

# Another talk about CAW?



NGI Stockholm CAWterly meeting

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Maxime Garcia

@gau

@MaxUlysse

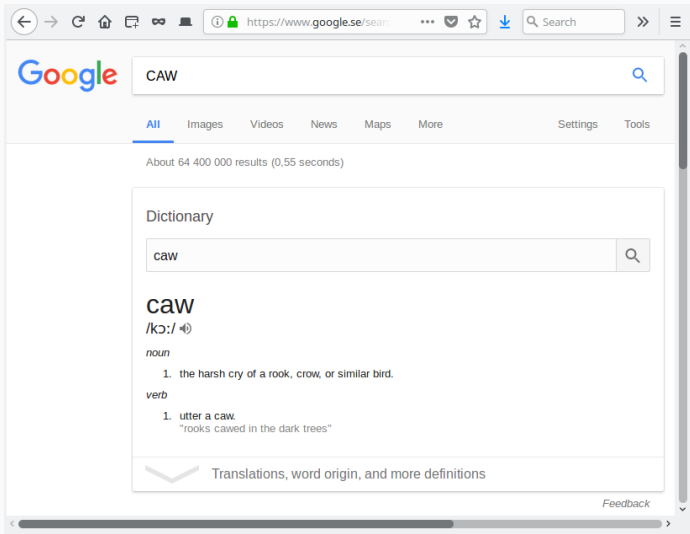
<https://maxulyse.github.io/>

2017-10-06

SciLifeLab NGI / BarnTumörBanken



# What is CAW?



A screenshot of a web browser showing a Google search for "CAW". The browser's address bar displays "https://www.google.se/search". The Google logo is on the left, and the search bar contains "CAW". Below the search bar, navigation tabs for "All", "Images", "Videos", "News", "Maps", and "More" are visible, with "All" selected. To the right of these tabs are links for "Settings" and "Tools". Below the tabs, it says "About 64 400 000 results (0,55 seconds)". The main content area shows a "Dictionary" section with a search bar containing "caw". Below this, the word "caw" is displayed in a large font, followed by its phonetic transcription "/kɔ:/". Underneath, the word is defined as a "noun" and a "verb". The noun definition is "the harsh cry of a rook, crow, or similar bird." The verb definition is "utter a caw." with an example sentence: "rooks cawed in the dark trees". At the bottom of the dictionary section, there is a link that says "Translations, word origin, and more definitions". A "Feedback" link is located at the bottom right of the page.

Google CAW

All Images Videos News Maps More Settings Tools

About 64 400 000 results (0,55 seconds)

Dictionary

caw

**caw**  
/kɔ:/  
noun

- the harsh cry of a rook, crow, or similar bird.

verb

- utter a caw.  
"rooks cawed in the dark trees"

Translations, word origin, and more definitions

Feedback

# What is CAW?



<http://opensource.scilifelab.se/projects/caw/>

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- Pipeline developed at NGI



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<http://opensource.scilifelab.se/projects/caw/>

- Pipeline developed at NGI
- In collaboration with NBIS
- Support of The Swedish Pediatric Tumor Biobank



# What does CAW do?



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- Tumor/Normal pair WGS analysis



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<http://opensource.scilifelab.se/projects/caw/>

- Tumor/Normal pair WGS analysis
- Based on GATK best practices for processing FASTQ files
- MuTect1, MuTect2, Strelka, and GATK HaplotypeCaller

# What does CAW do?



<http://opensource.scilifelab.se/projects/caw/>

- Tumor/Normal pair WGS analysis
- Based on GATK best practices for processing FASTQ files
- SNPs, SNVs and indels

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- Based on GATK best practices for processing FASTQ files
- SNPs, SNVs and indels
- Structural variants
- Heterogeneity, ploidy and CNVs



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- Docker-like containers technology
- Specific for HPC environment





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- Better reproducibility
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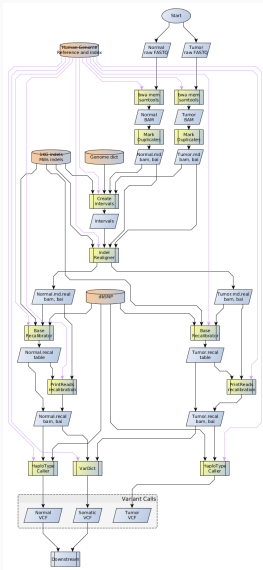


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- Supported by Nextflow
- Better reproducibility
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Containerization is not only portable but also reproducible.

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- Start from FASTQ files
- More or less processed BAM files
- Annotations with snpEff and/or VEP
- Reports with MultiQC

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- Reports with MultiQC
- Choose between GRCh37 or GRCh38
- We can also process normal only samples

Can CAW do more?





# CAW to replace Piper into production



- Kick of meeting was 2017-10-04

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- Faster than Piper

# CAW to replace Piper into production




- Kick of meeting was 2017-10-04
- Normal only processing of samples
- Handles GRCh38 and GRCh37
- Faster than Piper
- Has already been use to process the 1000 samples from SweGen



## 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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- We have a gitter channel   
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- We have a gitter channel   
`https://gitter.im/SciLifeLab/CAW`
- Our code is hosted on Github   
`https://github.com/SciLifeLab/CAW`

Any questions?

