

# Analysis tools and portals

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Boston College

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Sequences in a central place, variant recalled or aggregated, metadata and phenotype harmonized ...

... what tools are needed make the data useful for the community?

# What type of analyses can we do?

- Population genetic
  - Haplotype phasing
  - Single-variant allele frequencies
  - Variant burden
- Functional
  - Coding annotations
  - Disease databases
  - Non-coding annotations
  - Loss of Function analyses
- GWAS
  - Meta-analysis
  - De novo analysis
- Systems biology / higher order analyses
  - Network / pathway analysis

- Well-defined vs. open-ended
- Algorithmically easy vs. hard
- Tools mature vs. emerging
- Computation-heavy vs. light

# Who are we trying to serve?

Statistician / tool developer

How does my tool perform?

What's different about the non-responder?

Drug developer

Is this variant associated with any known phenotype?

Biologist in small laboratory

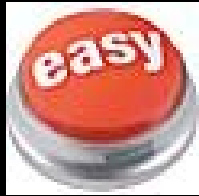
Do I get a bigger p-value from all the extra samples?

Medical consortium project analyst

I see a variant in this gene... should I alter the treatment of my patient?

Clinician

# How to make analysis accessible?

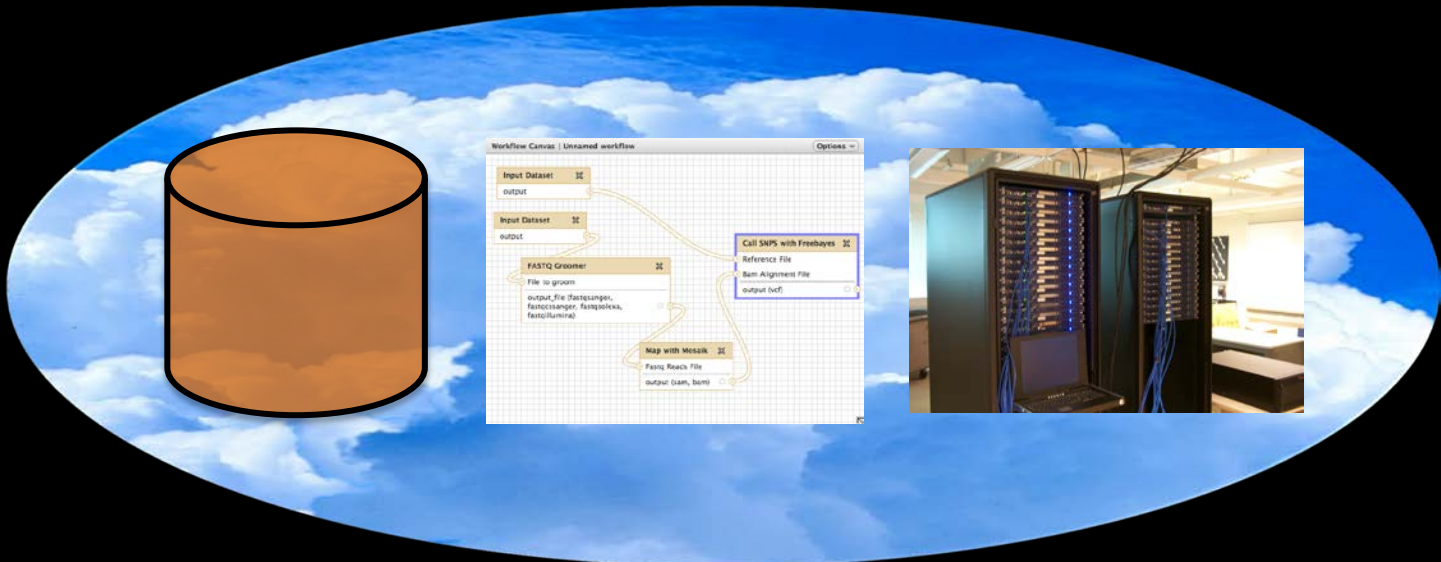


- Easy to install
- Easy to use
- Intuitive
- Fast
- Interactive
- **Web-based**
- Storage & hardware
- Informatics expertise



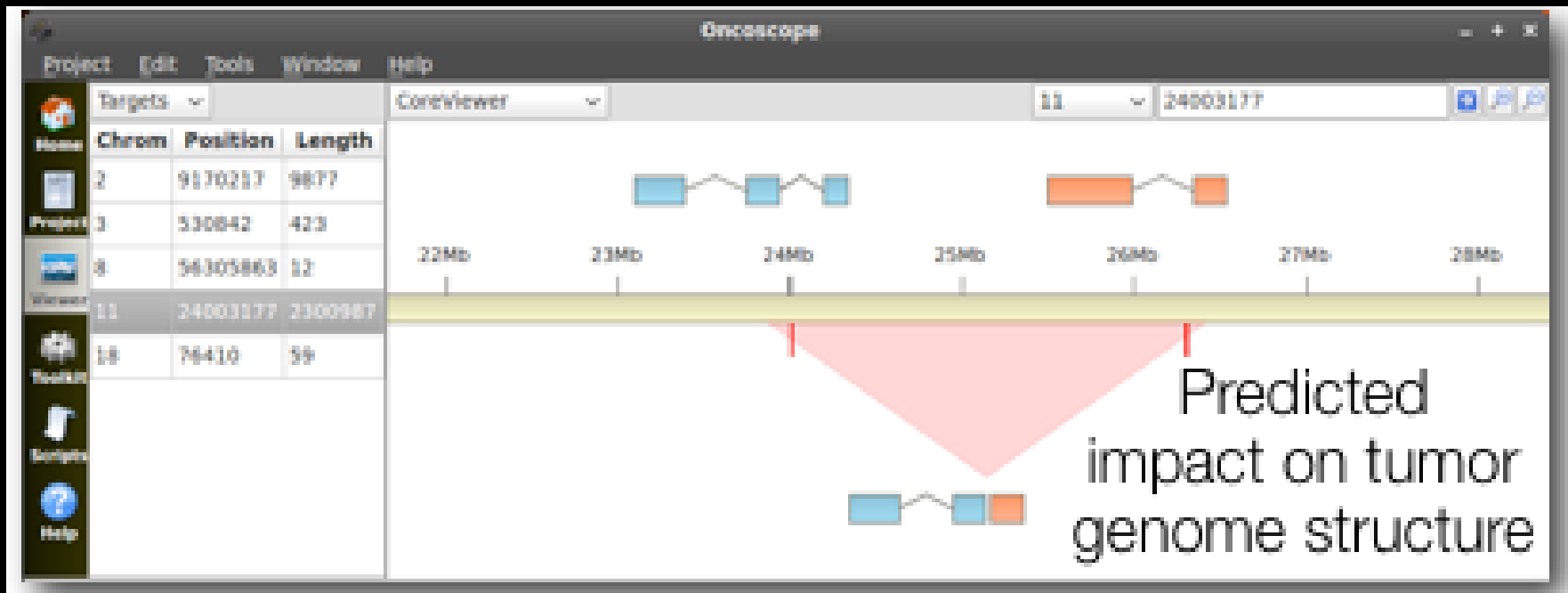
# How can we provide the analyses?

- Raw data download
- Query portals, viewers, data slicers
- Static variant annotations, pre-computed resources
- Analysis environment with **central data**, facilities for users to add their **own data**, **tools installed** and **computational resources** to run the analysis



# What static analyses make sense?

- Variants, variant allele frequencies, sample genotypes
- Phased haplotypes

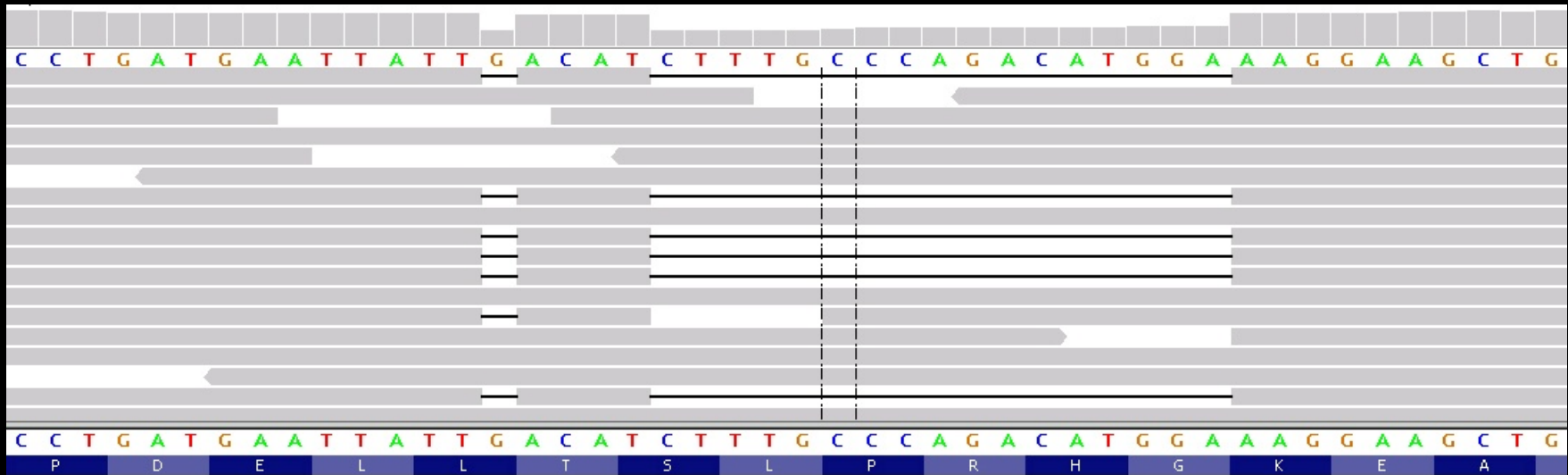


variant consequence

- Haplotype browsing
- Phenotype browsing

# What tasks require analysis services?

- Read mapping, and variant calling



(Daniel McArthur)

- This category has the highest tool development cost because of the additional engineering required



# One tool or multiple tools?

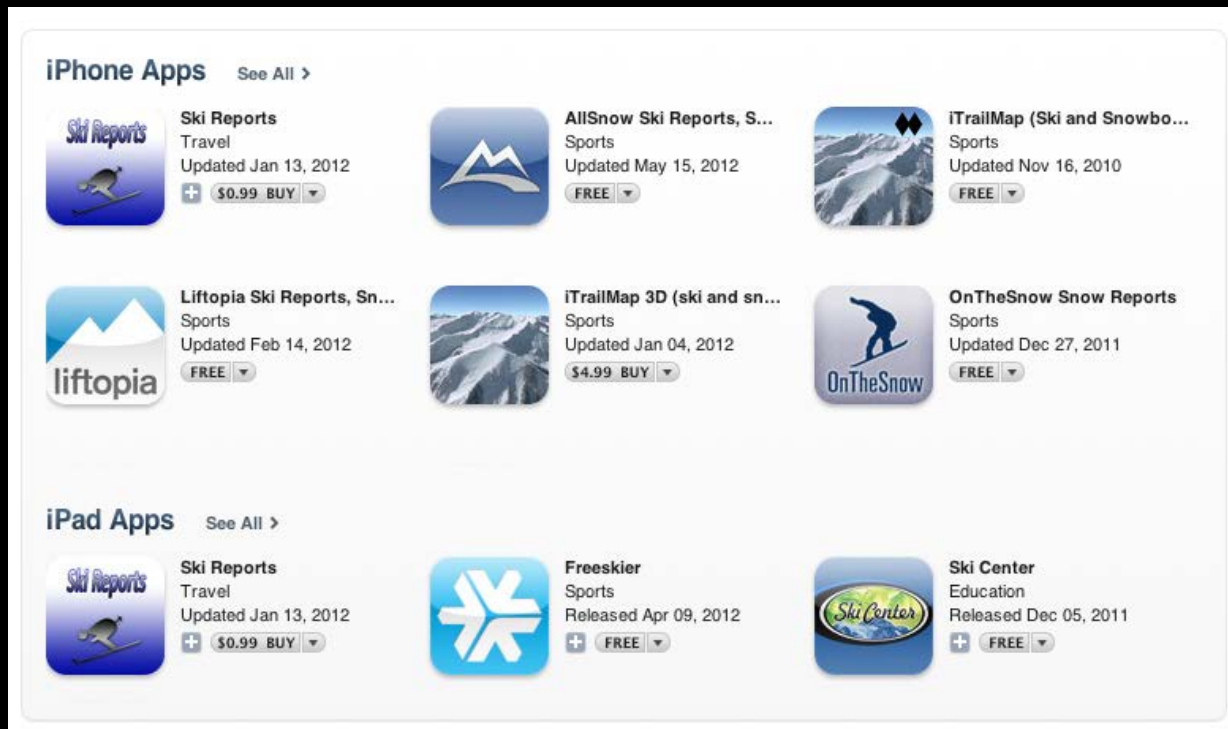
Dataset	SNPs	FP metric Total
Tool 1	632,344	2.32
Tool 2	547,173	2.34
Tool 3	576,125	2.36
Tool 4	629,761	2.26

Dataset	SNPs	FP metric Ts/Tv
4 of 4	410,243	<b>2.56</b>
3 of 4	518,407	<b>2.50</b>
2 of 4	593,538	<b>2.42</b>

There are inherent advantages to having alternative tools available

# Centralized or distributed development?

- Tool development is iterative... once we get an answer, we want to ask a new question
- Often users are better served by light, flexible tools for customized analysis... a **tool ecosystem**



# Who would develop the tools?

- Many current tools from large genome centers but the majority from smaller tool development groups
- There is also a large and successful “cottage industry” of tool development, where small informatics groups can produce very sophisticated software, and respond nimbly to user needs

# How to move forward?



- Focus on the cloud
- Build an open environment for tool deployment to pull in the widest possible developer base
- Models and technologies exist (iPhone apps, etc.)