

# MED AVANT AND PhenoTips

INTEGRATING GENOTYPE AND PHENOTYPE DATA



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**SickKids**<sup>®</sup>

**FORGE**  
CANADA CONSORTIUM

# From Genome to Genomic Medicine



- shift: **interpretation and analysis** challenge
- genome browsers made for single genomes, not cohorts
- disconnect between tools used for data analysis and visualization



Marc Fiume

SAVANT & MEDSAVANT: BROWSERS FOR MEDICAL SEQUENCING

# Savant Genome Browser



- Dynamic Visualization of HTS Datasets (BAMs, VCFs, etc.)
  - Local or Remote
- Integration with External Databases (e.g. UCSC)
- Plugin Framework Allows for Extension

# Savant Plugin Framework

- **unlocks the potential for performing visual analytics**
- **mutually beneficial** for both users and tool developers

**for users:** perform complex data analyses on-the-fly within a visual environment

**for programmers:** platform for simple development and deployment of new tools

- Some Savant Plugins
  - RNA-seq analyzer, EdgeR Differential Abundance Estimator, Application Wrapper, GO Navigator, WikiPathways Navigator, Data Table... (16 and counting)

# MedSavant: Where to look?



 SAVANT



MED  AVANT

# Database



## Contents

- patient: e.g. age, gender, family
- phenotype: e.g. symptoms and scores
- genotype: e.g. variants

# Query Engine



## Filters

- set of user specified rules that **remove low quality or uninteresting variants** on the basis of:
  - basic patient data, phenotype data, genotype



# Visualization Framework



## Charts and Tables

- graphical presentation of trends in the data:
  - **summary** : histograms, pie charts
  - **aggregate** : over genomics regions, ontology terms

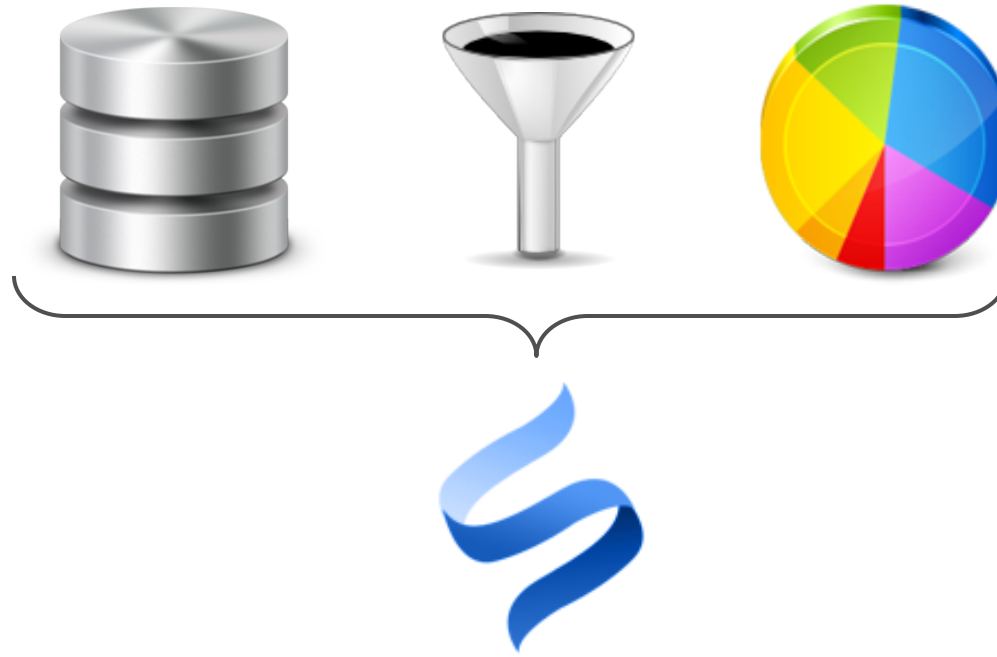
# Tools for processing genetic variants



- powerful
- expert use
- difficult to maintain

- not as powerful
- easy to use
- difficult to maintain

# Introducing MedSavant



- powerful
- easy to use
- easy to maintain

DEMONSTRATION

## Conclusions

- MedSavant is a platform for **efficient storage, filtering, and visualization** of genetic variants

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- **Accelerating the discovery of causal variants** in disease sequencing studies

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- Plugin framework enables **integration of cutting-edge tools for genetic variant analysis**

<http://medsavant.com/>



Marta Girdea

PHENOTIPS: PATIENT PHENOTYPING TOOL AND DATABASE

# Phenotyping for FORGE

- Rare Disorders Are not Always Named
  - Important to collect phenotype data to cross-reference against cases observed across the country
  - Currently Two Alternatives: free text or checkboxes

## Dysmorphic features

- df
- dysmorphic
- dysmorphic faces
- dysmorphic features

## Congenital malformation/anomaly:

- congenital anomaly
- congenital malformation
- congenital anomaly
- congenital anomaly
- congenital anomaly
- congenital anomaly
- congenital anomaly
- cong. m.
- cong. Mal
- cong. malfor
- congenital malform
- congenital m.
- multiple congenital anomalies
- multiple congenital abnormalities
- multiple congenital abnormalities

## Phenotypic description (Clinical symptoms)

### Behavior, Cognition and Development

- Global development delay
- Fine motor delay     Gross motor delay
- Language delay
- Learning disability
- Mental retardation

### Examples of lists:

\* Moderate dd. cong. malfor. behav. pro.

\* Severe dd. mental retardation

Attention deficit hyperactivity disorder

Autism

Pervasive developmental delay

Psychiatric disorders (Specify below)

Other: mental retard short stature

### Neurological

- Hypotonia
- Seizures
- Ataxia
- Dystonia
- Chorea

### Cardiac

- ASD
- VSD
- AV canal defect
- Coarctation of aorta
- Tetralogy of fallot
- Other: \_\_\_\_\_

### Craniofacial

- Craniosynostosis
- Cleft lip                       Cleft palate
- Microretrognathia         Retrognathia
- Facial dysmorphism (Specify below)
- Other: \_\_\_\_\_

### Eye Defects

- Blindness
- Coloboma
- Epicanthus
- Eyelid abnormality (Specify below)
- Other: \_\_\_\_\_

## What about Ontologies?

- Extensive Ontologies Describe Human Phenotypes:
  - London Dysmorphology Database
  - Human Phenotype Ontology
  - SNOMED
- Initial Reaction from Clinical Geneticists:
  - Absolutely not, too complicated
- So Can We Make it Simple?



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## PhenoTips

- All FORGE patient phenotypes will now be recorded through the web UI (NO PAPER!)
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- Working to install similar database at SickKids for Clinical Geneticists and Molecular Diagnostics
- 

- Simple User Interfaces can make (even) Clinicians use Computers 😊

# Acknowledgements

## MedSavant Team

Marc Fiume, Andrew Brook, Nirvana Nursimulu, Margie Manker, Justin Foong

<http://genomesavant.com/med>

## PhenoTips Team

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MITACS



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