

# Updates, musings and thoughts from CGP



# COSMIC

- ◆ Catalogue Of Somatic Mutations In Cancer.
  - ◆ <http://cancer.sanger.ac.uk>
- ◆ Using GBrowse since 2010.
- ◆ To switch to JBrowse Feb 4<sup>th</sup> 2014 (10 year anniversary).

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# Internally

- ◆ Fully migrating to JBrowse within next few weeks.
- ◆ Listing based configuration script
  - ◆ Simple TSV table of data files
  - ◆ Simple config file
  - ◆ 1,000s of JBrowse tracks in seconds

# JBrowse

- ◆ LDAP
- ◆ Tweaks to VCF
  - ◆ Filter descriptions on mouse over (in track menu)
  - ◆ Customise individual fields of default popup
- ◆ Legends in track menu

# VariantService

- ◆ Webservice for exposing VCF data.
  - ◆ Java/Resin
- ◆ REST(ish) – some polishing required.
- ◆ Range query and Filtering.
- ◆ Conversion to gff3 or tsv on fly.
  - ◆ Originally written to allow use of VCF data in GBrowse rather than converting to GFF3/SeqFeatureDb

# Vagrent

- ◆ Variation Annotation Generator
- ◆ All transcripts annotated, including effect on:
  - ◆ mRNA, CDS, protein sequence
- ◆ Uses SO terms (many added during development)
- ◆ Fast
  - ◆ Uses BED intersect to determine if variant is within gene footprints (+-5kb)
  - ◆ Optionally caches annotations for speed.
- ◆ Can plug in any gene/transcript source (with configuration).

# FileTrk

- ◆ File management system for groups with little IT support.
- ◆ Simple, can reference Database tables/PKs, rows of a spreadsheet or stored metadata for file meta-data.
- ◆ Pg, Oracle, MySQL and SQLite for management.
- ◆ Can use any underlying filesystem for storage
  - ◆ Concept of *reserving* space before computation.
- ◆ Perl API, but others may follow.
- ◆ Expected release in next 6 months.