Practical Introduction

Variant Calling and Filtering for INDELs

December 9, 2014

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Goals of This Session

- Aligned sequences -> indel calls
- Examine INDELs at particular genomic positions
- Evaluate quality of INDEL calls

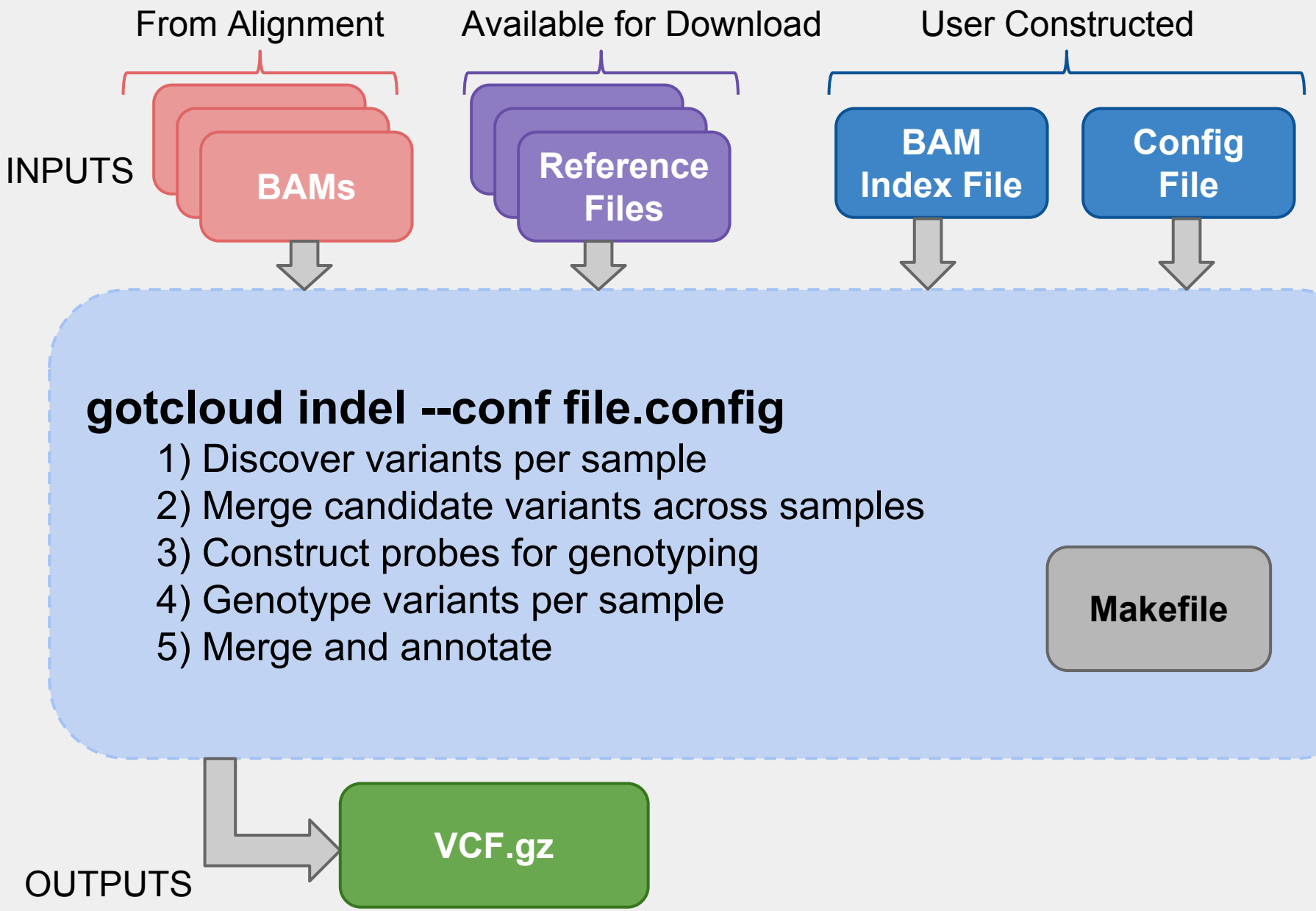
High Quality INDEL Calls from BAMs

- Many tools & best practices to choose from
- Our solution:

Genomes on the Cloud (GotCloud)

  - Yes, it has an indel pipeline too.

GotCloud INDEL Pipeline Overview



GotCloud indel Input Files

- Same inputs as GotCloud snpcall
  - BAMs->INDELs instead of BAMs->SNPs

Looking at INDELs

- Use *vt*
  - http://genome.sph.umich.edu/wiki/Vt
  - view - look at VCF
  - peek - summarize VCF

- Your favorite VCF viewer/analyzer
  - tabix

Try it yourself

http://genome.sph.umich.edu/wiki/SeqShop:_Variant_Calling_and_Filtering_for_INDELs_Practical