3-6 February 2020 - Athens, Greece

# Human Brain Project SUMMIT & OPEN DAY

Co-funded by
the European Union

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# Developing pipelines for multi- scale/species/method analysis

## adaptable, reusable, UseCase-driven

05.02.2020 HBP Summit, *Athens*

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JÜLICH Forschungszentrum

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# Where we are - Where we want to be

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## Towards large research collaborations and long-lasting projects

- Data sharing becomes easier and more common
- Open Access becomes more prominent
- "Reproducibility Crisis"

- Easy publishing of analysis workflows
- Easy replication of published results
- Easy reuse of published data/results/analysis

## How can we adapt our computational research practices?

- There is no one-size-fit-all solution
- A lot of little, incremental improvements
- Many solutions and tools already exist
- There is progress in bringing tools together
- There is progress in co-developing new features and bridges

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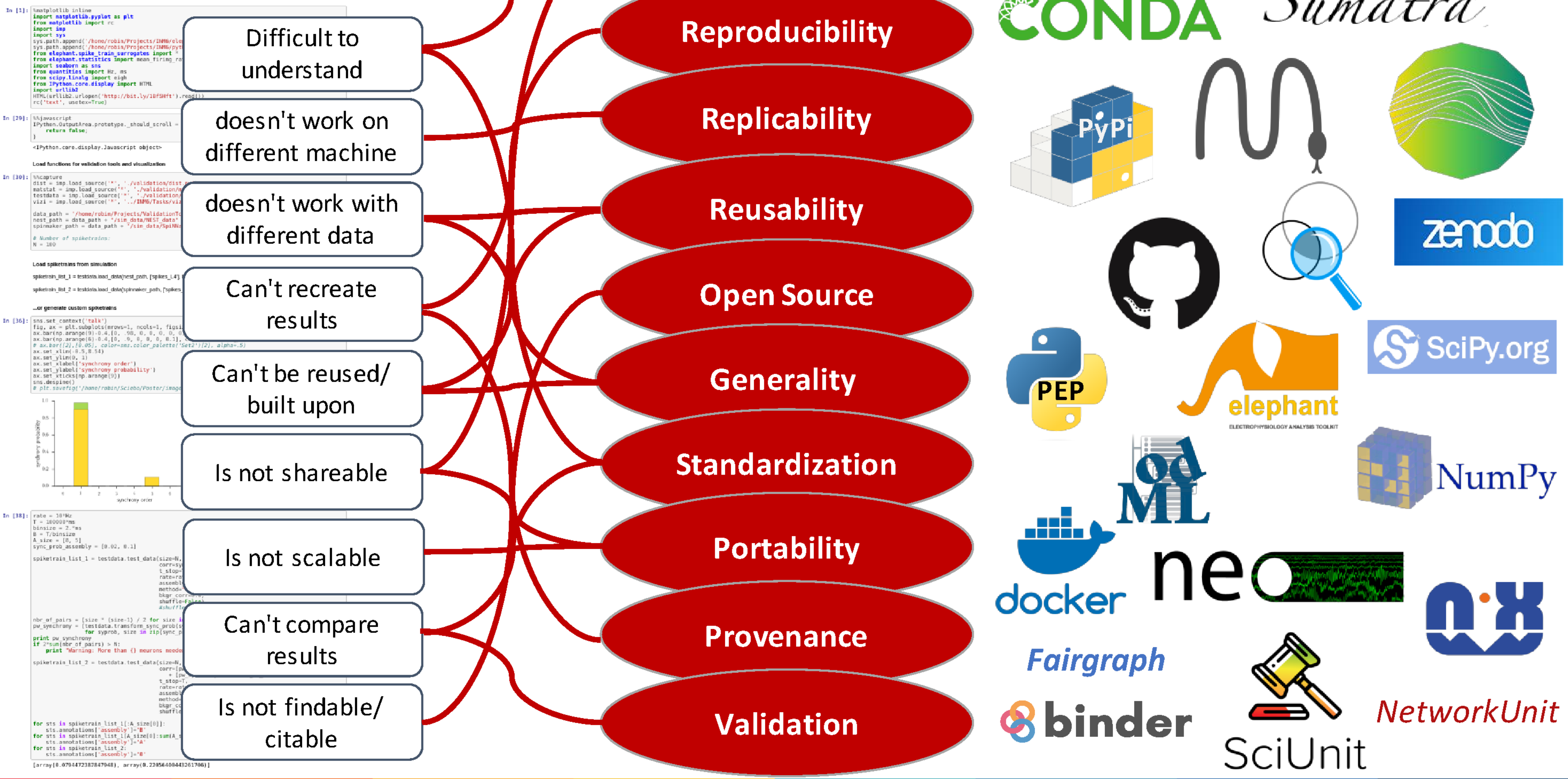
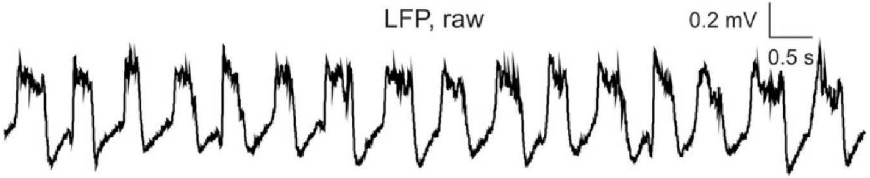


# Slow Wave Analysis (SP3 UseCase002)

## Slow Waves

- periodic transition between Up and Down state (0-5Hz)
- in sleep and anasthesia
- across measurements and species
- relevance for memory and consciousness research




*Szabó et. al. 2017*

## Analysis Pipeline

- identifying a generalized structure of analysis steps

  -> sequential *Stages*, and modular *Blocks*
- implemention with a workflow management sytem
- precisely defining the interfaces and (meta-)data requirements
- integrating existing analysis approaches & algorithms

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# Flowchart

Pipeline | Stage | Block

Calcium Imaging

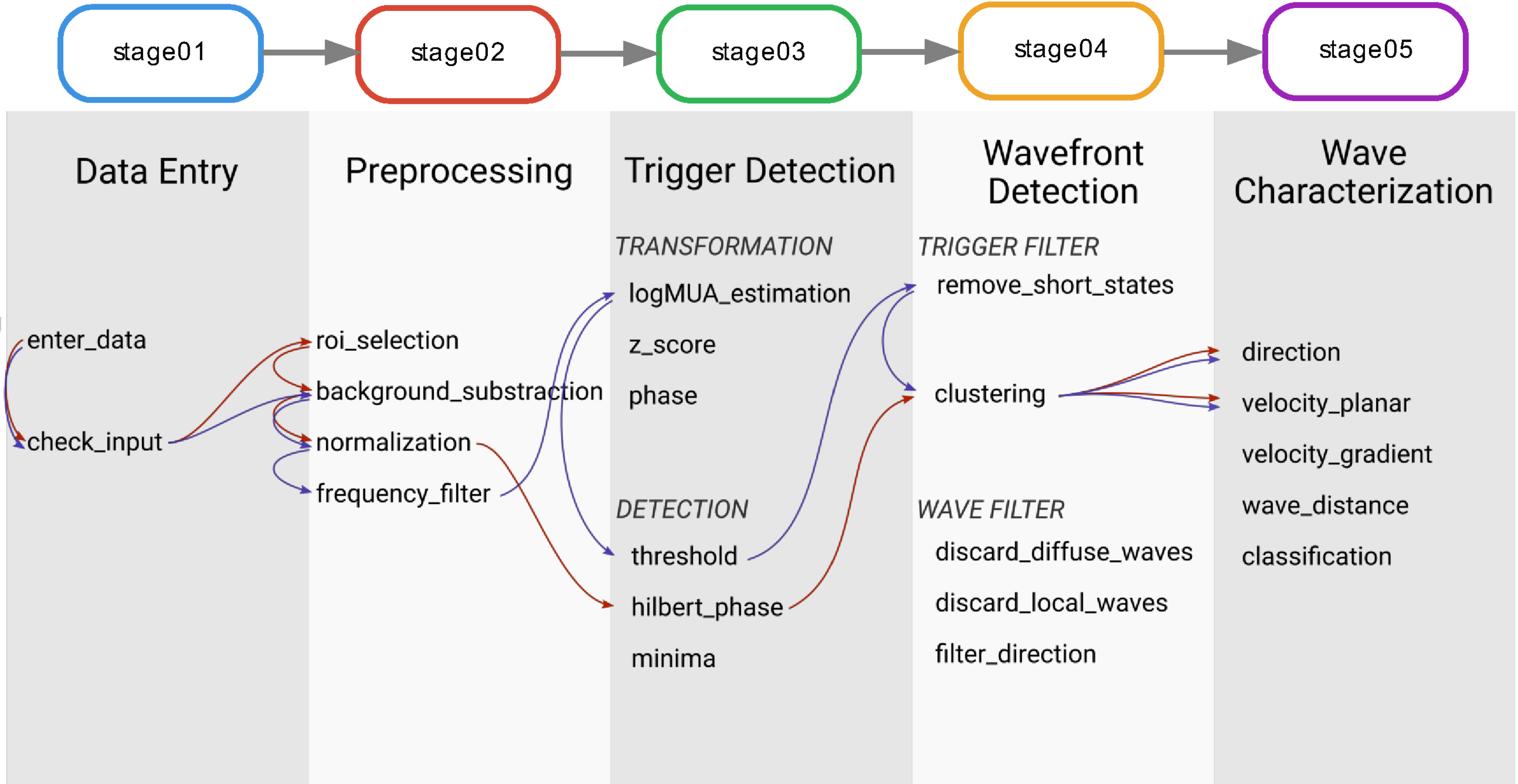
ECoG

EEG

LFP

Spikes

*Simulation*




*Data curtesy of: F.S. Pavone Lab, LENS, Florence, Italy / M.V. Sanchez-Vives Lab, IDIBABS, Barcelona, Spain*

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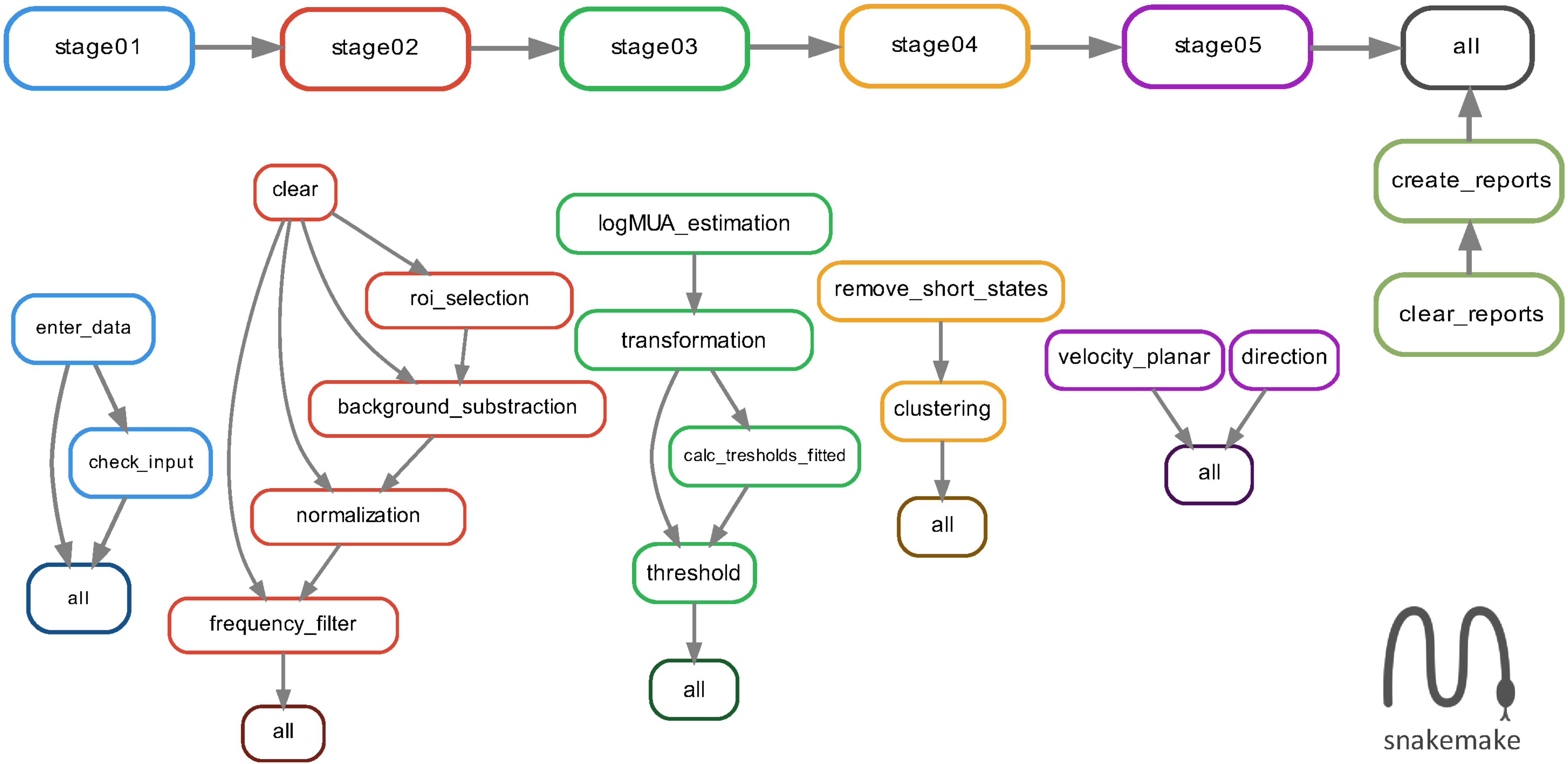
# Dependency Trees

Pipeline Stage Block




snakemake

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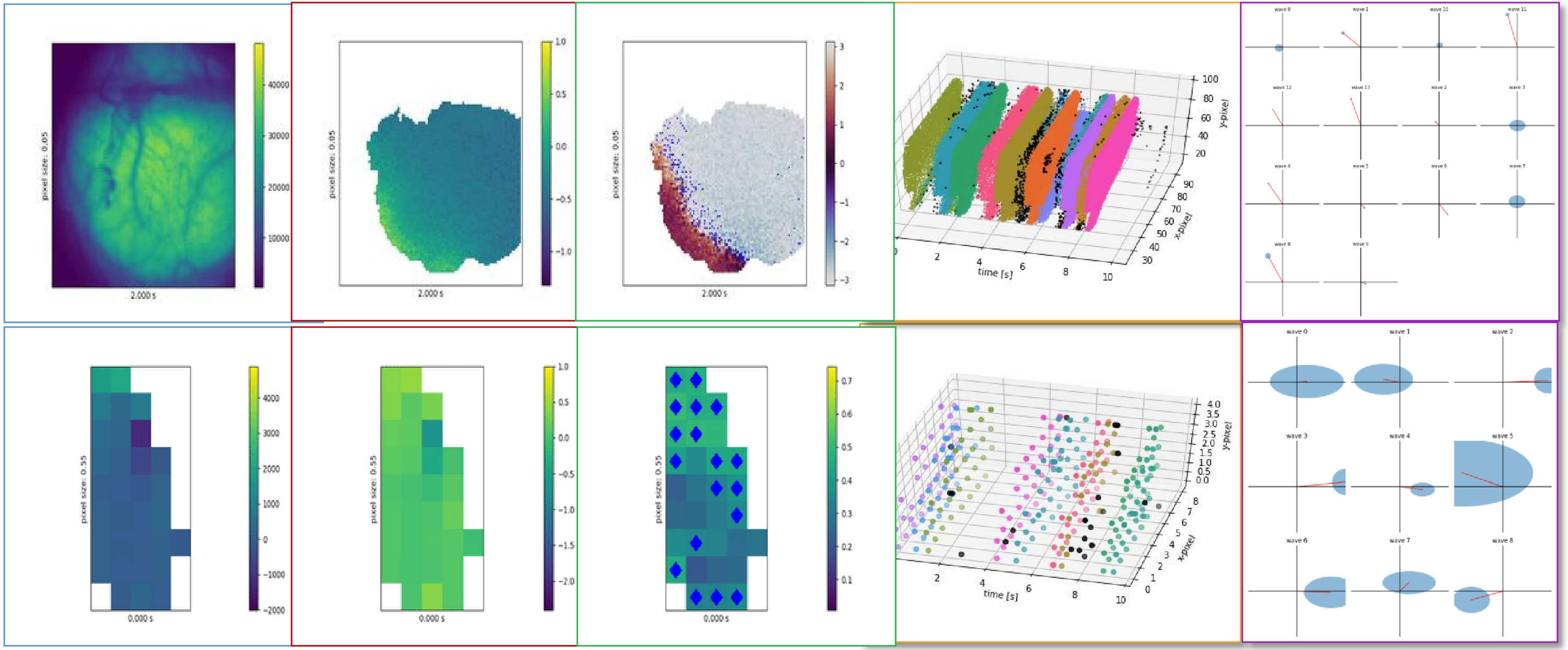
# Stage Outputs

Pipeline | Stage | Block

stage01 → stage02 → stage03 → stage04 → stage05



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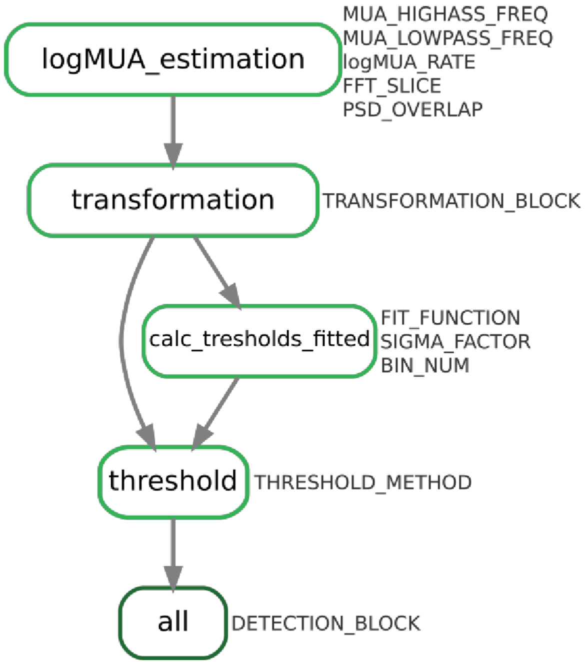
# Folder Hierachy

Pipeline | Stage | Block




```
(wavescalephant_env) ✔ ~/pipeline/stage03_trigger_detection
13:54 $ snakemake
```

## Source Files

- stage03_trigger_detection
  - config.yaml
  - Snakefile
  - README.md
  - report.rst
  - scripts
    - transformation
      - z_score.py
      - time_slice.py
      - phase_transform.py
      - logMUA_estimation.py
    - detection
      - calc_thresholds_fixed.py
      - minima.py

## Output Files

- stage03_trigger_detection
  - threshold
    - amplitude_distribution_channel18.png
    - fitted_thresholds.npy
    - transitions.nix
    - transitions.png
  - transformation
    - logMUA_estimation
      - logMUA_estimation.nix
      - logMUA_trace_1-10s_channel18.png
    - transformed_signal.nix
    - transformed_trace_1-10s_channel18.png
  - trigger_times.nix
  - report.html

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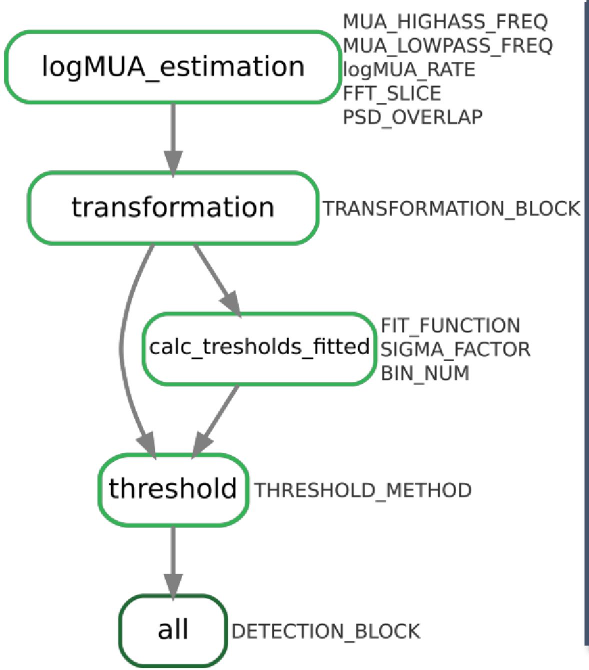
Pipeline | Stage | Block

# Config & Snakefile

## How to flexibly adapt the trigger detection method?




config.yaml

```
# int or None. default 'None' -> randomly selected
```

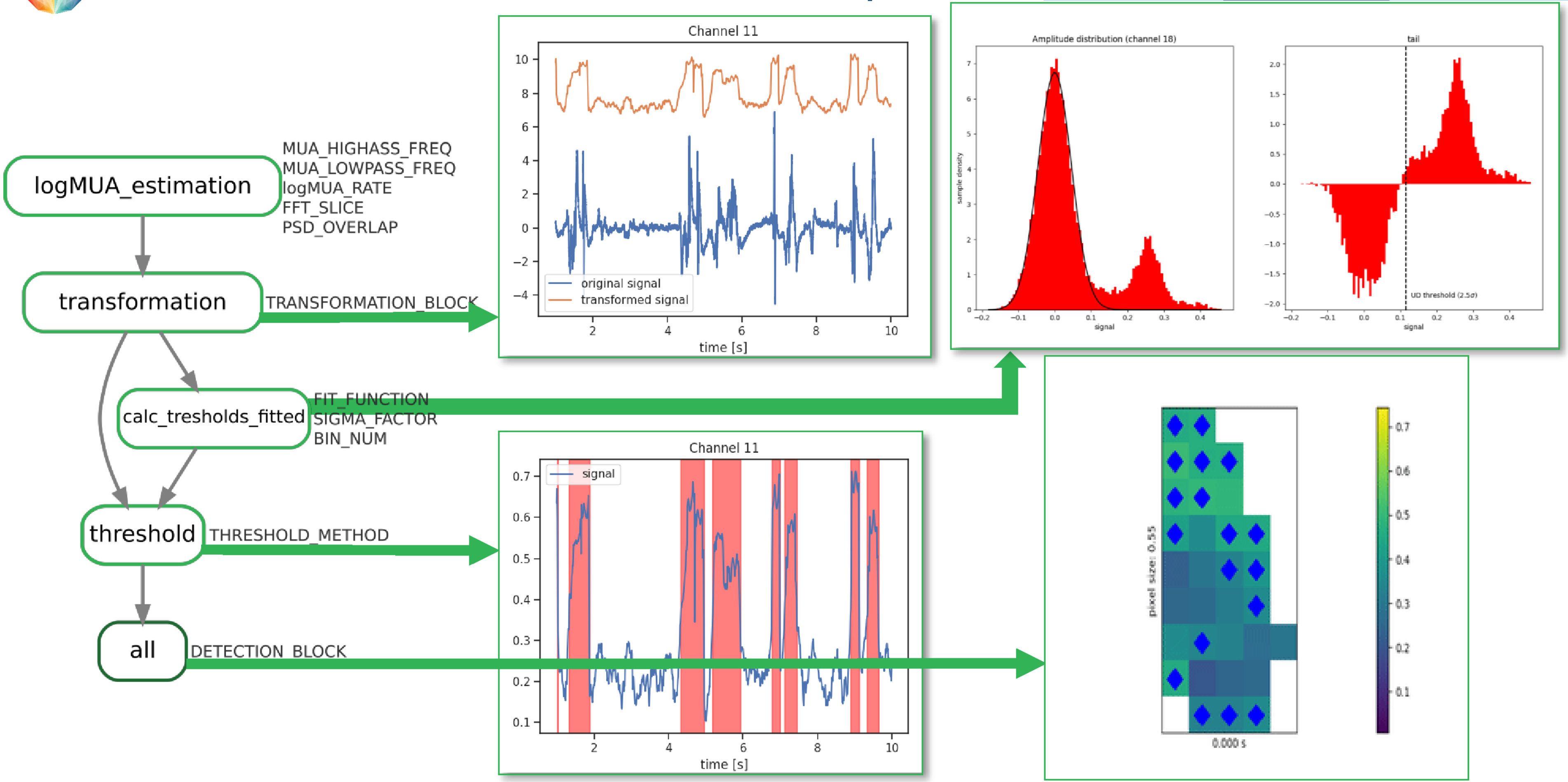
Snakefile

```
    def transformation_input_file(wildcards):
        if wildcards.rule_name == 'transformation':
            return os.path.join(output_path, 'transformation',
                                TRANSFORMATION_BLOCKS[-1],
                                TRANSFORMATION_BLOCKS[-1]+neo_format)
        else:
            idx = locate(TRANSFORMATION_BLOCKS, wildcards.rule_name)
            if idx:
                return os.path.join(output_path, 'transformation',
                                    TRANSFORMATION_BLOCKS[idx-1],
                                    TRANSFORMATION_BLOCKS[idx-1]+neo_format)
            else:
                return stage_input

    def trigger_detection_input_file(wildcards):
        if len(TRANSFORMATION_BLOCKS):
            return os.path.join(output_path, 'transformation',
                                'transformed_signal'+neo_format)
        else:
            return stage_input
```

# Block Outputs





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# Block Structure



**Block** = Instructions to create output from input (*snakemake rule*)

**Block**

```
rule frequency_filter:
    input:
        data = input_file,
        script = 'scripts/frequency_filter.py',
        config = 'config.yaml'
    output:
        data = os.path.join(output_path, 'frequency_filter.nix'),
    shell:
        """
        python {input.script} --data "{input.data}" \
                              --output "{output.data}" \
                              --highpass_freq {config['HIGHPASS_FREQ']} \
                              --lowpass_freq {config['LOWPASS_FREQ']} \
                              --order {config['FILTER_ORDER']} \
                              --filter_function {config['FILTER_FUNCTION']}
        """
```

elephant
signal_processing.butter

## Snakemake Advantages

- Can use any shell executables
- Handles portability
- Determines execution order
- Captures execution details

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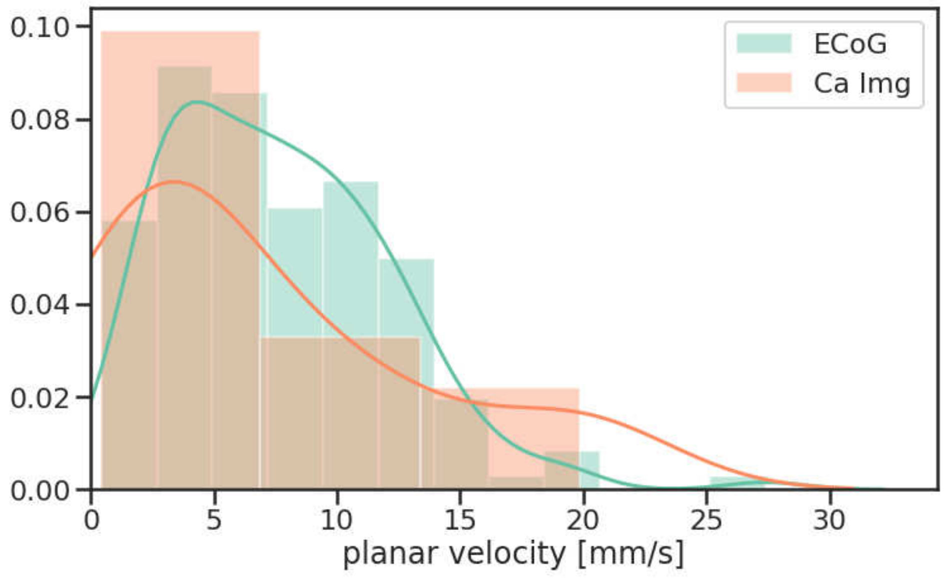
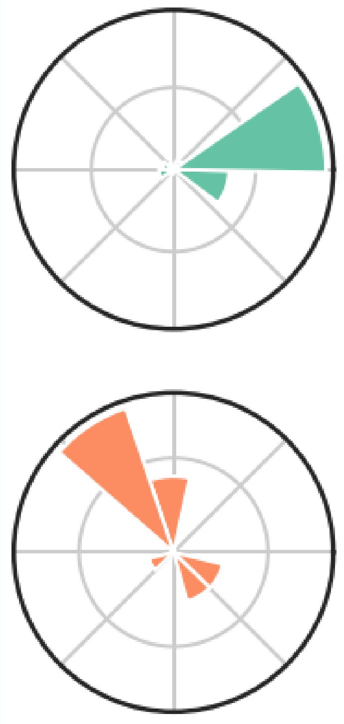
# The Payoff

## Direct comparability between different data types

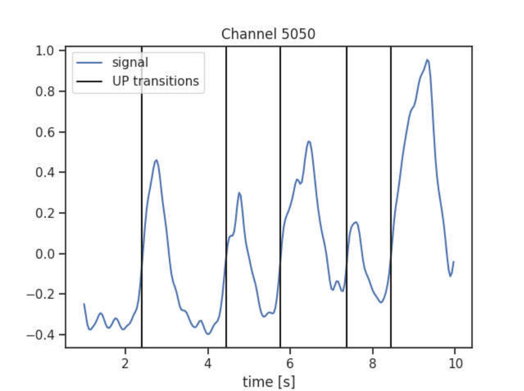


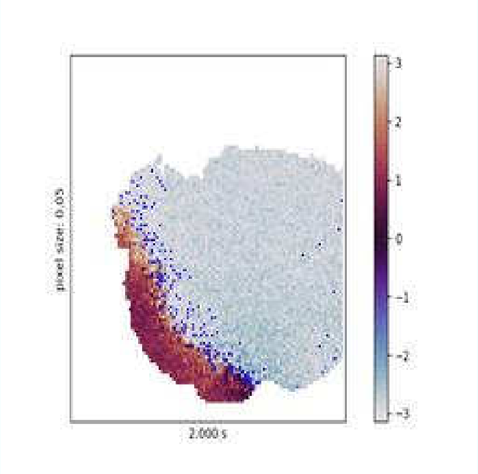



# The Payoff

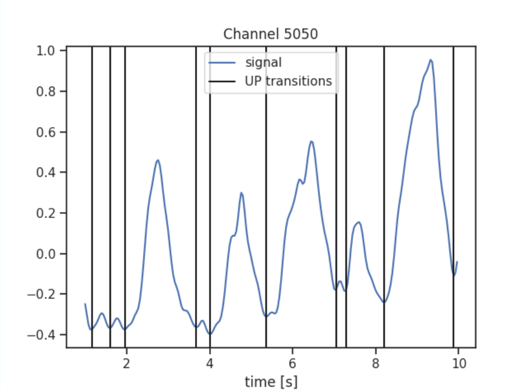
## Benchmarking of analysis algorithms

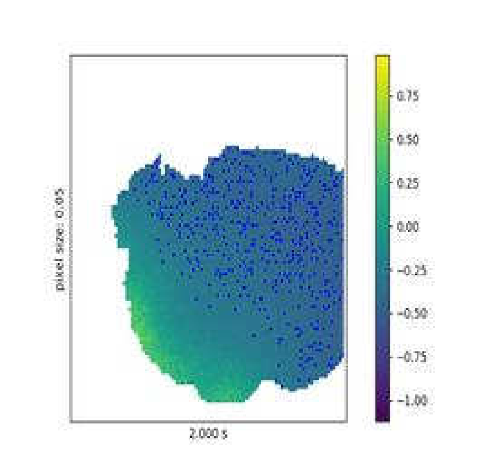
**via Hilbert phase**




**via minima**



# The Payoff

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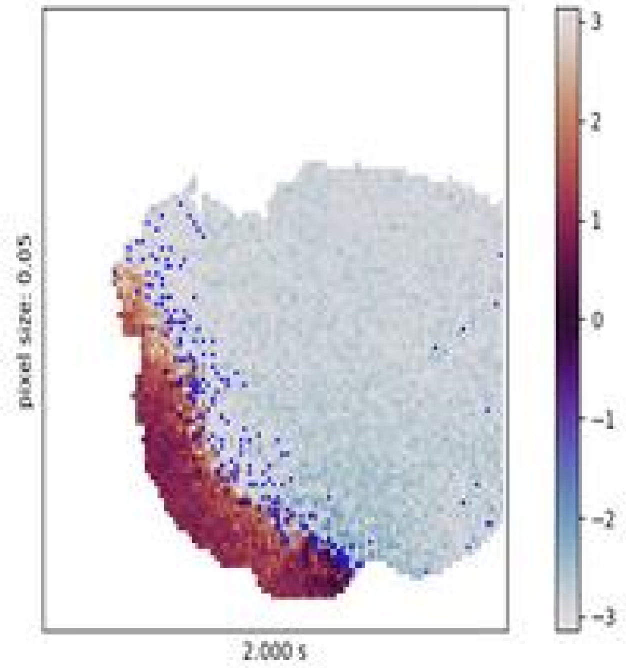
## Basis for meaningful validation tests

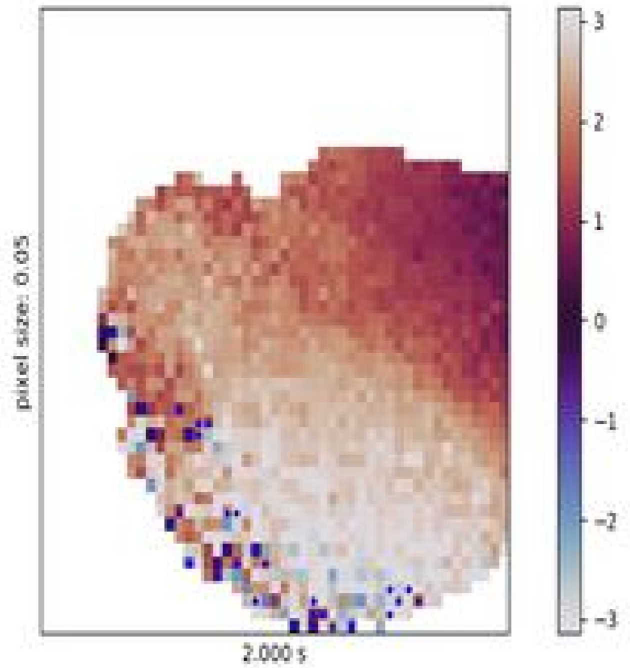
NetworkUnit

SciUnit

recorded activity




simulated activity




*Model by Cristiano Capone*

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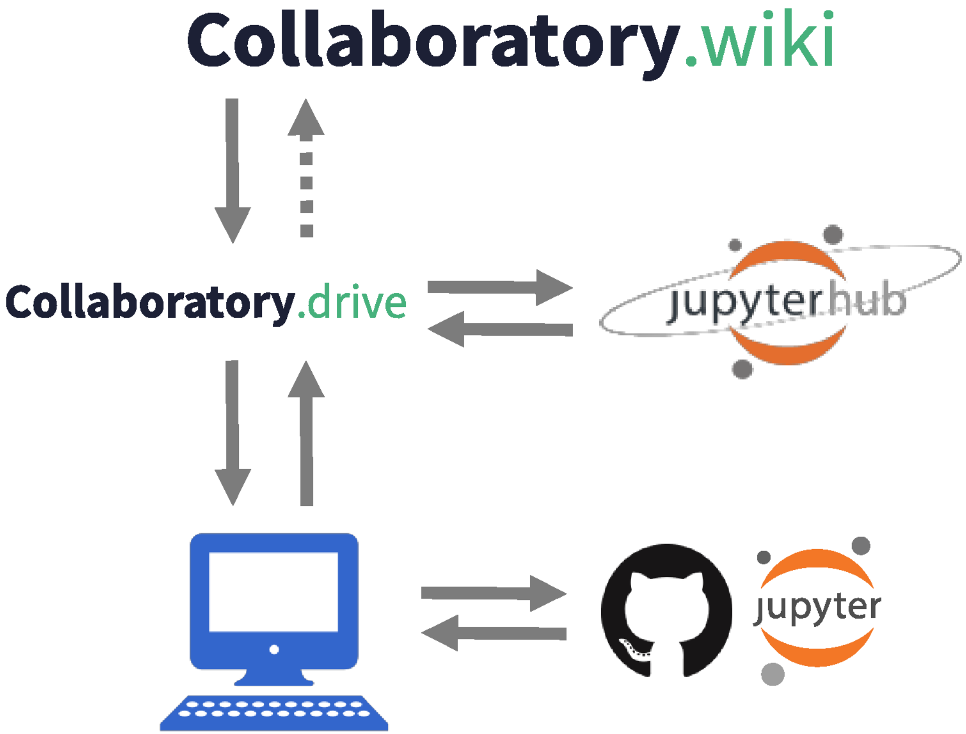
# Collab Integration




## Wishlist

- GitHub Integration / Version Control
- (Python) Environment Management
- Easy HPC Access
- Workflow Engine

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# Thank you!

Giulia De Bonis

Cristiano Capone

Elena Pastorelli

Pier Stanislao Paolucci

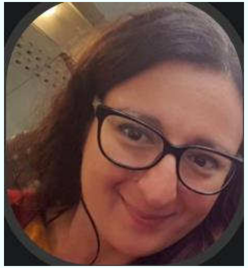
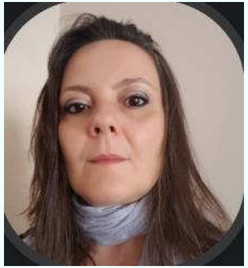
Yann Zerlaut

Glynis Mattheis

Andrew Davison

Robin Gutzen

Michael Denker





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