



Cancer Analysis Workflow

Yes we can run it on Irma with Singularity containers

Maxime Garcia

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- Can pull containers from Docker-hub

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- of every version used

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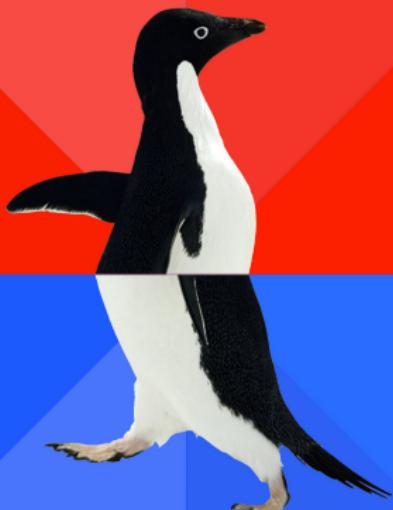
- For a better control
- of every tool used
- of every version used
- For a better reproducibility

Why would we want to do that?

- For a better control
- of every tool used
- of every version used
- For a better reproducibility
- Containerization is reproducible and portable

We can do everything!

WE CAN USE ANY VERSION
OF ANY TOOL WE WANT



WE ARE RESPONSIBLE FOR
EVERY TOOL WE NEED

The CAW-containers repository

README.md



Containers for CAW

[release v1.1](#) [license MIT License](#) [nextflow >0.23.2](#) [chat on gitter](#) [build passing](#)

CAW is a complete open source pipeline to detect somatic variants from WGS data developed at the [National Genomics Infrastructure](#) at [SciLifeLab Stockholm](#), Sweden.

For further information/help contact: maxime.garcia@scilifelab.se or szilveszter.juhos@scilifelab.se, or join the gitter chat: gitter.im/SciLifeLab/CAW

Documentation

This repo comes with documentation about the different containers, found in the `doc/` directory:

1. Documentation about containers
2. Documentation about building

Author

• Maxime Garcia

The One Script

SciLifeLab/CAW-containers

- 24 different Docker containers for all the different processes

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SciLifeLab/CAW-containers

- 24 different Docker containers for all the different processes
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One Script to push them

- One Script to pull them all,

and with Singularity run them

Inside the script

SciLifeLab/CAW-containers/main.nf

```
docker build -t $repository/$container:$tag \
$baseDir/containers/$container/.

docker push $repository/$container:$tag

singularity pull --name $container-${tag}.img \
docker://$repository/$container:$tag
```

Nextflow and Singularity for the win



- Nextflow natively support Singularity



- Nextflow natively support Singularity
- Easy configuration



- Nextflow natively support Singularity
- Easy configuration
- Automatic pull of the containers

Easy configuration

SciLifeLab/CAW/configuration/singularity.config

```
singularity {
    autoMounts = true
    enabled = true
}
process {
    $RunFastQC.container      = 'docker://maxulysse/fastqc:1.1'
    $RunFreeBayes.container   = 'docker://maxulysse/freebayes:1.1'
    $RunGenotypeGVCFs.container = 'docker://maxulysse/gatk:1.1'
    $RunManta.container       = 'docker://maxulysse/runmanta:1.1'
    $RunMultiQC.container     = 'docker://maxulysse/multiqc:1.1'
    $RunMutect1.container     = 'docker://maxulysse/mutect1:1.1'
}
```

Easy configuration

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    $RunMultiQC.container     = 'docker://maxulysse/multiqc:1.1'
    $RunMutect1.container     = 'docker://maxulysse/mutect1:1.1'
}
process.container = 'shub://MaxUlysse/shubcontainer'
```

What to do on a secure cluster?

- How about running CAW with Singularity on Bianca or Irma?

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What to do on a secure cluster?

- How about running CAW with Singularity on Bianca or Irma?
- No automatic pull of the containers
- The configuration is still easy

Still an easy configuration

```
SciLifeLab/CAW/configuration/singularity-download.config
```

```
singularity {
    autoMounts = true
    enabled = true
}
process {
    $RunFastQC.container      = 'containers/fastqc-1.1.img'
    $RunFreeBayes.container   = 'containers/freebayes-1.1.img'
    $RunGenotypeGVCFs.container = 'containers/gatk-1.1.img'
    $RunManta.container       = 'containers/runmanta-1.1.img'
    $RunMultiQC.container     = 'containers/multiqc-1.1.img'
    $RunMutect1.container     = 'containers/mutect1-1.1.img'
}
```

How to get the containers?

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- To pull all containers from Docker-hub into Singularity containers

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- Use the script that does the thing
- To pull all containers from Docker-hub into Singularity containers
- Transfer the containers to the secure cluster

One last detail

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- /pica

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- /proj

One last detail

- Do not forget to create the UPPMAX specific directories in the containers
- /pica
- /proj
- /sw

Let the magic happen

SciLifeLab/CAW/main.nf

```
nextflow run ~/CAW/main.nf --project project --step preprocessing \
--genome GRCh38 --sample sample.tsv -profile singularityLocal
```

Using parallelization to do multiple tests

SciLifeLab/CAW/.travis.yml

```
^^Isudo: required
^^Ilanguage: java
^^Ijdk: openjdk8
^^Iservices:
^^I - docker
^^Ienv:
^^I - NXF_VER=0.25.6 SGT_VER=2.3.1 TEST=ANNOTATE PROFILE=singularity
^^I - NXF_VER=0.25.6 SGT_VER=2.3.1 TEST=ANNOTATE PROFILE=docker
^^I - NXF_VER=0.25.6 SGT_VER=2.3.1 TEST=RECALIBRATE PROFILE=singularity
^^I - NXF_VER=0.25.6 SGT_VER=2.3.1 TEST=RECALIBRATE PROFILE=docker
^^I - NXF_VER=0.25.6 SGT_VER=2.3.1 TEST=REALIGN PROFILE=singularity
^^I - NXF_VER=0.25.6 SGT_VER=2.3.1 TEST=REALIGN PROFILE=docker
^^I - NXF_VER=0.25.6 SGT_VER=2.3.1 TEST=MAPPING PROFILE=singularity
^^I - NXF_VER=0.25.6 SGT_VER=2.3.1 TEST=MAPPING PROFILE=docker

^^Iinstall: # Install Nextflow
^^I - "./scripts/install.sh --tool nextflow"

^^Iscript:
^^I - "./scripts/test.sh --profile $PROFILE --test $TEST --install --travisci"
```

All your test are belong to us.

SciLifeLab / CAW  build passing

Current Branches Build History Pull Requests Build #433 More options 

✓ Pull Request #457 Update Manta and Strelka  #433 passed 

↳ Commit 2be368b  ↳ #457: Update Manta and Strelka  ↳ Branch master 

⌚ about 3 hours ago 

Maxime Garcia authored and committed 

Build Jobs

✓ # 433.1	 ↳ JDK: openjdk8	 NXF_VER=0.25.6 PROFILE=dockerTest TEST=ANNOTATION  22 min 12 sec	
✓ # 433.2	 ↳ JDK: openjdk8	 NXF_VER=0.25.6 SGT_VER=2.3.1 PROFILE=singularit  23 min 57 sec	
✓ # 433.3	 ↳ JDK: openjdk8	 NXF_VER=0.25.6 PROFILE=dockerTest TEST=ANNOTATION  22 min 6 sec	
✓ # 433.4	 ↳ JDK: openjdk8	 NXF_VER=0.25.6 SGT_VER=2.3.1 PROFILE=singularit  11 min 53 sec	
✓ # 433.5	 ↳ JDK: openjdk8	 NXF_VER=0.25.6 PROFILE=dockerTest TEST=RECALIBRATION  11 min 15 sec	
✓ # 433.6	 ↳ JDK: openjdk8	 NXF_VER=0.25.6 SGT_VER=2.3.1 PROFILE=singularit  11 min 29 sec	
✓ # 433.7	 ↳ JDK: openjdk8	 NXF_VER=0.25.6 PROFILE=dockerTest TEST=REALIGNMENT  9 min 43 sec	
✓ # 433.8	 ↳ JDK: openjdk8	 NXF_VER=0.25.6 SGT_VER=2.3.1 PROFILE=singularit  14 min 13 sec	
✓ # 433.9	 ↳ JDK: openjdk8	 NXF_VER=0.25.6 PROFILE=dockerTest TEST=MAPPING  6 min 14 sec	

The List of People Involved

Sebastian DiLorenzo

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Marcel Martin

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Pelin Sahlén

Johanna Sandgren

Teresita Díaz De Ståhl

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?



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