



# CAW 1.1 review

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Maxime Garcia

2017-09-27

SciLifeLab

NATIONAL  
CTAC  
ATCA GENOMICS  
INFRASTRUCTURE

NBIS  
NATIONAL BIOINFORMATICS  
INFRASTRUCTURE SWEDEN

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Institutet

KTH  
KTH Royal Institute of Technology

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universitet

Uppsala  
UNIVERSITET



# Today's agenda

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- First clinical case with CAW
- Discussions about what to do next
- Bugs report

# What is Singularity?

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<http://singularity.lbl.gov/>  
<https://singularity-hub.org/>

- Docker-like containers technology
- Specific for HPC environment

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- Docker-like containers technology
- Specific for HPC environment
- Supported by Nextflow

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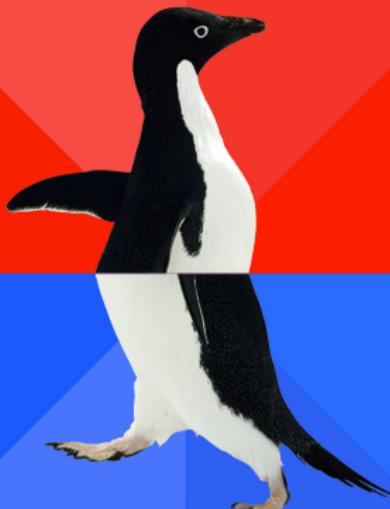
## Why would we want to use that?

- For a better control
  - of every tool used
  - of every version used
- For a better reproducibility

Containerization is not only portable but also reproducible.

We can do everything!

WE CAN USE ANY VERSION  
OF ANY TOOL WE WANT



WE ARE RESPONSIBLE FOR  
EVERY TOOL WE WANT

## We do not rely on UPPMAX modules anymore

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- Tools already updated
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  - Strelka: 1.0.15 -> 2.8.2
- What was gained?
  - Manta: Single Diploid Sample + Tumor-Only Analysis
  - Strelka: Germline variants + Manta's candidate indels supplied as input to Strelka

We're currently updating every other tools in our containers.



- Markus Mayrhofer & Markus Ringnér

## Switch to Szilva's presentation

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- Szilva's slides

## Where we are right now

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- What we have
- What we need
- What we are working on

## Switch to Teresita's presentation

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- Teresita's slides

# What do we have now?

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CAW 1.1

- From FASTQ to annotated VCF

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## CAW 1.1

- From FASTQ to annotated VCF
- A core set of Variant Callers:
  - MuTect1, MuTect2
  - HaplotypeCaller, Freebayes
  - Strelka, Manta, Ascat

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- VEP and snpEFF for annotation
- Rely on UPPMAX modules
- Singularity support

## CAW 1.2

- Singularity support
- Up to date tools
- Add Control-FREEC

## What to do next?

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- Scout

## Bugs report

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## The List of People Involved

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Sebastian DiLorenzo	Monica Nistèr
Jesper Eisfeldt	Björn Nystedt
Maxime Garcia	Pall Olason
Szilveszter Juhos	Markus Ringnér
Max Käller	Pelin Sahlén
Malin Larsson	Johanna Sandgren
Marcel Martin	Teresita Díaz De Ståhl
Markus Mayrhofer	

## Where to find us?

- We are on the SciLifeLab Slack  
#cancer-pipeline

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- We have a gitter channel  
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- We are on the SciLifeLab Slack  
`#cancer-pipeline`
- We have a gitter channel  
<https://gitter.im/SciLifeLab/CAW>
- Our code is hosted on Github  
<https://github.com/SciLifeLab/CAW>

# Any questions?

