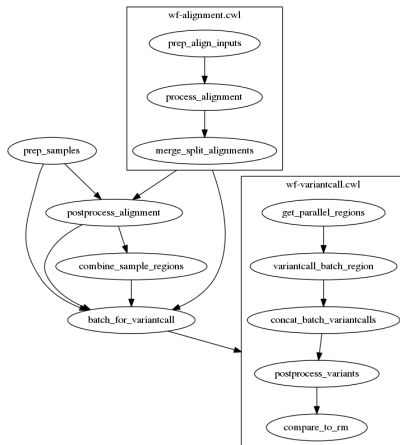


Building a community menagerie of automated variant validations

Brad Chapman
Bioinformatics Core, Harvard Chan School
<http://j.mp/bcbiolinks>

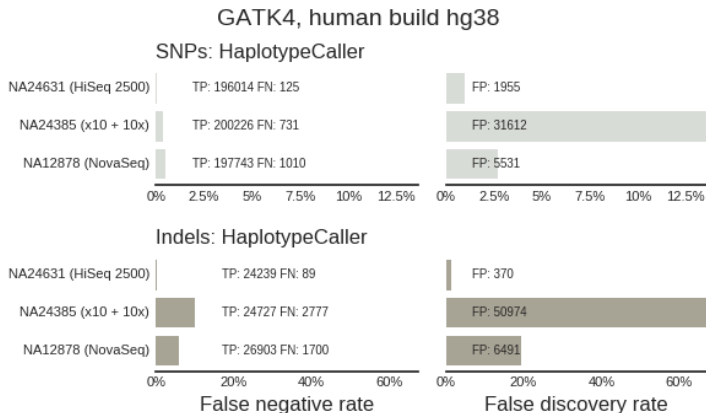
27 June 2018

You have a variant calling pipeline



<https://github.com/bcbio/bcbio-nextgen>

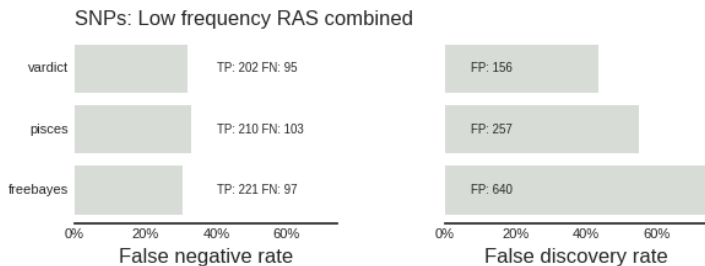
Is it good? How good? What data types?



https://github.com/bcbio/bcbio_validations/tree/master/gatk4

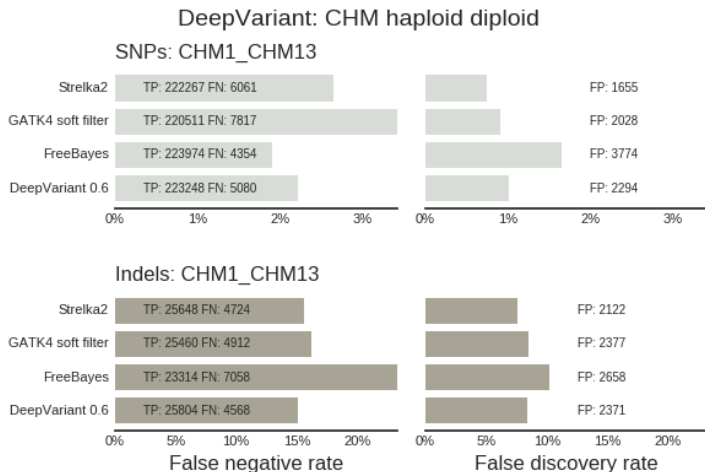
Does it work on my difficult samples?

Somatic tumor-only FFPE



https://github.com/bcbio/bcbio_validations/tree/master/somatic-lowfreq

Can I use it to improve callers?



https://github.com/bcbio/bcbio_validations/tree/master/deepvariant

Will it run correctly on my platform?

- Local machines and HPC: Cromwell, Toil
- AWS, GCP, Azure
- Arvados
- DNAnexus
- SevenBridges

<http://bcbio-nextgen.readthedocs.io/en/latest/contents/cwl.html>

■ Workflows

https://github.com/bcbio/bcbio_validation_workflows

■ Analyses

https://github.com/bcbio/bcbio_validations

■ Join the community: GiaB, GA4GH, NIH Data Commons

<https://github.com/bcbio/bcbio-nextgen>