source ontology or controlled vocabulary list that ontology terms have been obtained from.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Ontology_source	 Identifiable
Association Source or name space of the term.	Card. Role Name	* Ontology_term	0..1 Ontology_source

Attributes:

Attribute	Lower bound	Notes
ontology_URI	0	A URI is short for Uniform Resource Identifier. A URI is a compact sequence of characters that identifies an abstract or physical resource.

7.2.1.78 Ontology_term

Type: **Class Identifiable**

Package: **FUGE**

Document:

Ontology term, defined in more detail in FuGE (http://fuge.sourceforge.net/). This is just a place holder.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Ontology_term	 Identifiable
Association Source or name space of the term.	Card. Role Name	* Ontology_term	0..1 Ontology_source

Attributes:

Attribute	Lower bound	Notes
term	1	Ontology term

7.2.1.79 BasicTypes

Package: PAGE-OM

Document:

XML basic types (http://www.w3.org/TR/xmlschema-2).

7.2.1.80 anySimpleType

Type: Class anyType

Package: BasicTypes

Document:

Connections:

Connector		Source	Target
Generalization	Card. Role Name	decimal	anySimpleType
Generalization	Card. Role Name	float	anySimpleType
Generalization	Card. Role Name	anyURI	anySimpleType
Generalization	Card. Role Name	dateTime	anySimpleType
Generalization	Card. Role Name	time	anySimpleType

Connector		Source	Target
Generalization	Card. Role Name	double	anySimpleType
Generalization	Card. Role Name	anySimpleType	anyType
Generalization	Card. Role Name	string	anySimpleType
Generalization	Card. Role Name	date	anySimpleType
Generalization	Card. Role Name	boolean	anySimpleType

7.2.1.81 anyType

Type: **Class**

Package: **BasicTypes**

Document:

Connections:

Connector		Source	Target
Generalization	Card. Role Name	anySimpleType	anyType

7.2.1.82 anyURI

Type: **Class anySimpleType**

Package: **BasicTypes**

Document:

Connections:

Connector		Source	Target
Generalization	Card. Role Name	anyURI	anySimpleType

7.2.1.83 boolean

Type: **Class anySimpleType**

Package: **BasicTypes**

Document:

Connections:

Connector		Source	Target
Generalization	Card. Role Name	boolean	anySimpleType

7.2.1.84 date

Type: **Class anySimpleType**

Package: **BasicTypes**

Document:

Connections:

Connector		Source	Target
Generalization	Card. Role Name	date	anySimpleType

7.2.1.85 dateTime

Type: **Class anySimpleType**

Package: **BasicTypes**

Document:

Connections:

Connector		Source	Target
Generalization	Card. Role Name	dateTime	anySimpleType

7.2.1.86 decimal

Type: **Class anySimpleType**

Package: **BasicTypes**

Document:

Connections:

Connector		Source	Target
Generalization	Card. Role Name	decimal	anySimpleType
Generalization	Card. Role Name	integer	decimal

7.2.1.87 double

Type: **Class anySimpleType**

Package: **BasicTypes**

Document:

Connections:

Connector		Source	Target
Generalization	Card. Role Name	double	anySimpleType

7.2.1.88 float

Type: **Class anySimpleType**

Package: **BasicTypes**

Document:

Connections:

Connector		Source	Target
Generalization	Card. Role Name	float	anySimpleType

7.2.1.89 int

Type: **Class long**

Package: **BasicTypes**

Document:

Connections:

Connector		Source	Target
Generalization	Card. Role Name	int	long
Generalization	Card. Role Name	short	int

7.2.1.90 integer

Type: **Class decimal**

Package: **BasicTypes**

Document:

Connections:

Connector		Source	Target
Generalization	Card. Role Name	long	integer
Generalization	Card. Role Name	integer	decimal

7.2.1.91 long

Type: **Class integer**

Package: **BasicTypes**

Document:

Connections:

Connector		Source	Target
Generalization	Card. Role Name	int	long
Generalization	Card. Role Name	long	integer

7.2.1.92 short

Type: **Class int**

Package: **BasicTypes**

Document:

Connections:

Connector		Source	Target
Generalization	Card. Role Name	short	int

7.2.1.93 string

Type: **Class anySimpleType**

Package: **BasicTypes**

Document:

Connections:

Connector		Source	Target
Generalization	Card. Role Name	string	anySimpleType

7.2.1.94 time

Type: **Class anySimpleType**

Package: **BasicTypes**

Document:

Connections:

Connector		Source	Target
Generalization	Card. Role Name	time	anySimpleType

7.2.1.95 SNP

Package: **PAGE-OM**

Document:

Module replicating part of OMG specification SNP (Single Nucleotide Polymorphism).

7.2.1.96 Anatomic_location

Type: **Class Identifiable**

Package: **SNP**

Document:

Description of the anatomical location the molecular sample is derived from. Best expressed as a controlled vocabulary of anatomical terms.

Connections:

Connector		Source	Target
Association Anatomic location from which sample was taken.	Card. Role Name	* Molecular_sample	* Anatomic_location
Association	Card. Role Name	0..1 Page	* Anatomic_location
Generalization	Card. Role Name	 Anatomic_location	 Identifiable

7.2.1.97 Annotation

Type: **Class**

Package: **SNP**

Document:

A free text of name and value pair. Note: name should be Ontology_term.

Connections:

Connector		Source	Target
Association	Card. Role Name	* Identifiable	* Annotation
Association	Card. Role Name	0..1 Page	* Annotation

Attributes:

Attribute	Lower bound	Notes
name	0	Name of the annotation feature
value	0	Value of annotation feature

7.2.1.98 CDS

Type: **Class Sequence**

Package: **SNP**

Document:

Region in a reference sequence that determines the start, end, and strand of the gene coding region.

Connections:

Connector		Source	Target
Association Coding region that is part of the gene structure.	Card. Role Name	0..1 CDS	0..1 Genomic_gene_structure
Generalization	Card. Role Name	 CDS	 Sequence
Association	Card. Role Name	0..1 Page	* CDS

7.2.1.99 Contributor

Type: **Class Source**

Package: **SNP**

Document:

Person who has edited data in the data set. Synonym: curator.

Connections:

Connector		Source	Target
Association	Card. Role Name	0..1 Page	* Contributor
Generalization	Card. Role Name	 Contributor	 Source

Attributes:

Attribute	Lower bound	Notes
date	0	Date of the editing.

7.2.1.100 Cytogenetic_location

Type: **Class Ordered_location**

Package: **SNP**

Document:

A location in a cytogenetic map expressed as a band or a range of bands.

Connections:

Connector		Source	Target
Association	Card. Role Name	0..1 Cytogenetic_map	* Cytogenetic_location
Generalization	Card. Role Name	 Cytogenetic_location	 Ordered_location
Association	Card. Role Name	0..1 Page	* Cytogenetic_location

7.2.1.101 Cytogenetic_map

Type: **Class Ordered_map**

Package: **SNP**

Document:

Map of cytogenetic bands describing their relative order.

Connections:

Connector		Source	Target
Association	Card. Role Name	0..1 Cytogenetic_map	* Cytogenetic_location
Generalization	Card. Role Name	 Cytogenetic_map	 Ordered_map
Association	Card. Role Name	0..1 Page	* Cytogenetic_map

7.2.1.102 Db_xref

Type: **Class Identifiable**

Package: **SNP**

Document:

Cross reference between two Identifiables in different databases.

Connections:

Connector		Source	Target
Association	Card. Role Name	* Identifiable	* Db_xref
Association	Card. Role Name	0..1 identifier Db_xref	0..1 Bibliographic_reference
Association	Card. Role Name	0..1 Page	* Db_xref
Generalization	Card. Role Name	 Db_xref	 Identifiable

Attributes:

Attribute	Lower bound	Notes
db	0	The remote database name or abbreviation.
db_version	0	Version of the database
field	0	Field in the remote database where the UID value is found (e.g., ID or AC in EMBL). Optional
uid	1	Unique identifier in the remote database.
url	0	Full URL to the cross-referenced entry.

7.2.1.103 Exon

Type: **Class Sequence**

Package: **SNP**

Document:

Region in a reference sequence that determines the start, end, and strand of the transcript that is not spliced away.

Connections:

Connector		Source	Target
Association Exons that are part of gene structure.	Card. Role Name	1..* Exon	0..1 Genomic_gene_structure
Association	Card. Role Name	0..1 Page	* Exon
Generalization	Card. Role Name	 Exon	 Sequence

7.2.1.104 Gene_product_change

Type: **Class Identifiable**

Package: **SNP**

Document:

Free form description of change in gene product.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Structural_change	Gene_product_change
Generalization	Card. Role Name	Gene_product_change	Identifiable
Generalization	Card. Role Name	Residue_change	Gene_product_change
Generalization	Card. Role Name	Functional_change	Gene_product_change

Attributes:

Attribute	Lower bound	Notes
label	0	Human understandable term for the change (e.g., missense, truncation).

7.2.1.105 Genetic_location

Type: **Class Ordered_location**

Package: **SNP**

Document:

A relative location of a marker in a genetic map based on recombination.

Connections:

Connector		Source	Target
Association	Card. Role Name	0..1 Genetic_map	* Genetic_location
Generalization	Card. Role Name	 Genetic_location	 Ordered_location
Association	Card. Role Name	0..1 Page	* Genetic_location

7.2.1.106 Genetic_map

Type: **Class Ordered_map**

Package: **SNP**

Document:

A map containing the order and non-metric distance between genetic markers for identifiable sequence features. Unit: centiMorgan.

Connections:

Connector		Source	Target
Association	Card. Role Name	0..1 Genetic_map	* Genetic_location
Generalization	Card. Role Name	 Genetic_map	 Ordered_map
Association	Card. Role Name	0..1 Page	* Genetic_map

7.2.1.107 Genomic_reference_allele

Type: **Class Genomic_allele**

Package: **SNP**

Document:

The DNA sequence of a Genomic_variation as it appears in the public database.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Genomic_reference_allele	Genomic_allele
Association	Card. Role Name	* Reference_genomic_assembly	* present_in Genomic_reference_allele
Association The DNA sequence of a genomic variation as it appears in the public database.	Card. Role Name	0..1 one_of Genomic_reference_allele	0..1 Genomic_allele
Association	Card. Role Name	0..1 Page	* Genomic_reference_allele

7.2.1.108 Geographic_location

Type: **Class Identifiable**

Package: **SNP**

Document:

Location of an individual or population in a geographic map. Locations are expressed in decimal degrees. Northern latitudes (if north of the equator) and eastern longitudes (if east of GM) have positive values by convention.

Connections:

Connector		Source	Target
Association Geographic location of individual or group of individuals (panel)	Card. Role Name	* Abstract_population	0..1 Geographic_location
Association	Card. Role Name	0..1 Page	* Geographic_location
Generalization	Card. Role Name	 Geographic_location	 Identifiable

Attributes:

Attribute	Lower bound	Notes
max_latitude	0	Upper bound of a geographical location expressed in degrees from the equator.
max_longitude	0	Upper bound of a geographical location expressed in degrees from the Greenwich meridian.
min_latitude	0	Lower bound of a geographical location expressed in degrees from the equator.
min_longitude	0	Lower bound of a geographical location expressed in degrees from the Greenwich meridian.

7.2.1.109 Identifiable

Type: **Class**

Package: **SNP**

Document:

Anything with a unique identifier.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Latent_genotype	Identifiable
Generalization	Card. Role Name	Plate	Identifiable
Aggregation *supporting_source* Supporting evidences: Citations, studies, ontology terms, etc.	Card. Role Name	* Identifiable	0..1 Evidence
Generalization	Card. Role Name	Subject_descriptor	Identifiable
Generalization	Card. Role Name	Hypothesis	Identifiable
Generalization	Card. Role Name	Abstract_run	Identifiable
Association	Card. Role Name	* Identifiable	* Annotation
Association	Card. Role Name	* Identifiable	* Publication
Association	Card. Role Name	* Identifiable	* Db_xref
Generalization	Card. Role Name	Bibref_scope	Identifiable

Generalization	Card. Role Name	Journal	Identifiable
Association Source of identifiable.	Card. Role Name	0..1 Identifiable	0..1 Source
Generalization	Card. Role Name	Gene_product_change	Identifiable
Generalization	Card. Role Name	Ontology_source	Identifiable
Generalization	Card. Role Name	Algorithm	Identifiable
Generalization	Card. Role Name	Abstract_value	Identifiable
Generalization	Card. Role Name	Ontology_term	Identifiable
Generalization	Card. Role Name	Genomic_observation	Identifiable
Generalization	Card. Role Name	Provider	Identifiable
Generalization	Card. Role Name	Map	Identifiable
Generalization	Card. Role Name	Taxon	Identifiable

Generalization	Card. Role Name	Anatomic_location	Identifiable
Generalization	Card. Role Name	Study	Identifiable
Generalization	Card. Role Name	Conclusion	Identifiable
Generalization	Card. Role Name	Observation_method	Identifiable
Generalization	Card. Role Name	Methodology	Identifiable
Generalization	Card. Role Name	Abstract_observation_target	Identifiable
Generalization	Card. Role Name	Genotype_phenotype_correlation_experiment	Identifiable
Generalization	Card. Role Name	Observable_feature_category	Identifiable
Generalization	Card. Role Name	Abstract_observable_feature	Identifiable
Generalization	Card. Role Name	Geographic_location	Identifiable
Generalization	Card. Role Name	Locatable	Identifiable

Generalization	Card. Role Name	Location	Identifiable
Generalization	Card. Role Name	Db_xref	Identifiable

Attributes:

Attribute	Lower bound	Notes
creation_date	0	Date of creation of the object.
delete_date	0	Date of deletion of the object.
lsid	1	Life Science Identifier.
modify_date	0	Date of last modification of the object.
name	0	Name can be non unique. Display name

7.2.1.110 Locatable

Type: **Class Identifiable**

Package: **SNP**

Document:

Abstract class for anything that can be placed on a sequence (i.e., can act as a sequence feature).

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Genomic_gene_structure	Locatable
Generalization	Card. Role Name	Genomic_variation	Locatable
Association *Locations* Locations	Card. Role Name	* Locatable	* Location
Generalization	Card. Role Name	Residue_change	Locatable
Generalization	Card. Role Name	Sequence	Locatable
Generalization	Card. Role Name	Locatable	Identifiable

7.2.1.111 Location

Type: **Class Identifiable**

Package: **SNP**

Document:

A position in an abstract map.

Connections:

Connector		Source	Target
Association Source location.	Card. Role Name	* Location	0..1 Location
Generalization	Card. Role Name	 Reference_genomic_location	 Location
Association	Card. Role Name	0..1 Map	* Location
Generalization	Card. Role Name	 Ordered_location	 Location
Association *Locations* Locations	Card. Role Name	* Locatable	* Location
Generalization	Card. Role Name	 Location	 Identifiable

7.2.1.112 Map

Type: **Class Identifiable**

Package: **SNP**

Document:

An abstract map.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Physical_map	Map
Association	Card. Role Name	0..1 Map	* Location
Generalization	Card. Role Name	Ordered_map	Map
Generalization	Card. Role Name	Map	Identifiable

7.2.1.113 Methodology

Type: **Class Identifiable**

Package: **SNP**

Document:

Abstract class for a laboratory method or a computational protocol.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Variation_assay	Methodology
Generalization	Card. Role Name	Haplotype_derivation_methods	Methodology
Generalization	Card. Role Name	Methodology	Identifiable

7.2.1.114 Oligo

Type: **Class Sequence**

Package: **SNP**

Document:

A DNA oligonucleotide used for detection and assay of Genomic_variations in Variation_assays. Synonym: primer

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Oligo	 Sequence
Association PCR primers.	Card. Role Name	* Variation_assay	* Oligo
Association	Card. Role Name	0..1 Page	* Oligo

7.2.1.115 Ordered_location

Type: **Class Location**

Package: **SNP**

Document:

A location on a secondary map that gives ordering information. That map can be a genetic or a cytogenetic map.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Genetic_location	Ordered_location
Generalization	Card. Role Name	Ordered_location	Location
Association Ordered location of variation (e.g., cytogenetic location)	Card. Role Name	* Ordered_location	0..1 Genomic_variation
Generalization	Card. Role Name	Cytogenetic_location	Ordered_location

Attributes:

Attribute	Lower bound	Notes
position	0	Location description

7.2.1.116 Ordered_map

Type: **Class Map**

Package: **SNP**

Document:

A non-metric map category.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Cytogenetic_map	Ordered_map
Generalization	Card. Role Name	Genetic_map	Ordered_map
Generalization	Card. Role Name	Ordered_map	Map

7.2.1.117 Organization

Type: **Class Provider**

Package: **SNP**

Document:

Affiliation of a group of unidentified persons.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Organization	Provider
Association	Card. Role Name	0..1 Page	* Organization

7.2.1.118 Person

Type: **Class Provider**

Package: **SNP**

Document:

An individual identified by name who is involved with creating or disseminating publications. Possible roles are author, editor, contributor, publisher, or applicant.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Person	Provider
Association	Card. Role Name	* editor Person	0..1 Book
Association	Card. Role Name	0..1 Page	* Person
Association Curator of evidence.	Card. Role Name	0..1 Evidence	0..1 curator *Curator of evidence* Person

Attributes:

Attribute	Lower bound	Notes
affiliation	0	Name of the organization the person is affiliated with.
email	0	Email address
et_al	0	Indicator that there are more persons in the list of persons; used typically for the bibliographic reference that contains only an abbreviated author list. Last listed author should have et_al set to true.
first_name	0	First name
mid_initials	0	Initials of any subsequent personal names.
postal_address	0	Full postal address
surname	0	Last name.

7.2.1.119 Physical_map

Type: **Class Map**

Package: **SNP**

Document:

Map of physical entities (e.g., clones, contigs).

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Physical_map	Map
Generalization	Card. Role Name	Haplotype_map	Physical_map
Generalization	Card. Role Name	Sequence_map	Physical_map

7.2.1.120 Reference_genomic_assembly

Type: **Class Sequence_map**

Package: **SNP**

Document:

Set of reference sequences (Reference_genomic_landmarks) with an algorithm to define the genome and its constituents.

Connections:

Connector		Source	Target
Association Set of genomic landmarks that are part of the reference genomic assembly.	Card. Role Name	* Reference_genomic_landmark	0..1 Reference_genomic_assembly
Association Reference assembly on which locations are defined (coordinate system).	Card. Role Name	0..1 Reference_genomic_assembly	* Reference_genomic_location
Association	Card. Role Name	* Reference_genomic_assembly	0..1 Taxon
Generalization	Card. Role Name	 Reference_genomic_assembly	 Sequence_map
Association	Card. Role Name	* Reference_genomic_assembly	* present_in Genomic_reference_allele
Association	Card. Role Name	0..1 Page	* Reference_genomic_assembly

7.2.1.121 Reference_genomic_landmark

Type: **Class Sequence**

Package: **SNP**

Document:

An accessioned genomic sequence that can be unambiguously assigned to a location in an assembly based on information in public databases.

Connections:

Connector		Source	Target
Association Set of genomic landmarks that are part of the reference genomic assembly.	Card. Role Name	* Reference_genomic_landmark	0..1 Reference_genomic_assembly
Association Landmark of the location. Identified region on assembly.	Card. Role Name	0..1 Reference_genomic_landmark	* Reference_genomic_location
Association Genomic landmark (part of sequence assembly)	Card. Role Name	0..1 Genomic_variation	0..1 Reference_genomic_landmark
Generalization	Card. Role Name	 Reference_genomic_landmark	 Sequence
Association	Card. Role Name	0..1 Page	* Reference_genomic_landmark

7.2.1.122 Residue_change

Type: **Class Gene_product_change, Locatable**

Package: **SNP**

Document:

Abstract superclass for classes describing residue changes in gene-related sequences.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Translation_change	 Residue_change
Generalization	Card. Role Name	 Genic_variation	 Residue_change

Generalization	Card. Role Name	Residue_change	Gene_product_change
Generalization	Card. Role Name	Residue_change	Locatable
Generalization	Card. Role Name	Transcription_change	Residue_change

Attributes:

Attribute	Lower bound	Notes
changed_residue	0	The new residue in the reference sequence.
original_residue	0	The affected residue in the reference sequence.

7.2.1.123 Sequence

Type: **Class Locatable, Sequence_map**

Package: **SNP**

Document:

Biological sequence. A sequence accessioned by a public database and associated with an accessioned taxon, a version number, and a release date.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Oligo	Sequence
Generalization	Card. Role Name	CDS	Sequence
Generalization	Card. Role Name	Genomic_allele	Sequence
Generalization	Card. Role Name	Reference_genomic_landmark	Sequence
Generalization	Card. Role Name	Sequence	Locatable
Generalization	Card. Role Name	Exon	Sequence
Generalization	Card. Role Name	Sequence	Sequence_map

Attributes:

Attribute	Lower bound	Notes
molecule	0	Indicates the alphabet of the sequence molecule (e.g., ‘DNA,’ ‘RNA,’ ‘protein’).
sequence	0	The residue sequence string.

7.2.1.124 Sequence_map

Type: **Class Physical_map**

Package: **SNP**

Document:

A map composed of one or more biological sequences.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Reference_genomic_assembly	Sequence_map
Generalization	Card. Role Name	Sequence	Sequence_map
Generalization	Card. Role Name	Sequence_map	Physical_map

7.2.1.125 Subject_descriptor

Type: **Class Identifiable**

Package: **SNP**

Document:

Subject term and vocabulary name container.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Subject_descriptor	 Identifiable
Association	Card. Role Name	* subject_heading Subject_descriptor	0..1 Bibref_subject
Association	Card. Role Name	* code Subject_descriptor	0..1 Bibref_subject
Association	Card. Role Name	* keyword Subject_descriptor	0..1 Bibref_subject
Association	Card. Role Name	0..1 Page	* Subject_descriptor

Attributes:

Attribute	Lower bound	Notes
term	0	The keyword, code, or subject heading value string.
vocabulary_name	0	Name of the controlled vocabulary. For example, Sears List of Subject Headings (SEARS), Library of Congress Subject Headings (LCSH), or Medical Subject Headings (MeSH).

7.2.1.126 Taxon

Type: **Class Identifiable**

Package: **SNP**

Document:

Taxonomic unit. The UID is typically a species TaxID from the Taxonomy Database (http://www.ncbi.nih.gov/Taxonomy/).

Connections:

Connector		Source	Target
Association Taxonomic name (e.g., species) of individual or population.	Card. Role Name	* Abstract_population	* Taxon
Association	Card. Role Name	* Reference_genomic_assembly	0..1 Taxon
Association	Card. Role Name	0..1 Page	* Taxon
Generalization	Card. Role Name	 Taxon	 Identifiable

Attributes:

Attribute	Lower bound	Notes
rank	0	Rank (taxonomic category) of the taxon in the hierarchy. Typically ‘species’ or ‘family.’
scientific_name	0	Scientific name, e.g., Homo sapiens.

7.2.1.127 BREF

Package: PAGE-OM

Document:

Module covering bibliographic references as defined in OMG specification SNP (Single Nucleotide Polymorphism), located at: http://www.omg.org/spec/SNP/.

7.2.1.128 Article

Type: Class Bibliographic_reference

Package: BREF

Document:

Non fictional prose forming an independent part of a publication.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Journal_article	Article
Generalization	Card. Role Name	Article	Bibliographic_reference
Generalization	Card. Role Name	Book_article	Article

Attributes:

Attribute	Lower bound	Notes
first_page	0	First page in an article
last_page	0	Last page in an article

7.2.1.129 Bibliographic_reference

Type: **Class Publication**

Package: **BREF**

Document:

The BibliographicReference class is the core of the data model. It is a super-class for all specialized citation types, but it can also be instantiated and represent an additional type not specifically defined in this specification.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Article	Bibliographic_reference
Generalization	Card. Role Name	Book	Bibliographic_reference
Generalization	Card. Role Name	Patent	Bibliographic_reference
Generalization	Card. Role Name	Thesis	Bibliographic_reference
Generalization	Card. Role Name	Web_resource	Bibliographic_reference
Association	Card. Role Name	0..1 desciption Bibref_description	0..1 Bibliographic_reference
Generalization	Card. Role Name	Tech_report	Bibliographic_reference
Association	Card. Role Name	0..1 status Entry_status	0..1 Bibliographic_reference
Generalization	Card. Role Name	Proceeding	Bibliographic_reference
Generalization	Card. Role Name	Bibliographic_reference	Publication

Association	Card. Role Name	0..1 identifier Db_xref	0..1 Bibliographic_reference
Association	Card. Role Name	0..1 publisher Provider	0..1 Bibliographic_reference
Association	Card. Role Name	* Provider	0..1 Bibliographic_reference
Association	Card. Role Name	* author Provider	0..1 Bibliographic_reference
Association	Card. Role Name	0..1 subject Bibref_subject	0..1 Bibliographic_reference
Association	Card. Role Name	0..1 coverage Bibref_scope	0..1 Bibliographic_reference
Association	Card. Role Name	* contributor Provider	0..1 Bibliographic_reference
Association	Card. Role Name	0..1 Page	* Bibliographic_reference

Attributes:

Attribute	Lower bound	Notes
date	0	Defines a date associated with an event in the life cycle of the cited resource, when this resource became available. Usually, it is a date of publishing, however, for not yet published resources, it can be a date of creation.
format	0	Describes the physical or digital manifestation of the cited resource. It can have very different content depending on the citation type.
language	0	Defines a language of the intellectual contents of the cited resource. The recommendation is to use values as defined by RFC1766 that includes a two-letter Language Code (taken from the ISO639 standard, followed optionally by a two-letter Country Code (taken from the ISO3166 standard). For example, “en” for English, “fr” for French, or “en-uk” for English used in the United Kingdom. Another possibility is to use MARC List of Languages.
rights	0	Specifies information about rights over the cited resource. Typically, it contains a rights management statement for the resource, or it refers to a service providing such information. Rights information often encompasses Intellectual Property Rights [IPR], Copyrights, and various Property Rights.
title	0	A title given to the cited resource (a name by which the resource is formally known).
type	0	It defines the nature or genre of the cited resource. Although a working draft of Dublin Core Types recommends a type classification, the proposed types are mostly out of scope of this specification. The majority of cited resources would fall in the same category “text.” For the future, however, Dublin Core is considering the addition of subtypes to the high level types, or other ways of making sub-categories

7.2.1.130 Bibref_description

Type: **Class**

Package: **BREF**

Document:

A brief account of the content of the cited resource. It can be either the abstract, or the table of contents, or both. It can be written in a language different from the language of the cited resource.

Connections:

Connector		Source	Target
Association	Card. Role Name	0..1 description Bibref_description	0..1 Bibliographic_reference
Association	Card. Role Name	0..1 Page	* Bibref_description

Attributes:

Attribute	Lower bound	Notes
abstract_type	0	Format of the abstract expressed in MIME (Multipurpose Internet Mail Extensions)
language	0	Language of the description
table_of_contents	0	A list of divisions (chapters or articles) and the pages on which they start
the_abstract	0	Summary of the main points of the publication.
toc_type	0	Format of the table of contents expressed in MIME (Multipurpose Internet Mail Extensions).

7.2.1.131 Bibref_scope

Type: **Class Identifiable**

Package: **BREF**

Document:

It defines the extent or scope of the content of the cited resource. It can include spatial location (a place name or geographic co-ordinates), temporal period (a period label, date, or date range), or both. Finally, it can have additional dynamic properties such as jurisdiction.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Bibref_scope	 Identifiable
Association	Card. Role Name	0..1 coverage Bibref_scope	0..1 Bibliographic_reference

Attributes:

Attribute	Lower bound	Notes
spatial_location	0	A place or area name or geographic coordinates in string format.
temporal_period	0	A period label, date, or date range.

7.2.1.132 Bibref_subject

Type: **Class**

Package: **BREF**

Document:

It defines the topic of the content of the cited resource.

Connections:

Connector		Source	Target
Association	Card. Role Name	* subject_heading Subject_descriptor	0..1 Bibref_subject
Association	Card. Role Name	* code Subject_descriptor	0..1 Bibref_subject
Association	Card. Role Name	* keyword Subject_descriptor	0..1 Bibref_subject
Association	Card. Role Name	0..1 subject Bibref_subject	0..1 Bibliographic_reference

7.2.1.133 Book

Type: **Class Bibliographic_reference**

Package: **BREF**

Document:

A written work or composition that has been published; usually printed on pages bound together.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Book	 Bibliographic_reference
Association	Card. Role Name	1 from_book Book	0..1 Book_article
Association	Card. Role Name	* editor Person	0..1 Book

Attributes:

Attribute	Lower bound	Notes
edition	0	Name of the edition.
isbn	0	International Standard Book Number
series	0	Name of a collection of books.
volume	0	Volume number of the book in a series.

7.2.1.134 Book_article

Type: **Class Article**

Package: **BREF**

Document:

Article that forms part of a book.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Book_article	 Article
Association	Card. Role Name	1 from_book Book	0..1 Book_article

7.2.1.135 Distributor

Type: **Class Source**

Package: **BREF**

Document:

The original source of the data.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Distributor	Source

7.2.1.136 Entry_status

Type: **Class Publication**

Package: **BREF**

Document:

Defines information related to the citation itself rather than to the cited resource.

Connections:

Connector		Source	Target
Association	Card. Role Name	0..1 status Entry_status	0..1 Bibliographic_reference
Generalization	Card. Role Name	Entry_status	Publication

Attributes:

Attribute	Lower bound	Notes
last_modified_date	0	last date the citation entry was changed
subset	0	Some bibliographic repositories consist of several, or even many, databases. The subset helps to locate the citation.

7.2.1.137 Journal

Type: **Class Identifiable**

Package: **BREF**

Document:

A class describing a journal; a periodical dedicated to a particular subject. The citations referring to the journal articles have a reference to this class. There are only few explicit attributes defined, the rest are accessible using dynamic properties.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Journal	 Identifiable
Association	Card. Role Name	1 from_journal Journal	0..1 Journal_article
Association	Card. Role Name	0..1 Page	* Journal

Attributes:

Attribute	Lower bound	Notes
abbreviation	0	Accepted abbreviated form of the journal name.
issn	0	The ISSN (International Standard Serial Number) is an eight-digit number that identifies periodical publications as such.

7.2.1.138 Journal_article

Type: **Class Article**

Package: **BREF**

Document:

Article, especially a scientific one that forms part of a journal.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Journal_article	 Article
Association	Card. Role Name	1 from_journal Journal	0..1 Journal_article

Attributes:

Attribute	Lower bound	Notes
issue	0	Integer indicating the ordering of the issue within a volume.
issue_supplement	0	Additional identifier for a separate supplement of the issue.
volume	0	Volume number of the journal. Typically all issues of a journal published within a year belong to the same volume.

7.2.1.139 Patent

Type: **Class Bibliographic_reference**

Package: **BREF**

Document:

A document granting an inventor sole rights to an invention.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Patent	 Bibliographic_reference
Association	Card. Role Name	0..1 applicant Provider	0..1 Patent

Attributes:

Attribute	Lower bound	Notes
doc_number	0	Patent identifier
doc_office	0	Name of the patent office (e.g., European Patent Office).
doc_type	0	Type of a patent (e.g., ‘utility,’ ‘design,’ and ‘plant.’

7.2.1.140 Proceeding

Type: **Class Bibliographic_reference**

Package: **BREF**

Document:

Printed communication from a scientific organization.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Proceeding	Bibliographic_reference

7.2.1.141 Provider

Type: **Class Identifiable**

Package: **BREF**

Document:

Bibliographic resources. The most obvious examples are authors, but it includes also publishers and other contributors.

These attributes define the active participants. They may be persons, organizations, or even services. A publisher is responsible for making the resource available. The authors and contributors are in ordered lists. The authors and contributors are responsible for creating the contents of the cited resource. There is no formal definition of how this Single Nucleotide Polymorphisms Specification responsibility is divided between them. However, the authors are usually primary creators while contributors may be illustrators, translators, or other creative providers. Their role may be specified in a separate attribute in dynamic properties.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Organization	Provider
Generalization	Card. Role Name	Person	Provider
Association	Card. Role Name	0..1 publisher Provider	0..1 Bibliographic_reference
Association	Card. Role Name	* Provider	0..1 Bibliographic_reference
Association	Card. Role Name	* author Provider	0..1 Bibliographic_reference
Association	Card. Role Name	0..1 applicant Provider	0..1 Patent
Association	Card. Role Name	* contributor Provider	0..1 Bibliographic_reference
Generalization	Card. Role Name	Service	Provider
Generalization	Card. Role Name	Provider	Identifiable

7.2.1.142 Publication

Type: **Class**

Package: **BREF**

Document:

A Citation. REF BibRef OMG standard. Not identifiable (Defined in model).

Connections:

Connector		Source	Target
Association	Card. Role Name	* Identifiable	* Publication
Generalization	Card. Role Name	 Bibliographic_reference	 Publication
Generalization	Card. Role Name	 Entry_status	 Publication

7.2.1.143 Service

Type: **Class Provider**

Package: **BREF**

Document:

Provider of software service

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Service	 Provider
Association	Card. Role Name	0..1 Page	* Service

7.2.1.144 Source

Type: **Class**

Package: **BREF**

Document:

Source of the data. Individual or institute.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	 Distributor	 Source
Association Source of identifiable.	Card. Role Name	0..1 Identifiable	0..1 Source
Generalization	Card. Role Name	 Contributor	 Source
Association	Card. Role Name	0..1 Page	* Source

Attributes:

Attribute	Lower bound	Notes
address	0	Street address.
email	0	Contact e-mail.
fax	0	Fax number.
institution	0	Name of the institution
name	0	Name of the Source.
tel	0	Telephone number.

7.2.1.145 Tech_report

Type: **Class Bibliographic_reference**

Package: **BREF**

Document:

Technical report

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Tech_report	Bibliographic_reference

7.2.1.146 Thesis

Type: **Class Bibliographic_reference**

Package: **BREF**

Document:

A treatise advancing a new point of view resulting from original research; usually a requirement for an advanced academic degree.

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Thesis	Bibliographic_reference

7.2.1.147 Web_resource

Type: **Class Bibliographic_reference**

Package: **BREF**

Document:

A referred web address

Connections:

Connector		Source	Target
Generalization	Card. Role Name	Web_resource	Bibliographic_reference

Attributes:

Attribute	Lower bound	Notes
cost	0	Cost of accessing the information
estimated_size	0	Rough size of the retrieved reference entry.
url	0	Uniform Resource Locator

8 Platform Specific Model

The previous chapter defines a platform independent model. The real implementations, however, are expected to depend on a more specific platform. This chapter shows an XML-based platform specific model expressing exchange format for data that conforms to platform independent model described above.

The platform specific model for XML derives its architecture according to the XML as suggested by W3C document "Extensible Markup Language (XML) 1.0 (http://www.w3.org/TR/REC-xml/)."

The model is defined by XML Schema as suggested by following W3C documents.

- XML Schema Part 0: Primer (http://www.w3.org/TR/xmlschema-0/)
- XML Schema Part 1: Structure (http://www.w3.org/TR/xmlschema-1/)
- XML Schema Part 2: Datatypes (http://www.w3.org/TR/xmlschema-2/)

The normative XML schema was generated from the modeling tool Enterprise Architect (EA), version 7.0.817.1. The target namespaces were propagated by the EA tool into the resulting XML Schema. However, because these target namespaces are not part of the XMI, when using a different tool, the namespaces must be changed in the resulting XML Schema manually as follows:

UML Package name	Target namespace
SNP	http://www.openpml.org/page-om/snp
SNP2	http://www.openpml.org/page-om/snp2
PAGE	http://www.openpml.org/page-om/page
BREF	http://www.openpml.org/page-om/bref
FUGE	http://www.openpml.org/page-om/fuge

Also following manual modifications were done into the XML schema files:
SchemaLocations attributes were added into the import elements for all packages (snp.xsd, snp2.xsd, page.xsd, bref.xsd and fuge.xsd) respectively.

Duplicate attributes coming from diamond inheritance are removed manually from snp.xsd file by editing out first occurrences of attributes from lsid to Source in Sequence and Residue elements.

The normative XML schema also consistently uses constructs `xs:choice minOccurs="0" maxOccurs="unbounded"` instead of constructs `xs:sequence`.

The normative XML Schema is attached in the "Associated files" as file *page-om.xsd*.

Annex A
Accompanying Files

(Informative)

This annex is a set of the accompanying files. Some of these files are normative and some of them contain examples and convenient images. If there is a discrepancy between the contents of the normative files and this document, then the normative files take precedence.

The accompanied files are divided into two sections, PIM and PSM. The PIM section includes files related directly to the "Platform Independent Model," the PSM section contains the files used in the "Platform Specific Model."

Platform Independent Model

PAGE-OM_uml_2.1_xmi_2.1.xml

A normative representation of the PAGE-OM specification.

PAGE-OM.EAP

This is the main file created by the Enterprise Architect (http://www.sparxsystems.com/) modeling tool. It served as a base for generating the XMI and description files, mentioned above.

01_Association_study.tiff

02_Sample.tiff

03_Genotype_overview.tiff

04_Phenotype_overview.tiff

05_Genotype_in_details.tiff

06_Frequency.tiff

07_Haplotype.tiff

08_Sequence.tiff

09_Map.tiff

90_Identifiable.tiff

91_Evidence_and_Value.tiff

Diagrams of the PAGE-OM specification. These are the same diagrams as in this document but perhaps with a better resolution.

Platform Specific Model

basictypes.xsd
bref.xsd
fuge.xsd
page-om.xsd
snp.xsd

Annex B
References

(Informative)

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Annex C
Glossary

(Informative)

Term	Definition
Abstract_observable_feature [in PAGE-OM]	An extension point for other kinds of observable features.
Abstract_observation_target [in PAGE-OM]	It is an abstract class for all entities from which one can make genotype or phenotype measurements or observations. It deals with entities capable of being observed.
Abstract_population [in PAGE-OM]	An interbreeding set of individuals, from whom a Panel is drawn. (Population in SNP-PML). Extends Abstract_observation_target, which is abstract class for all entities from which one can make genotype or phenotype measurements or observations.
Abstract_run [in PAGE-OM]	An extension point for other kinds of runs.
Abstract_value [in PAGE-OM]	An extension point for kinds of values.
Algorithm [in PAGE-OM]	Step-by-step procedure for solving a problem.
Anatomic_location [in SNP]	Description of the anatomical location the molecular sample is derived from. Best expressed as a controlled vocabulary of anatomical terms.
Annotation [in SNP]	A free text of name and value pair. Note: name should be Ontology_term.
Article [in BREF]	Non fictional prose forming an independent part of a publication.
Assayed_genomic_genotype [in PAGE-OM]	The result of applying a variation assay to an individual, to reveal one or more of the genomic alleles carried by that individual. This term applies to the observed data rather than to the inferred state of the individual. Thus the same individual might have several different genotypes at the same site, where the variation might be due to differing assays, experimental error, dominant systems, missing data, and so forth. Synonym: Measurement.
Association_study [in PAGE-OM]	Association study is core concept of the specification. It captures relationships between phenotypes and genotypes. It is an examination of genetic variation across the genome, designed to identify genetic associations with observable phenotypes. Association studies are results of correlation experiments.
Band_size [in PAGE-OM]	DNA fragment length estimated from gel electrophoresis.

Bibliographic_reference [in BREF]	The BibliographicReference class is the core of the data model. It is a super-class for all specialized citation types, but it can also be instantiated and represent an additional type not specifically defined in this specification.
Bibref_description [in BREF]	A brief account of the content of the cited resource. It can be either the abstract, or the table of contents, or both. It can be written in a language different from the language of the cited resource.
Bibref_scope [in BREF]	It defines the extent or scope of the content of the cited resource. It can include spatial location (a place name or geographic co-ordinates), temporal period (a period label, date, or date range), or both. Finally, it can have additional dynamic properties such as jurisdiction.
Bibref_subject [in BREF]	It defines the topic of the content of the cited resource.
Book [in BREF]	A written work or composition that has been published; usually printed on pages bound together.
Book_article [in BREF]	Article that forms part of a book.
Boolean [in PAGE-OM]	Value of type boolean.
CDS [in SNP]	Region in a reference sequence that determines the start, end, and strand of the gene coding region.
Conclusion [in PAGE-OM]	A reasoned judgment of an experiment.
Consensus_genomic_genotype [in PAGE-OM]	This class represents consensus from several experiments providing genotypes of the same sample on the same site.
Constraint [in PAGE-OM]	The contents of a Value can be limited by Constraints. Different types of Constraints allow various ways how to limit or validate one or more Value instances. The Constraint superclass only stores a string description of the Constraint. The actual full semantics of a constraint are specified in various subclasses described below. But there are no subclasses in the PAGE-OM - because they are out of scope of PAGE-OM.
Contributor [in SNP]	Person who has edited data in the data set. Synonym: curator
Cytogenetic_location [in SNP]	A location in a cytogenetic map expressed as a band or a range of bands.
Cytogenetic_map [in SNP]	Map of cytogenetic bands describing their relative order.
Db_xref [in SNP]	Cross reference between two Identifiables in different databases.
Defining_feature [in PAGE-OM]	Is an association class that has list of values, which are used in defining the instance of Latent_genotype_specifications (for example intensity values used in allele calling). The class captures information how alleles are called (observed) from raw measurement values like intensity values.
Distributor [in BREF]	The original source of the data.
Entry_status [in BREF]	Defines information related to the citation itself rather than to the cited resource.

Enum [in PAGE-OM]	Enumeration contains list of Values.
Environment_feature [in PAGE-OM]	Circumstances, objects, or conditions by which one is surrounded.
Error [in PAGE-OM]	Error value is numeric value of accuracy. Quality score
Evidence [in PAGE-OM]	Evidence indicates reliability of a feature or simply documents its authoritative origin.
Evidence_code [in PAGE-OM]	Evidence can be an EvidenceCode (which is a controlled vocabulary term such as a GO evidence code or ICIS Method code) but can be a more fully documented Evidence object (inheriting from EvidenceCode) generally curated by a specified person, a curator modeled as a Contact. Its strength is expressed by the score (which is usually a numeric value between 0 and 1, but also other types of Value are allowed - e.g., an ontology term value). The core of an evidence is its supporting source, which can be anything (because it is identified by a SimpleIdentifier). Usual evidence sources are BiblioReferences, Studies, and OntologyTerms. Reference (generationcp - http://pantheon.generationcp.org/demeter/Features.html)
Exon [in SNP]	Region in a reference sequence that determines the start, end, and strand of the transcript that is not spliced away.
Experiment_result [in PAGE-OM]	The experiment result (for example a single p-value) gathers correlation between genomic observation and phenotypic observed values. A correlation experiment can consist of more than one experiment result.
Float_value [in PAGE-OM]	Value of type float
Frequency [in PAGE-OM]	Abstract class for frequencies, expressed in percentages. Alleles (Genomic_alleles), genotypes (Consensus_genomic_genotype), and haplotypes (Genomic_haplotype) can have measured frequencies in population samples (Panels). In addition, heterozygosity (Heterozygosity) is a measure of observed variability of a polymorphic site (Genomic_variation) in a sub-population (Panel).
Frequency_set [in PAGE-OM]	Set of frequencies
Functional_change [in PAGE-OM]	Change in the function of the final gene product.
Gene_based_haplotype [in PAGE-OM]	Collection of variable nucleotides (Genomic_alleles in Genomic_variations) that define a gene. In older usage synonym locus.
Gene_product_change [in SNP]	Free form description of change in gene product.
Genetic_location [in SNP]	A relative location of a marker in a genetic map based on recombination.
Genetic_map [in SNP]	A map containing the order and non-metric distance between genetic markers for identifiable sequence features. Unit: centiMorgan.
Genic_variation [in PAGE-OM]	Genomic variation with location in genic coordinates. Synonym: mutation (when change from a common allele affects phenotype)

Genomic_allele [in PAGE-OM]	One of several alternative DNA sequences of a Reference_genomic_location as it appears in the population of organisms. Synonym: variant, allele
Genomic_allele_population_frequency [in PAGE-OM]	The frequency with which a particular Genomic_allele is seen in a particular Panel. This frequency can be measured from pooled samples. Synonyms: Genomic_allele_panel_frequency, allele_frequency.
Genomic_gene_structure [in PAGE-OM]	A structure of a gene expressed as location of the CDS and exons. Defines genic coordinate system from start of the CDS downstream.
Genomic_genotype_population_frequency [in PAGE-OM]	Frequency of a Consensus_genomic_genotype in a Panel. OSAGE-OM Has many to one relationship to Latent_genotype (Consensus_genomic_genotype in SNP-PML)
Genomic_haplotype [in PAGE-OM]	A set of Genomic_alleles across an equal number of Genomic_variations in a single chromosome and in a single individual. The Genomic_haplotype is derived from a set of Consensus_genomic_genotype. For each Genomic_variation, the haplotype contains one and only one Genomic_allele. Furthermore, the Genomic_alleles are required to be in phase on the individual, meaning that they are located on the same contiguous strand of DNA. Synonym: Haplotype.
Genomic_haplotype_population_frequency [in PAGE-OM]	Frequency of a Genomic_haplotype in a Panel.
Genomic_observation [in PAGE-OM]	Genomic observation
Genomic_reference_allele [in SNP]	The DNA sequence of a Genomic_variation as it appears in the public database.
Genomic_variation [in PAGE-OM]	A variable site in a Reference_genomic_landmark sequence. Synonyms: polymorphic site, marker, (Genomic_polymorphism in SNP-PML).
Genotype_phenotype_correlation_experiment [in PAGE-OM]	Family or case control based association study experiment. Represents set of experiment sub-sections that would normally be listed in the results section in manuscripts.
Geographic_location [in SNP]	Location of an individual or population in a geographic map. Locations are expressed in decimal degrees. Northern latitudes (if north of the equator) and eastern longitudes (if east of GM) have positive values by convention.
Haplotype_block [in PAGE-OM]	Large (spanning a few kb to >100 kb) blocks of Genomic_alleles in linkage disequilibrium (LD) and a few haplotypes per block, separated by regions of recombination.
Haplotype_derivation_methods [in PAGE-OM]	Association class describing methods used to derive Genomic_haplotypes from Consensus_genomic_genotypes.

Haplotype_map [in PAGE-OM]	Map of haplotypes. Features include: Block length distribution, measures of block variability, relative proportions of common haplotypes, block coverage of chromosomes and/or genome. LD and other values between haplotypes, markers, alleles.
Heterozygosity [in PAGE-OM]	Heterozygosity (Heterozygosity) is a measure of observed variability of a polymorphic site (Genomic_variation) in a sub-population (Panel).
Hypothesis [in PAGE-OM]	Free text description of hypothesis of study.
Identifiable [in SNP]	Anything with a unique identifier.
Individual [in PAGE-OM]	A single member of a species, where a species is an accessioned taxon defined by a public database, and the individual is accessioned in a public or private database. Synonym: “inbred strain” in homozygous lineages.
Integer_value [in PAGE-OM]	Value of type integer
Journal [in BREF]	A class describing a journal; a periodical dedicated to a particular subject. The citations referring to the journal articles have a reference to this class. There are only a few explicit attributes defined, the rest are accessible using dynamic properties.
Journal_article [in BREF]	Article, especially a scientific one that forms part of a journal.
Latent_genotype [in PAGE-OM]	Potentially existing genotypes on specific site that could be observed by Variation_assays. Application of a Variation _assay on one Molecular_sample generates a single Latent_genotype that has one or more Latent_genotype _specifications (this depends on ploidy level in case of Genomic_allele). Latent_genotypes associated to one instance of a Variation_assay can have only one type of Latent_genotype_specifications, as defined by Defining_feature. This class is a holder for one or many observable variation objects (Latent_genotype_specification). Latent_genotype is used to attach possible variations to measurements (Assayed_genomic_genotype), variation assays (Variation_assay), and marker loci (Genomic_variation).
Latent_genotype_specification [in PAGE-OM]	Abstract super class of observable variation objects, like alleles, melting temperatures (Melting_temperature), band sizes (Band_size). The class is an extension point to other kinds of variations.
Lifestyle_feature [in PAGE-OM]	Way of life of an individual or panel
Locatable [in SNP]	Abstract class for anything that can be placed on a sequence, i.e., can act as a sequence feature.
Location [in SNP]	A position in an abstract map.

Location_on_plate [in PAGE-OM]	X,Y plate_positions (wells). Numbering starts from one. Each well can contain one or more observation targets (molecular samples) prepared for measurement using one or more variation assays (e.g. assay multiplexing Assay_set). Note: These are optional laboratory specific details (Sample and Assay information is in Assayed_genomic_genotype).
Map [in SNP]	An abstract map.
Melting_temperature [in PAGE-OM]	The temperature at which DNA goes from a double-stranded to a single-stranded state. Unit of temperature is Celsius.
Methodology [in SNP]	Abstract class for a laboratory method or a computational protocol.
Molecular_sample [in PAGE-OM]	A sample from an Individual or from a Panel defining the molecule and tissue/cell used (Anatomic_locations) in the Variation_assay. Synonym: Sample of individual
Multi_vartiation_assay [in PAGE-OM]	Multi_variation_assay is a collection of assays that may be used simultaneously. Examples would be multiplex assays, micro-array based assays, or a panel of single-plex assays that share some common feature or purpose.
Neighbour_variation [in PAGE-OM]	Another Genomic_variation close enough to affect the primer design.
Numeric_value [in PAGE-OM]	Numeric value
Observable_feature [in PAGE-OM]	Measurable feature of observable (e.g., size of nose)
Observable_feature_category [in PAGE-OM]	All features considered by this model can be categorized by using this class. The category should be expressed by an ontology term.
Observation_method [in PAGE-OM]	Observable features can be measured by different methods. This class specifies which method has been used. For example, a method can be usage of a ruler or filling a questionnaire.
Observed_value [in PAGE-OM]	Observation done at specific point in time.
Oligo [in SNP]	A DNA oligonucleotide used for detection and assay of Genomic_variations in Variation_assays. Synonym: primer
Ontology_source [in FUGE]	The source ontology or controlled vocabulary list that ontology terms have been obtained from.
Ontology_term [in FUGE]	Ontology term, defined in more detail in FuGE (http://fuge.sourceforge.net/). This is just a place holder.
Ordered_location [in SNP]	A location on a secondary map that gives ordering information. That map can be a genetic or a cytogenetic map.
Ordered_map [in SNP]	A non-metric map category.
Organization [in SNP]	Affiliation of a group of unidentified persons.
Page [in PAGE-OM]	This class does not contain any scientific meaning. Its main purpose is to be the root element for the situations where this specification is used for data exchange formats (e.g., xml-schema). Therefore, it has optional direct associations to all important classes so that implementations can exchange only relevant data.

Panel [in PAGE-OM]	A set of samples from individuals drawn from the same species and used for genetic studies. A panel must be identifiable with a list of accessioned individuals, if possible. Panel can have subpanels. Synonym: SampleSet, Sample from population(s), “Plate” in Coriel sense.
Patent [in BREF]	A document granting an inventor sole rights to an invention.
Person [in SNP]	An individual identified by name who is involved with creating or disseminating publications. Possible roles are author, editor, contributor, publisher, or applicant.
Phenotype_disease_category [in PAGE-OM]	Specialized category of features representing diseases.
Phenotype_feature [in PAGE-OM]	Observable part of the structure, function, or behavior of a living organism.
Physical_map [in SNP]	Map of physical entities, e.g., clones, contigs.
Plate [in PAGE-OM]	A sample holder, for example a microtiter plate used in one or many runs, represented by instances of Run. Samples, represented by instances of Molecular_sample, are positioned on the plate using instances of Location_on_plate.
Proceeding [in BREF]	Printed communication from a scientific organization.
Provider [in BREF]	Bibliographic resources. The most obvious examples are authors, but it includes also publishers and other contributors. These attributes define the active participants. They may be persons, organizations, or even services. A publisher is responsible for making the resource available. The authors and contributors are in ordered lists. The authors and contributors are responsible for creating the contents of the cited resource. There is no formal definition of how this 60 Single Nucleotide Polymorphisms Specification responsibility is divided between them. However, the authors are usually primary creators while contributors may be illustrators, translators, or other creative providers. Their role may be specified in a separate attribute in dynamic properties.
Publication [in BREF]	A Citation. REF BibRef OMG standard. Not identifiable (Defined in model)
Reference_genomic_assembly [in SNP]	Set of reference sequences (Reference_genomic_landmarks) with an algorithm to define the genome and its constituents.
Reference_genomic_landmark [in SNP]	An accessioned genomic sequence that can be unambiguously assigned to a location in an assembly based on information in public databases.
Reference_genomic_location [in PAGE-OM]	A location within a Reference_genomic_landmark. Attributes of the location are the Reference_genomic_assembly and/or the Reference_genomic_landmark, the start and end range and strand of the feature relative to the Reference_genomic_landmark.

Reference_genomic_location_in_assembly [in PAGE-OM]	A location in one chromosome of a reference genomic assembly. Instead of the reference sequence being an accessioned sequence, it is a versioned assembly.
Residue_change [in SNP]	Abstract superclass for classes describing residue changes in gene-related sequences.
Run [in PAGE-OM]	The class contains information on measurement of samples, done on a physical device connected to plate. This information includes time of execution, name of instrument, etc.
Sequence [in SNP]	Biological sequence. A sequence accessioned by a public database and associated with an accessioned taxon, a version number, and a release date.
Sequence_map [in SNP]	A map composed of one or more biological sequences.
Service [in BREF]	Provider of software service
Set_of_haplotypes [in PAGE-OM]	An extension point for collections of haplotypes.
Source [in BREF]	Source of the data - Individual or institute
String_value [in PAGE-OM]	Value of type string
Structural_change [in PAGE-OM]	Change in the 3D structure of the polypeptide chain.
Study [in PAGE-OM]	An extension point for adding other kind of studies in the future.
Subject_descriptor [in SNP]	Subject term and vocabulary name container.
Taxon [in SNP]	Taxonomic unit. The UID is typically a species TaxID from the Taxonomy Database (http://www.ncbi.nih.gov/Taxonomy/)
Tech_report [in BREF]	Technical report
Thesis [in BREF]	A treatise advancing a new point of view resulting from original research; usually a requirement for an advanced academic degree.
Time_accuracy [in PAGE-OM]	Accuracy code contains information on incompleteness of time of measurement or information on reason why the time of measurement is unknown or incomplete.
Transcription_change [in PAGE-OM]	Change in the quality or quantity of the mature RNA product.
Translation_change [in PAGE-OM]	Change in the quality or quantity of (predicted) polypeptide chain (2D).
Unit [in PAGE-OM]	Unit of value. Unit is defined using ontology term.
Value [in PAGE-OM]	Abstract class. Extension point for Value implementations. Value model is based on concept developed in Generation Challenge Program: http://pantheon.generationcp.org/demeter/Values.html
Value_range [in PAGE-OM]	Inclusive value range
Variation_assay [in PAGE-OM]	An experimental lab protocol and set of reagents for detecting the Genomic_alleles of Genomic_variations carried by an individual or a panel of individuals. Synonym: Assay. Non instrument part of the experiment - same assay can be used in different instrument runs.
Web_resource [in BREF]	A referred web address

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