

# Workflows for Copy Number Variants in VarSeq A Users Perspective

Steve Hystad – Field Application Scientist

**CIOReview**

20 most promising  
Biotech Technology  
Providers

**pharma**  
TECH OUTLOOK

Top 10 Analytics  
Solution Providers

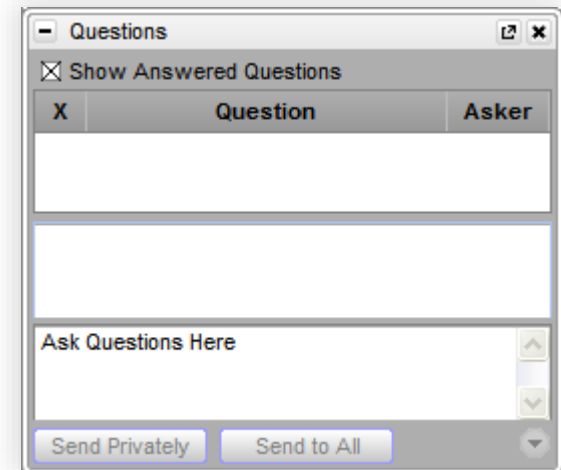
**Gartner.**

Hype Cycle for  
Life sciences



# Questions during the presentation

Use the Questions pane in your GoToWebinar window



# Golden Helix – Who We Are



Golden Helix is a global bioinformatics company founded in 1998.



Variant Calling  
Filtering and Annotation  
Clinical Reports  
CNV Analysis  
Pipeline: Run Workflows

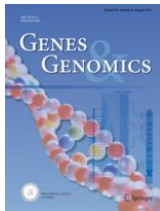
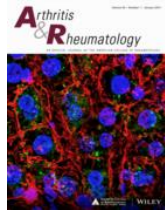
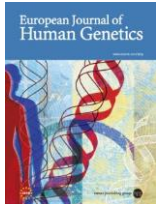
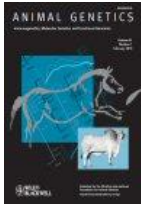
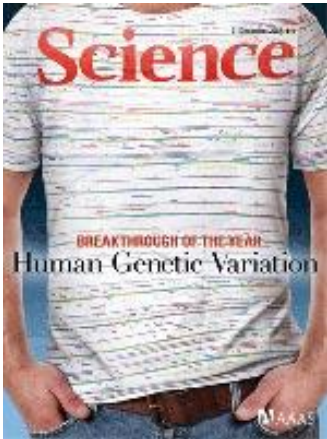


Variant Warehouse  
Centralized Annotations  
Hosted Reports  
Sharing and Integration

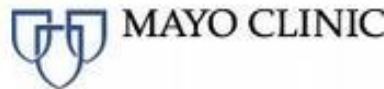


GWAS  
Genomic Prediction  
Large-N-Population Studies  
RNA-Seq  
Large-N CNV-Analysis

# Cited in over 1100 peer-reviewed publications



Over 350 customers globally

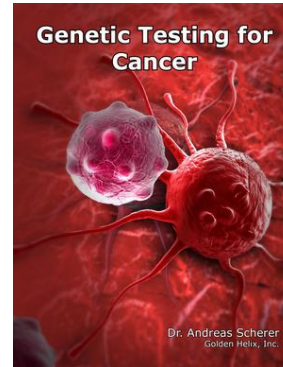


# Golden Helix – Who We Are



When you choose a Golden Helix solution, you get more than just software

- REPUTATION
- TRUST
- EXPERIENCE



- INDUSTRY FOCUS
- THOUGHT LEADERSHIP
- COMMUNITY

- TRAINING
- SUPPORT
- RESPONSIVENESS



- INNOVATION and SPEED
- CUSTOMIZATIONS

**SEQUENCER**

**PRODUCTS**

**BIOINFORMATICS PIPELINE**

**FUNCTION**



VS-CNV



SENTIEON DNASEQ



SENTIEON TNSEQ

OMIM SIFT & POLYPHEN CLINVAR ENSEMBL GENES  
CADD EXAC & GNOMAD EXOMES DBSNP REFSEQ GENES  
ONCO MD CONSERVATION SCORES COSMIC

FASTQ

SINGLE NUCLEOTIDE VARIATION

BAM

COPY NUMBER VARIATION & LOSS OF HETEROZYGOSITY

VCF

CHROMOSOMAL ABERRATION

**ANNOTATE**

PUBLIC & COMMERCIAL ANNOTATIONS  
TO ENRICH GENOMIC DATA SETS



VARSEQ

VSREPORTS

VSPipeline

**CLINICAL REPORT**

ANNOTATE & FILTER  
VISUALLY INSPECT ALIGNMENTS  
VARIANT PRIORITIZATION  
CLINICAL ASSESSMENT



WAREHOUSE

**DATA WAREHOUSING**

CLINICAL ASSESSMENT CATALOG  
ADVANCED DATA QUERYING  
VERSIONING

WEB-ENABLED INTERFACE  
+ POWERFUL API: JSON, XML  
TSV, CSV, SQL, FHIR

INTEROPERABILITY  
COMPLIANCE WITH HIPAA, CLIA, & CAP  
DATA DISCOVERY



## ■ VS-CNV

- Call CNVs from Gene Panels

## ■ VS-CNV 2.0

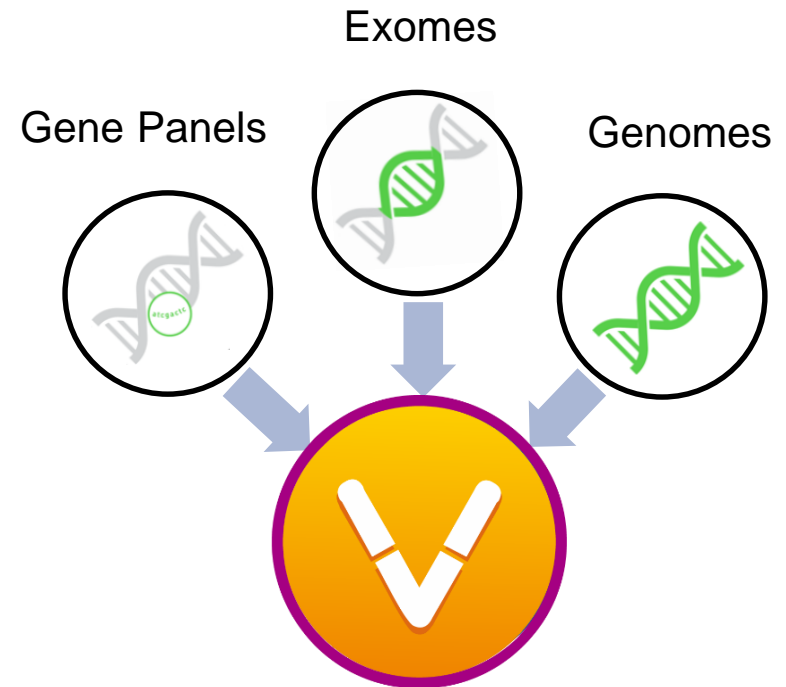
- Call large and small CNVs & LOH on Exome datasets

## ■ Whole Genome Sequence CNV Caller

- Call CNVs from low and ultra low read depth datasets.
- Call CNVs from the command line

## ■ CNV annotations

- Quickly examine clinically relevant CNVs
- Reduce false positives and filter out common CNVs
- Capture and store clinical CNV assessments



**Annotate and Filter**

**VS-CNV**



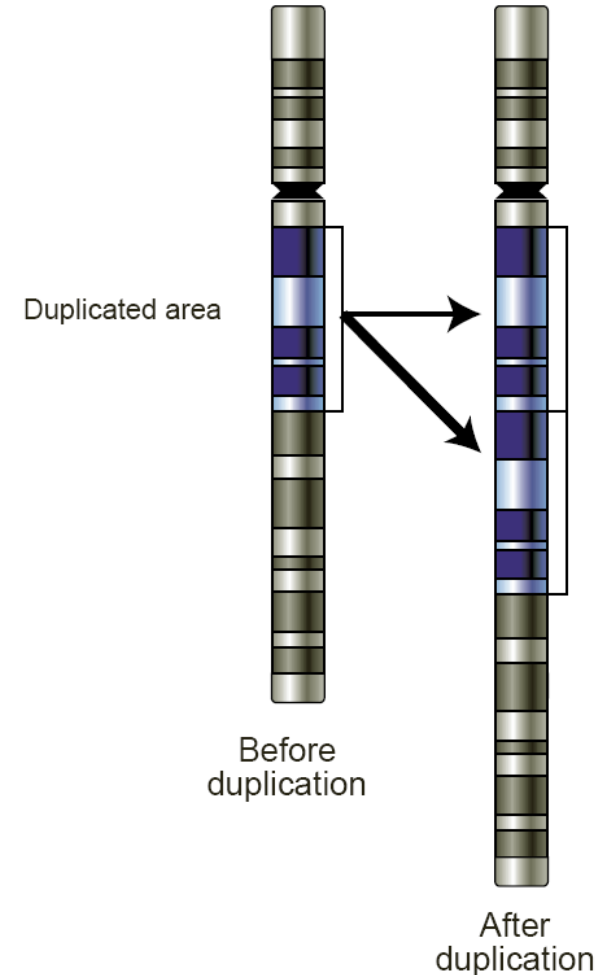


- **Chromosomal microarray**

- Current best practice
- Slow
- Additional expense
- Only detects large events

- **CNV calling from NGS data**

- Calls from existing coverage data
- Detects small single-exon events
- Provides faster results, simplified clinical workflow

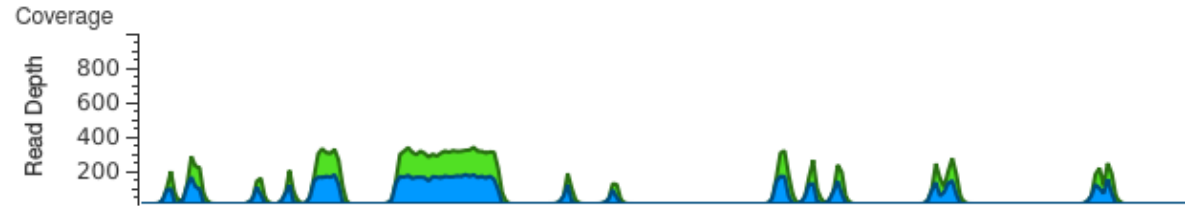


# CNV Detection via NGS

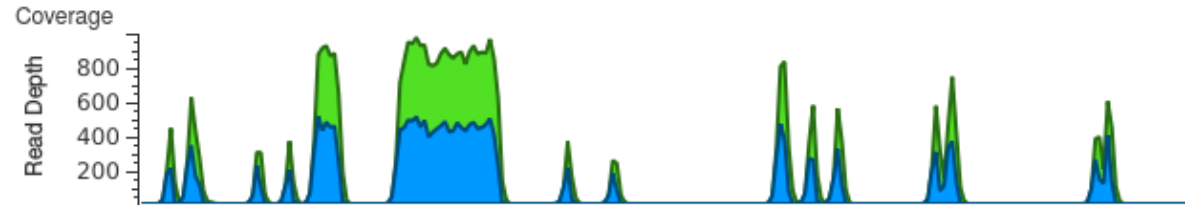


- **CNVs are called from coverage data**
- **Challenges**
  - Coverage varies between samples
  - Coverage fluctuates between targets
  - Systematic biases impact coverage
- **Solutions**
  - Data Normalization
  - Reference Sample Comparison

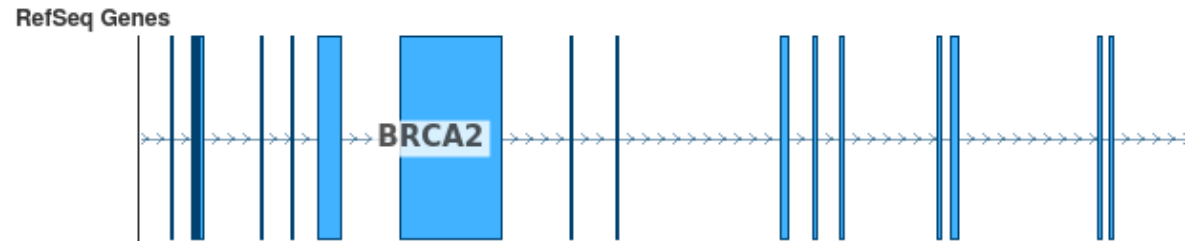
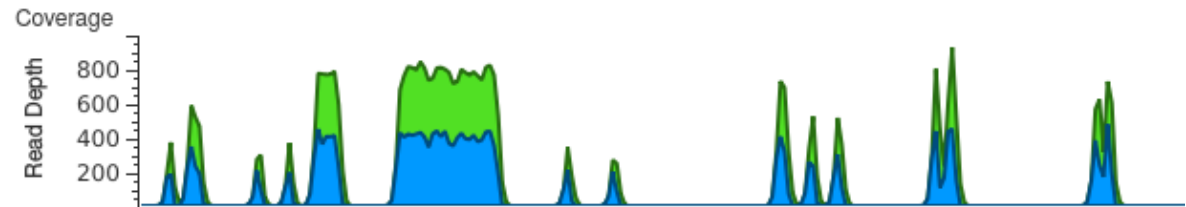
Current Sample: RD-NGSPROGENITYCANCER-SAMPLE11



Current Sample: RD-NGSPROGENITYCANCER-SAMPLE12



Current Sample: RD-NGSPROGENITYCANCER-SAMPLE13



# CNV calling in VarSeq



- **Reference samples used for normalization**

- **Metrics**

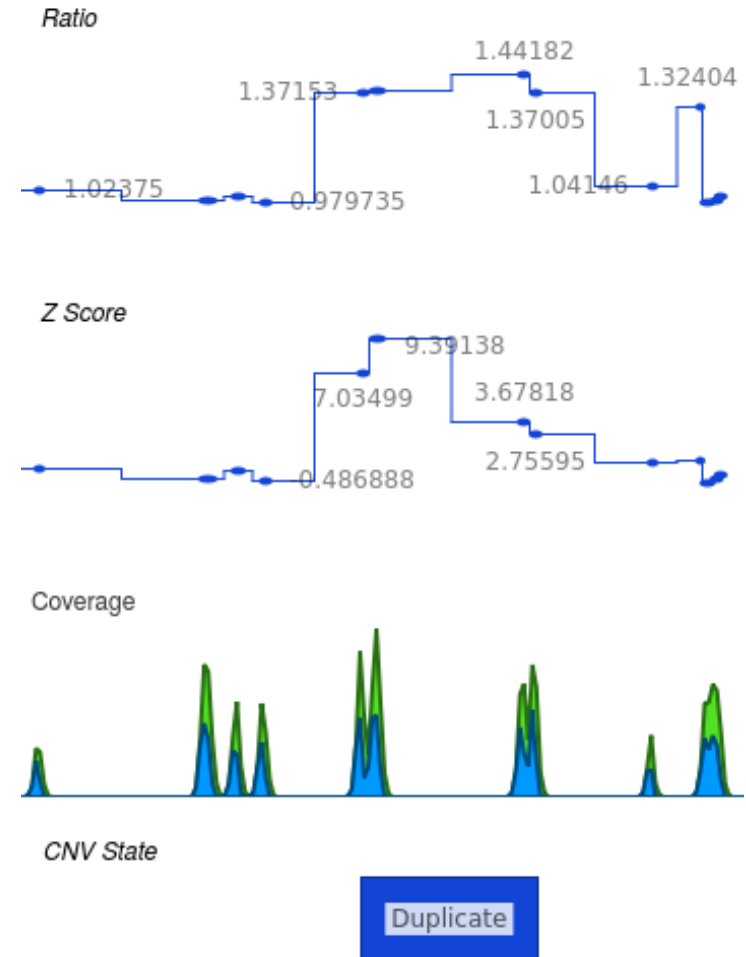
- Z-score: number of standard deviations from reference sample mean
- Ratio: sample coverage divided by reference sample mean
- VAF: Variant Allele Frequency

- **For Gene Panels and Exomes**

- Probabilistic model used to call CNVs
- Segmentation identifies large cytogenetic events

- **For Whole Genome Data**

- Targets segmented using Z-scores
- Events called based on Z-score and Ratio thresholds



# Annotations



- **Genes**



- **Clinical Assessments**



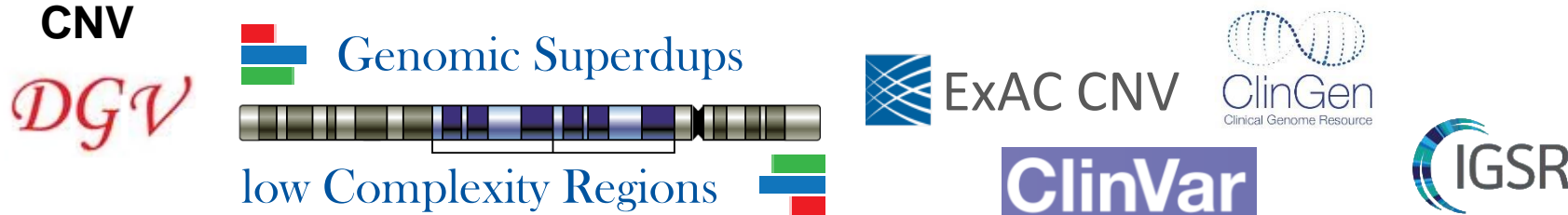
- **Population Frequencies**



- **Cancer**



- **CNV**



# Sample Data for Single Exome Analysis



- **Four Single Exome Samples**
- **BAM files from 1000 Genomes Phase 3 Illumina Exome Alignment**
- **Used Sentieon tools for variant calling.**

Sample CRExome-18 has chronic history of stomach ulcers and reported hearing impairment phenotype.





## ■ VS-CNV

- Call CNVs from Gene Panels, Exomes, and WGS

## ■ CNV annotations

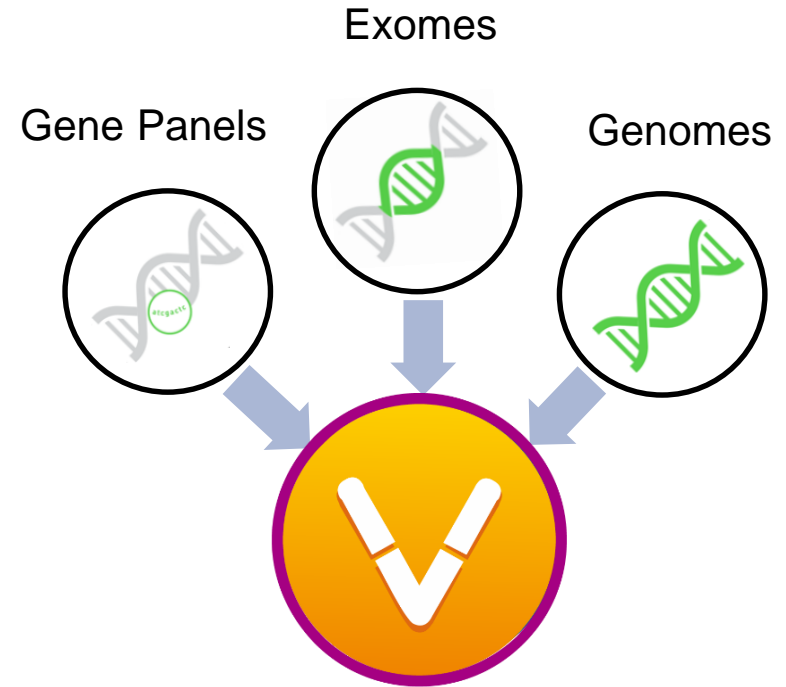
- Quickly examine clinically relevant CNVs
- Reduce false positives and filter out common CNVs

## ■ CNV algorithms

- Complete control over annotations
- Match Gene linked to Phenotype
- CNV Phorank!

## ■ CNV Assessment Catalogs

- Build knowledge base
- Plot, Annotate, and Repeat



**Annotate and Filter**

**VS-CNV**



## ■ Webcasts

- **CNV Analysis in VarSeq** – December 7<sup>th</sup> 2016
- **Calling Large LOH and CNV Events with NGS Exomes** – March 8<sup>th</sup> 2017
- **CNV Analysis in VarSeq – A User’s Perspective** – April 19<sup>th</sup> 2017
- **Comprehensive Clinical Workflows for CNVs in VarSeq** – Sept 27<sup>th</sup> 2017

## ■ Tutorials

- VarSeq CNV Caller Tutorial

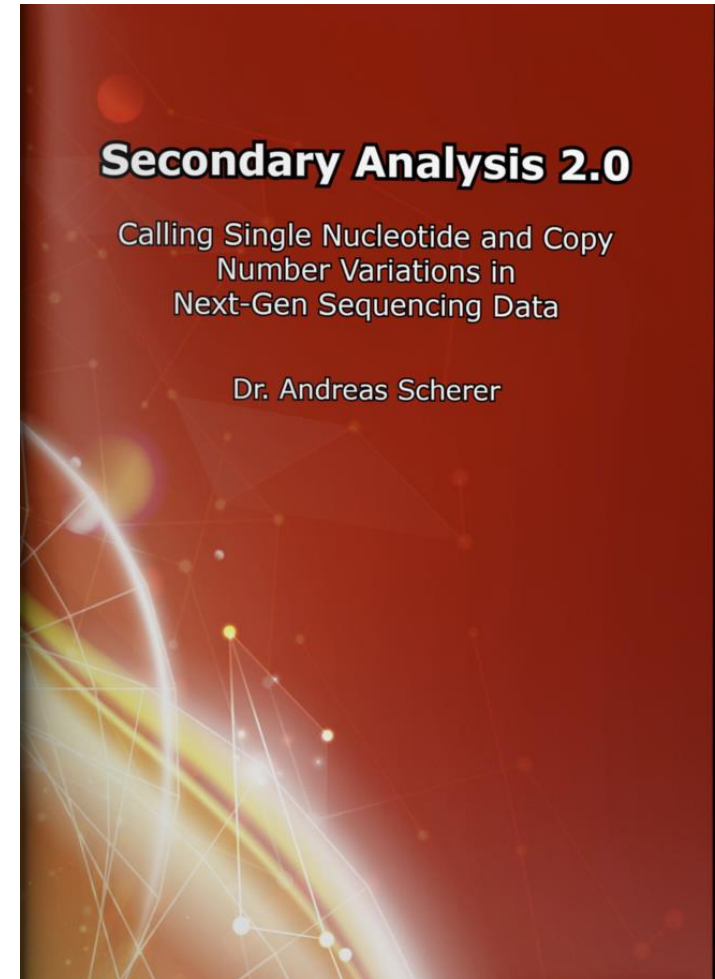
## ■ Support from Field Application Scientists

- [Support@Goldenhelix.com](mailto:Support@Goldenhelix.com)





- **Secondary Analysis ebook**
  - Calling SNVs & CNVs from NGS data
  
- **Golden Helix at ASHG 2017!**
  - Booth 902
  - Come see demos and ask us questions!
  
- **VarSeq CNV Powerpack (end Oct)**
  - *VarSeq + VSCNV + Sentieon + VSReports* - \$ 15,995
  
- **SVS & VarSeq Bundle**
  - CADD & OMIM included - \$7,995
  
- **Small Lab Warehouse + VS-CNV**
  - 2 users \$36,00





# Questions or more info:

- Email [info@goldenhelix.com](mailto:info@goldenhelix.com)
- Request an evaluation of the software at [www.goldenhelix.com](http://www.goldenhelix.com)

