The JBrowse Cancer Genome Browser

Ian Holmes
ITCR Meeting 2019
JBrowse

- All-JavaScript genome browser (can run as desktop app)
  - Grew out of the Generic Model Organism Database (GMOD) project, and its genome browser GBrowse
- Works as a static site: the most secure and performant way to web
  - Relies on fast pre-built indices (tabix, NCList)
- Emphasizes standards and code re-use
  - Parsers on GitHub for many standard formats (fasta, gff, bed, bigbed, sam, bam, wiggle, bigwig, cram, vcf…)
- >30k monthly active users, COSMIC one of biggest
gwasviewer

multibigwig

qualityglyphs

myvariantinfo

multivariantviewer

SVG Lollipop - Demo

HTML Features - Features with right-click menus

proportionalmultibw

JBrowse Plugin Registry
gmod.github.io/jbrowse-registry/
JBrowse 2: Priorities

- Modernization
  - **Web**: React components, state management, modularization, webpack/babel transpilation
  - **Genomics**: new formats (e.g., CRAM), track hubs, scaling

- Cancer applications
  - Genomic context of **structural variants**; breakpoints, circular view
  - Prebuilt human image at hg38.jbrowse.org (more to come)
    - Includes Dynamix (Monfort et al.), an AI for track recommendation
  - Rendering **genomic synteny** (c.f. GBrowse-Syn)
ITCR collaborations

- CIViC: protein variant browser (prototype)

- CNVnator: display output of CNVnator in JBrowse

- If you produce data that could benefit from visualization in genomic context, consider adapting a genome browser (they are extensible!) vs. developing your own
Thanks!

- Developers
  - Rob Buels
  - Colin Diesh
  - Garrett Stevens
  - Andrew Duncan
  - Eric Yao
- Outreach
  - Robin Haw
  - Scott Cain
- Lincoln Stein