HTSstation
A web application for High Throughput Sequencing data analysis

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Demultiplexing / Mapping

4C-seq
- Identification of long-range 3D interaction partners
  - Create library of fragments
  - Identify informative fragments
  - Calculate a normalized score per informative fragment

ChIP-seq
- Crosslinking
- Sonication
- Immunoprecipitation & reverse crosslinking
- Short read sequencing

RNA-seq
- Identification of interacting regions
- Running mean algorithm
  - Window size: 8 informative fragments, RNA O.5
- Translocation to interacting restriction fragment

SNP calling
- Detect & annotate SNPs
  - Detect SNPs from reads coverage and frequencies
  - Locate SNPs (exon, promoter, ...)
  - Indicate amino acid changes

Visualisation with GDV
- Genome browser
  - Fast, responsive and interactive visualisation
  - Manage, export and share data
  - Generate sub-dataset by selection
  - Link with gene documentation

Data manipulations with GDV
- Descriptive statistics
- Advanced plots

How to use HTSstation?
Standard analysis can be easily launched from the web interface: http://htsstation.epfl.ch. For advanced users, each module can be customised with configuration files. Developers can re-use all scripts available on github (http://github.com/bbcf) and integrate them with their own programs.