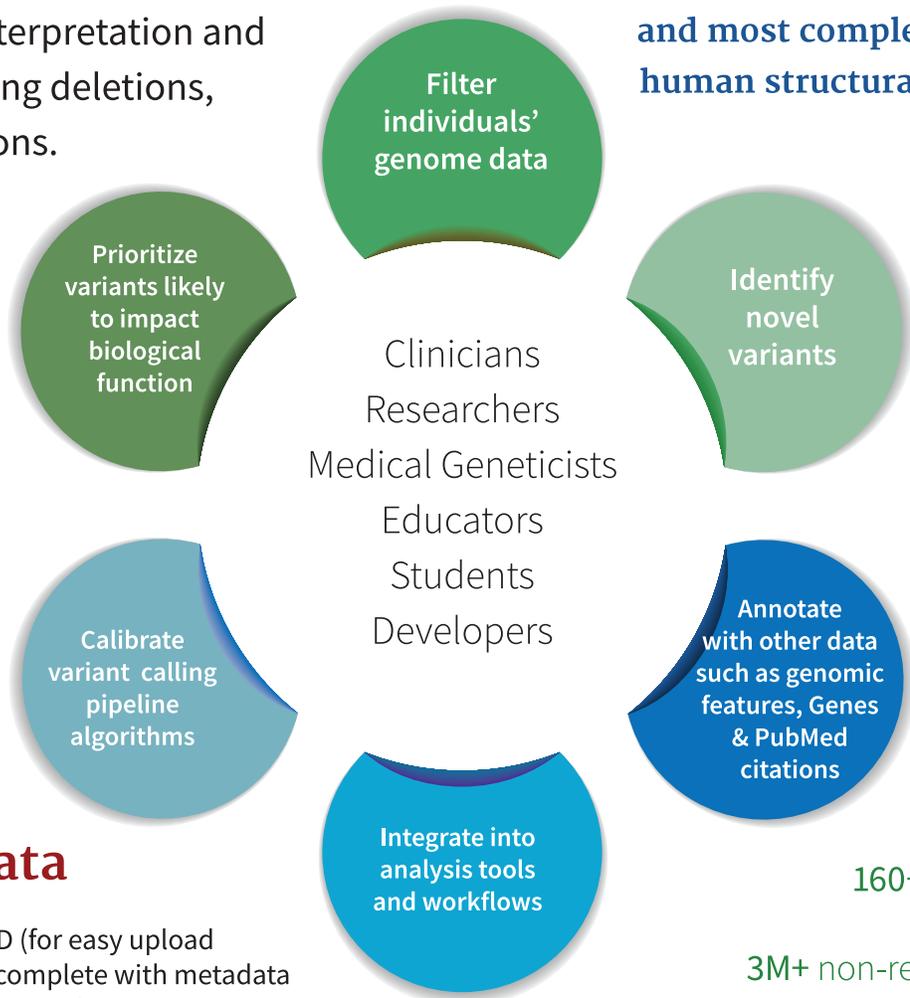


New non-redundant structural variant (NR-SV) datasets to aid variant interpretation and disease discovery including deletions, duplications, and insertions.

Your best source for the latest and most complete sets of human structural variants



How to Use dbVar Non-Redundant Data

- Available in three formats – BED (for easy upload to genome browsers), BEDPE (complete with metadata for more detailed analyses), and TSV (custom tab-delimited format for downstream annotation and analysis)
- Access on Github at <http://bit.ly/NCBIInrSVs>
- Review QuickStart.md and/or ToolGuide.md for use case examples
- Intersect dbVar's non-redundant (NR) files with other genomic interval files using popular tools and browsers, such as **NCBI's Sequence Viewer**, **Bedtools**, **Galaxy**, and **UCSC Genome Browser**
- Run a comparison or workflow using your custom data and dbVar NR-SV files. For example, use dbVar's NR-SV data to generate a map of ClinVar loci where SV has been implicated.

160+ Studies

3M+ non-redundant structural variants

updated monthly

