
# Sequana: a set of NGS pipelines

## overview and status (Feb-Aug 2016)

Thomas Cokelaer and Dimitri Desvillechabrol

Institut Pasteur

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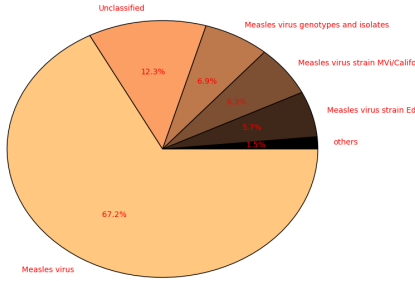
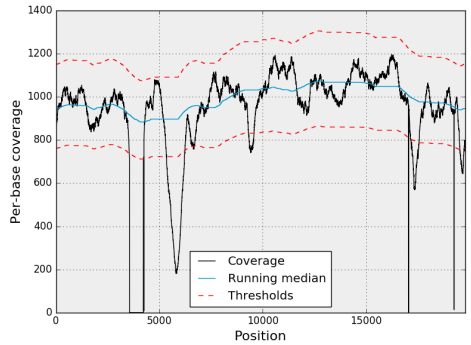
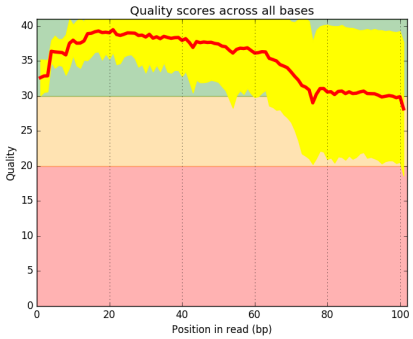
## Overview

- In the context of the Biomics platform, we are developing NGS pipelines to analyse DNA sequencing data (Illumina). Pipelines are available within the **Sequana** project.
- We aim at providing HTML reports and clean processed data that are reproduceable but also a common library to foster co-development within IP.
- Currently, we have pipelines to assess the quality of the sequences, detect variants, denovo assembly, taxonomic content, systematic study of the assembly coverage.
- A Continuous Integration guarantees a high quality software (reproducibility, tests, doc)


## Timeline and usage

- Sequana Project started in March 2016 and is entering production mode for the PF1 platform.
- Currently, Sequana is used to analyse paired or single-end Illumina seq. data (HiSeq, MiSeq)
- Future pipelines will include long reads analysis.
- Sequana can be used on the BIC or Tars IP cluster. A release is planed by the end of 2016

## Links and contributions

- For developers, please join the github : https://github.com/sequana/sequana
- For users, please see the on-line documentation on sequana.readthedocs.org
- Special thank you to Christiane Bouchier for her help and contributions