Relationships Help File

Column Headings:

- **Entity1_id**
  - Genes, chemicals (drugs) and diseases are designated by their ClinPGx IDs. Mappings for genes, chemicals and disease names to ClinPGx IDs are found in the “genes.zip”, "chemicals.zip" and “phenotypes.zip” files on the Downloads page. Variants are typically identified by dbSNP rsID, but may be labeled by chromosomal position. Haplotypes are typically identified by haplotype or star allele name, i.e. CYP2D6*4.
- **Entity1_type**
  - Gene, Chemical, Disease, Variant or Haplotype.
- **Entity2_id**
  - Genes, chemicals (drugs) and diseases are designated by their ClinPGx IDs. Mappings for genes, chemicals and disease names to ClinPGx IDs are found in the “genes.zip”, "chemicals.zip" and “phenotypes.zip” files on the Downloads page. Variants are typically identified by dbSNP rsID, but may be labeled by chromosomal position. Haplotypes are typically identified by haplotype or star allele name, i.e. CYP2D6*4.
- **Entity2_type**
  - Gene, Chemical, Disease, Variant or Haplotype.
- ***Evidence***
  - VariantAnnotation, ClinicalAnnotation, GuidelineAnnotation, LabelAnnotation, Pathway, DataAnnotation, Literature, MultilinkAnnotation. Comma separated list because the evidence for a relationship could come from multiple sources in ClinPGx.
- ***Association***
  - Possible values: “associated”, “not associated” or “ambiguous”.
    - “associated” means an association between the entities is supported by the “Evidence” and “PMIDs” columns.
    - “not associated” means that the entities were evaluated but not found have a statistically significant association based on the “PMIDs” column.
    - “ambiguous” means that some of the items in the “Evidence” and/or “PMIDs” columns support an association and others do not.
- ***PK***
  - PK stands for “Pharmacokinetic”. Relationships are marked as PK if the pair of entities was found in a pharmacokinetic pathway on ClinPGx, or if the variant annotation was tagged with PK in some manner.
  - The absence of PK in this column does NOT necessarily mean that there is NO evidence of a pharmacokinetic relationship.
- ***PD***
  - PD stands for “Pharmacodynamic”. Relationships are marked as PD if the pair of entities was found in a pharmacodynamic pathway on ClinPGx, or if the variant annotation was tagged with PD in some manner.
  - The absence of PD in this column does NOT necessarily mean that there is NO evidence of a pharmacodynamic relationship.
- ***PMIDs***
  - PubMed IDs that were used to support the listed relationship. Semi-colon delimited list.

Relationship Types between Entity1 and Entity2:

- ***Variant-Chemical*** associations are derived from a variant annotation or clinical annotation.
- ***Variant-Disease*** associations are derived from a variant annotation or clinical annotation. - ***Variant-Disease*** associations derived from a variant annotation or clinical annotation are really referring to a variant that has an annotation with that “Disease” tag. ***These associations can be misleading because they are not necessarily indications that a variant is directly associated with a disease phenotype.*** For example, in the annotation for rs5275 in PTGS2:
  “Genotype AA is associated with increased progression-free survival and overall survival when treated with capecitabine and oxaliplatin in people with Colorectal Neoplasms as compared to genotypes GG + AG.” rs5275 will be listed in the relationships file as “associated” with “Colorectal Neoplasms”, but in reality the snp is associated with the treatment outcome for capecitabine and oxaliplatin in people who have the condition.
- ***Haplotype-Chemical*** associations are derived from a variant annotation or clinical annotation.
- ***Haplotype-Disease*** associations are derived from a variant annotation or clinical annotation.
  - ***Haplotype-Disease*** associations derived from a variant annotation or clinical annotation are really referring to a haplotype that has an annotation with that “Disease” tag. ***These associations can be misleading because they are not necessarily indications that a haplotype is directly associated with a disease phenotype (i.e., disease risk is not implied).***
- ***Gene-Chemical*** associations are derived from a ClinPGx pathway, a drug label annotation, a clinical guideline annotation, a variant annotation or clinical annotation.
- ***Gene-Disease*** associations are derived from a variant annotation or clinical annotation.
  - ***Gene-Disease*** associations derived from a variant annotation or clinical annotation are really referring to a variant in the gene that has an annotation with that “Disease” tag. ***These associations can be misleading because they are not necessarily indications that a gene is directly associated with a disease phenotype.*** For example, in the annotation for rs5275 in PTGS2: “Genotype AA is associated with increased progression-free survival and overall survival when treated with capecitabine and oxaliplatin in people with Colorectal Neoplasms as compared to genotypes GG + AG.” PTGS2 will be listed in the relationships file as “associated” with “Colorectal Neoplasms”, but in reality the gene is associated with the treatment outcome for capecitabine and oxaliplatin in people who have the condition.
- ***Gene-Gene*** associations are derived from a ClinPGx pathway in which one gene influences another gene (direct connection from pathway arrows).

NOTE: Relationships are listed 'bi-directionally' in the file so that each one is listed twice: "A - B" and "B - A". No biological directionality is implied in the relationship.