# MetLab: an in silico experimental design, simulation and validation tool for viral metagenomics studies

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The use of metagenomics for detection and characterisation of viruses has several difficult steps, including high throughput sequencing and bioinformatics analysis. We present MetLab, a new program aimed at providing scientists with a simple baseline for experimental design and analysis of viral metagenomics.

MetLab aims to provide support in planning the sequencing, by estimating coverage by implementing an adaptation of Stevens' theorem (Wendl *et al.* 2013). It also provides scientists with several pipelines aimed at simplifying the analysis of viral metagenomes, including quality control, assembly and taxonomic binning. We also implement a tool for simulating metagenomics datasets from a number of sequencing platforms. The overall aim is to provide virolo-gists within veterinary medicine with an easy to use tool for designing, simulating and analyzing viral metagenomes. The results presented here include a comprehensive benchmark towards other suitable software, with emphasis on detection of viruses as well as speed of applications. MetLab is packaged as one comprehensive software package, readily available for Linux and OSX users.

## Acknowledgements

## References

Wendl MC, Kota K, Weinstock GM and Mitreva M (2013) Coverage theories for metagenomic DNA sequencing based on a generalization of Stevens' theorem. *J. Math. Biol.* **67**(5), 1141–1161. http://dx.doi.org/10.1007/s00285-012-0586-x