## YAMP: Yet Another Metagenomic Pipeline

<u>Alessia Visconti</u>, Tiphaine Martine, Mario Falchi
TwinsUK, King's College London

Why?

## 1. Easy to use

#### 2. Portable

### 3. Flexible

## 4. Reproducible

How?

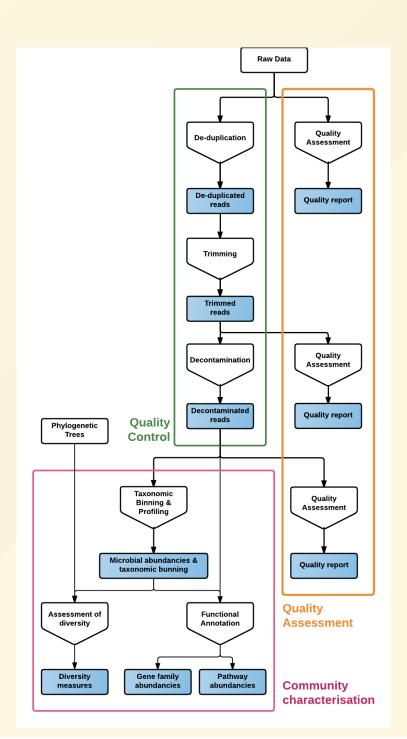
# nextlow

- Highly parallel
- Easily portable
- Very flexible and customisable



- Lightweight, self-contained systems
- Software version management

What?



## Raw Data De-duplication De-duplicated reads Trimming Trimmed reads Decontamination Decontaminated reads

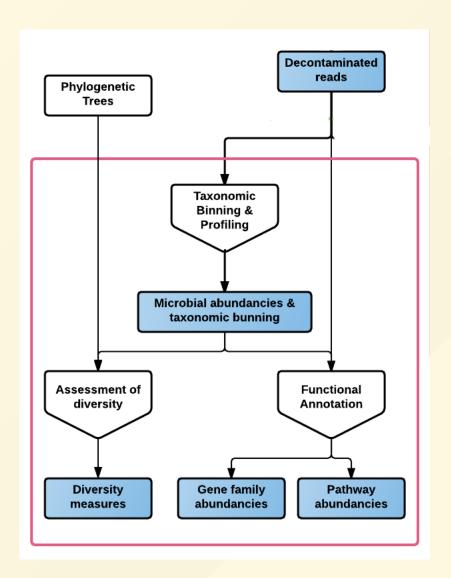
#### **Quality Control I**

- De-duplication: clumpify
- Trimming: BBduk
- Decontamination: BBwrap

#### Raw Data Quality De-duplication Assessment De-duplicated Quality report Trimming reads Quality Decontamination Assessment Decontaminated Quality report reads Quality Assessment Quality report

#### **Quality Control II**

• Assessment: FastQC



## **Community Characterisation**

- Taxonomy binning & profiling: metaphlan2
- Functional annotation: HUMAnN2
- Assessment of diversity: QIIME

Where?



https://github.com/alesssia/YAMP

https://github.com/alesssia/YAMP/wiki



https://hub.docker.com/r/alesssia/yampdocker

Who?

#### Acknowledgements

TwinsUK

Mario Falchi Tiphaine Martin

The "community"

Brian Bushnell Paolo Di Tommaso





