

- Targeted/Whole Exome Sequence Data Workflow
 - vcf file → SummarizedExperiment
 - SummarizedExperiment → FamilyExperiment
 - Construct trio-states
 - mendelian inconsistencies
 - TDT
 - ScanTrios
- Array Data Workflow
 - data files → GWASTools ncd files and objects
 - data files → trioSetList objects
 - trioSetList → de novo deletions (GRanges)
 - de novo deletions → CNVMatrix