Rules for Data Use

1. You may not upload specific patient identifying information into the system. You may upload (or have uploaded for you) any data relating to the "Aggregate Variant-Level Data Fields" indicated below.

2. Data from other laboratories on the network cannot be used for research or publication without prior permission from the laboratory owning the data (see below section on 'variant data access'). This includes use of datasets that originated from other laboratories even if currently housed in a single lab.

3. Any publications that result from knowledge/data shared through the COGR will acknowledge COGR in their publication.

Variant Data Access

- We will allow participating laboratories to initially upload their variant classifications into the system without turning on the sharing mechanism. This means that variant data will not be shared by them or with them until the laboratory has indicated their willingness to share data.

- We intend to support programmatic access for all variant classifications (without text-based interpretation summaries) so that labs can integrate this information into their bioinformatic pipelines. Laboratories will only have access to their own data and to the consensus data of the centralized COGR instance. A comprehensive list of shared data points is located below under "Aggregate Variant-Level Data Fields".

- Each laboratory retains rights to their own data and this data can only be accessed and downloaded by authorized users within that laboratory. Data uploaded to the COGR's centralized repository is automatically attributed to the contributing laboratory. If you choose to share your data with the COGR network, your variant level data can be viewed by other laboratories on a variant by variant basis. Individual laboratories can only download their own variant datasets and not variant data from other sharing laboratories. This function exists to discourage the download of other laboratories datasets without authorization, i.e., no bulk downloading (aka. 'leaching') of data from other members is allowed.. If members are found to try and exploit data and the principles of the COGR initiative, the members will be warned, censured and if necessary asked to leave.

- Variant consensus data (decided on by consensus workgroup meetings), will be made available for use by consortium members through the 'consensus' COGR instance. This consensus variant data will be made available to patient advocacy groups in an

aggregated form on the COGR website (www.opengenetics.ca). Specific laboratory related data or other information will not be made available to the broader community.

- Variant interpretation summaries must be viewed manually through the user interface. Each laboratory must make a variant by variant decision whether to "promote" another laboratories variant interpretation and make it their own. The purpose of this rule is to discourage wholesale copying of another laboratory's knowledge base. Each laboratory must review and accept other laboratory interpretations before incorporating them into their own knowledgebase.

- Rules for use: It is acceptable to bring in and use (with or without modification) variant interpretation summaries from clinical reports without acknowledging interpretation history. However, other uses require permission (e.g., publications, abstracts, third party sharing). The system will track importation of variant interpretation summaries. Note: If several labs contribute to a variant interpretation, all can claim full ownership. A future enhancement will show better visibility of the complete audit trail of a variant's interpretive history.

- It is recommended that if a lab uses any networked data to inform their own interpretation they should annotate what date and from what lab they imported the data.

- You may withdraw from the collaboration and have your variant data removed from the system at any time. To withdraw from the consortium you can do so by notifying the COGR management team. Any variant information that is shared and used to form a consensus variant interpretation will remain part of the COGR consortium.

- If a lab leaves the network, it is acceptable for them to maintain information on the variants they created or reported using the system, but other information (e.g., interpretation/classifications on non-reported variants) from the network must be removed/destroyed. It is the labs decision whether they would like to have their data removed from the network or if they would like to leave their data in the network with a note that this variant will no longer be updated.

- In the event the COGR Consortium is terminated, a 'data migration' plan will be formulated by discussion. This will guide the preservation of the consensus data and data already in the public domain for future use by the broader community. Members will be able to download their data without restriction and assistance offered with bulk extraction from the individual member's instances if needed.

- Future builds of GeneInsight will enable individual laboratory variant data or COGR consensus variant data to be pushed to ClinVar or other public databases by agreement of the data owners.

Aggregate Variant-Level Data Fields Shared among Network

- Alias(es)
- Allele name
- Amino Acid change
- Amino Acid change type
- DNA change
- DNA change type
- Compound type (in cis, in trans)
- Gene Region
- Transcript ID
- Alignment(s) (all validated alignments from source)
    - Genome build name
    - Start and End positions
    - Wild type sequence
    - Variant sequence
- Nested variant(s) (if parent variant is compound)
    - Same as variant info, but without interpretation revisions
- Reference(s)
- Abstract
- Comments
- Author
- Journal Details
- Publication Year
- Source (Identifier/Type)
- Title
- URL (if type is URL)
- Gene Identifier (first Gene Identifier with a code system associated to the variant's gene)
- External ID (A unique identifier which makes the record of that variant within a certain lab totally unique)
- Report Allele Name
- Report DNA Change
- Report AA Change
- Splicing Impact (if available)
- dbSNP ID
- # of Families
- # of Reports
- Source (ID/Name) (Modifiable fields that are intended to record the source of the variant information when it was originally entered. Typically this would be a database [e.g., COSMIC, dbSNP, CardioGenomics] and the identifier assigned to the variant in that database)
- Current Interpretation Revision Approval
    - Note 1: If variant currently has a proposed interpretation (i.e. has not been approved) only the date & time of the proposal will be displayed.

    - Note 2: Depending on the configuration of the receiving instance, only interpretations related to existing diseases in the receiving instance are processed.
    - Content Approval (by User, on Date)
    - Approval (by User, on Date)
    - Reason for Update
    - (For each interpretation)
        - Category Type (Med Sig, Unk. Sig, Incidental)
        - Category Code
        - Inheritance
        - Interpretation Text
        - List of Disease Codes (if applicable)

Working Groups

- Will be comprised of representatives from the participating COGR laboratories.

- Methods for evaluating discrepant variant classifications for each disease areas are currently under discussion. Either working groups or individual laboratories will be involved in resolving discrepant variants interpretations that can be shared with the broader community.

Objectives of Working Groups

- To provide guidance and recommendations leveraging the COGR and other national clinical genomics efforts/initiatives to support and advance genetic-based medicine through better clinical interpretations.

- To assist in developing overall strategy for the adoption and use of variant knowledge to drive/support high quality, reliability, and efficiency of clinical reporting.

- Stimulate concept development among thought leaders and enable dissemination of innovative approaches for the benefit of the COGR members and ultimately to the broader clinical genetics community.

Process for Resolving Governance Issues

- It is possible that governance issues could arise concerning differences of opinion on which laboratories to admit to the network, whether laboratories are adhering to these guidelines or whether there is a need for new guidelines. Should this occur, the COGR PIs will circulate a proposal for resolving the issue. Comments will be solicited and used to refine the proposal. If there is consensus on the proposal it will be adopted. If there is not consensus, the COGR PIs will make a decision. However, each member laboratory will always have the option of discontinuing sharing with any other member. They can choose to exercise this option if needed as a result of one of these decisions.