Sarek

A portable workflow for WGS/WES analysis of germline and somatic mutations

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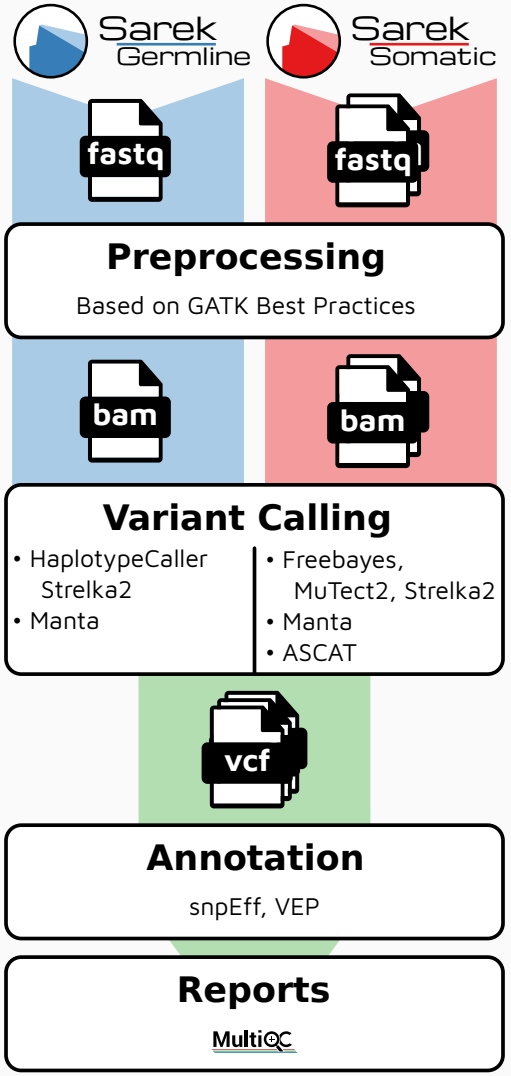
What is Sarek?

http://sarek.scilifelab.se/

- Analysis germline and somatic workflow
- Whole genome or targeted sequencing
- Developed with NGI and NBIS
- Support from The Swedish Childhood Tumor Biobank

Data and files workflow



Preprocessing

https://software.broadinstitute.org/gatk/best-practices/

Based on GATK Best Practices (GATK 4.0)

- Reads mapped to reference genome with `bwa`
- Duplicates marked with `picard MarkDuplicates`
- Recalibrate with `GATK BaseRecalibrator`

Germline Variant Calling

- SNVs and small indels:
  - HaplotypeCaller
  - Strelka2
- Structural variants:
  - Manta

Somatic Variant Calling

- SNVs and small indels:
  - MuTect2
  - Freebayes
  - Strelka2
- Structural variants:
  - Manta
- Sample heterogeneity, ploidy and CNVs:
  - ASCAT
  - Control-FREEC (🔧 adding)

Annotation

- VEP and SnpEff
- 🗄 ClinVar, COSMIC, dbSNP, GENCODE, gnomAD, polyphen, sift, etc.

Prioritization

- First step towards clinical use
- Rank scores are computed for all variants
  - COSMIC, ClinVar, SweFreq and MSK-IMPACT (cancerhotspots.org)
- Findings are ranked in three tiers
  - 1^{st} tier: well known, high-impact variants
  - 2^{nd} tier: variants in known cancer-related genes
  - 3^{rd} tier: the remaining variants

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Any questions?