



CAW 1.1 review

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SciLifeLab

NATIONAL
ATCA GENOMICS
INFRASTRUCTURE

NBIS
NATIONAL BIOINFORMATICS
INFRASTRUCTURE SWEDEN

Karolinska
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UNIVERSITET



Today's agenda

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- Discussions about what to do next
- Bugs report

What is Singularity?



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- Supported by Nextflow

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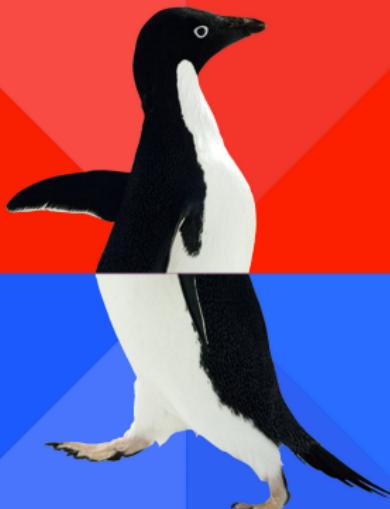
Why would we want to use that?

- 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 NEED

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- 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

- Szilva's slides

Where we are right now

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

Switch to Teresita's presentation

- Teresita's slides

What do we have now?

CAW 1.1

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- A core set of Variant Callers:
 - MuTect1, MuTect2
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 - Strelka, Manta, Ascat

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- Rely on UPPMAX modules
- Singularity support

CAW 1.2

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

What to do next?

- Scout

Bugs report

The List of People Involved

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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- Our code is hosted on Github
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Any questions?

