Genomic observations can be organized and grouped together in a wide variety of ways. Generally, grouping is used to provide a visualization which may be helpful to the developer. An exception is grouping a panel, when the appropriate panel code is used (e.g. a specific Panel LOINC code in an observation used to tie all the variants of the panel together).

Overview

Observations are the core representation of structured genomic information. Observations profiles are typically referenced directly by the [genomics report](http://build.fhir.org/ig/HL7/genomics-reporting/branches/withoutGrouper/StructureDefinition-genomics-report.html). The genetic findings, implications and region studied profiles all contain links to computably define their relationships (e.g. the variant observation is referenced within the implication profile using derivedFrom).

However, it is sometimes desired to connect observations for visualization. This may be done with a grouping observation. In this version of the specification, no guidance is provided on where or if a grouping observation should be used. This is left up to the discretion of the reporting organization. Observations might be organized for visualization purposes on the basis of subject, specimen, chromosome, gene, condition/disease, medication, etc. The recursive hasMember relationship in observation supports a nested tree-structure of observations when desired for grouping. Please note that more than two levels of grouping observations is likely excessive. This  [example](http://build.fhir.org/ig/HL7/genomics-reporting/branches/withoutGrouper/Bundle-oncologyexamples-r4.html) uses grouping to separately reference variants and other Observations on the report. For a version of the same report without grouping see this [example without grouping](http://build.fhir.org/ig/HL7/genomics-reporting/branches/withoutGrouper/Bundle-oncologyexamples-r4-noGrouping.html). In the examples, the NCI metathesaurus code C43359 (for 'Group' or 'Panel') is used for the grouping the Observation.code field. Genomic panels that have specific codes, such as a specific LOINC code, could also be used if the grouping observation contains all the elements typically reported by the specific panel.

Here is a figure showing a diagnostic report directly referencing the resultant genomic observations without grouping (similar to [this example without grouping](http://build.fhir.org/ig/HL7/genomics-reporting/branches/withoutGrouper/Bundle-oncologyexamples-r4-noGrouping.html) and [this pharmacogenomics example based on EMERGE but without grouping](http://build.fhir.org/ig/HL7/genomics-reporting/branches/withoutGrouper/DiagnosticReport-PGxGenomicsReportEMERGE.html)):