The overall aim is to provide virologists within veterinary medicine with an easy to use tool for experimental design, simulation and analysis of viral metagenomics experiments.

### Experimental design

Provide an estimate of needed sequencing depth

Ensure enough coverage to detect all viral species in a sample, even those of low abundance

- **- Estimation of the sequencing depth using an adaptation of Stevens’ theorem (1).**

- **- Prediction of the confidence value for finding all genomes present in a sample.**

### Bioinformatic analysis

Data preprocessing: quality control

Assembly of the sequencing reads

Taxonomic assignment / Binning

### Evaluation

Testing tools on datasets with known content:

- Simulated datasets

Results analysis and comparison

Validation

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**MetLab**

This module can be used to simulate viral metagenomic datasets from sequencing profiles, as well as create sequencing profiles from sequence data.

- Ion Proton
- Ion Torrent (200bp or 400bp)

Simulates datasets from:

- a selected sequencing technology

- a number of included species and their distribution.

Then downloads random viral genomes, generates the fastq file(s) and summarizes the taxonomic content.

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