



SciLifeLab



DNA  
club

INTERNATIONAL  
GENOMICS  
CENTRE  
INFRASTRUCTURE

NBS

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Barntumörbanken



# What is Sarek?



 <http://sarek.scilifelab.se/>

- Analysis germline and somatic workflow

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



nextflow

 <https://www.nextflow.io/>



 <https://www.sylabs.io/singularity/>

# nextflow

 <https://www.nextflow.io/>

Data-driven workflow language



 <https://www.sylabs.io/singularity/>

HPC specific container engine

## Sarek exists in multiple flavors





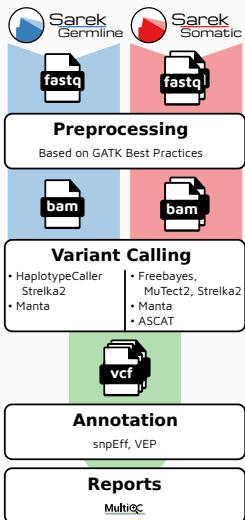
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# Data and files workflow





# AWS iGenomes

 <https://ewels.github.io/AWS-iGenomes/>

- Human GRCh37
- Human GRCh38

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- Human GRCh37
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- Dog CanFam3.1 
- Mouse GRCm38 



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

Based on GATK Best Practices (GATK 4.0)



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- Reads mapped to reference genome with `bwa mem`



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- Reads mapped to reference genome with `bwa mem`
  - FASTQs or BAMs 🔧





🌐 <https://software.broadinstitute.org/gatk/best-practices/>

Based on GATK Best Practices (GATK 4.0)

- Reads mapped to reference genome with `bwa mem`
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- Duplicates marked with `picard MarkDuplicates`









🌐 <https://software.broadinstitute.org/gatk/best-practices/>








Based on GATK Best Practices (GATK 4.0)











- Reads mapped to reference genome with `bwa mem`
  - FASTQs or BAMs 🔧
- Duplicates marked with `picard MarkDuplicates`
- Recalibrate with `GATK BaseRecalibrator`

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  - Freebayes 
  - HaplotypeCaller 
  - MuTect2 
  - Strelka2 / 



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- Sample heterogeneity, ploidy and CNVs:

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  - ASCAT 
  - Control-FREEC  

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



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- Prioritization 
  - Rank scores are computed for all variants, and can be explored



 <https://www.sylabs.io/singularity/>



 <https://www.sylabs.io/singularity/>

- Available on `rackham` and/or `bianca`
- `/sw/data/uppnex/ToolBox/sarek`



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- Next step `Sarek` module

**BIOCONDA<sup>®</sup>**

 <https://bioconda.github.io/>

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- Execute Sarek within a conda environment





 <https://aws.amazon.com/>



 <https://aws.amazon.com/>

- Improving AWS usage

# Acknowledgments



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# Any questions?

🌐 <https://maxulysse.github.io/dnacclub2019>

🐙 <https://github.com/SciLifeLab/Sarek>

📖 <https://gitter.im/SciLifeLab/Sarek>

🌐 <http://sarek.scilifelab.se/>

🔖 [#sarek-pipeline](#)

