



Aalborg Universitet

AALBORG UNIVERSITY
DENMARK

Global genome-centric metatranscriptomics unravels food webs in complex microbial communities

Yssing Michaelsen, Thomas; Hao, Liping; Brandt, Jakob; Karst, Søren Michael; Kirkegaard, Rasmus Hansen; Albertsen, Mads

Publication date:
2018

Document Version
Publisher's PDF, also known as Version of record

[Link to publication from Aalborg University](#)

Citation for published version (APA):

Yssing Michaelsen, T., Hao, L., Brandt, J., Karst, S. M., Kirkegaard, R. H., & Albertsen, M. (2018). *Global genome-centric metatranscriptomics unravels food webs in complex microbial communities*. Poster presented at 17th International Symposium on Microbial Ecology, Leipzig, Germany.

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- ? Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- ? You may not further distribute the material or use it for any profit-making activity or commercial gain
- ? You may freely distribute the URL identifying the publication in the public portal ?

Take down policy

If you believe that this document breaches copyright please contact us at vbn@aub.aau.dk providing details, and we will remove access to the work immediately and investigate your claim.

Global genome-centric metatranscriptomics unravels food webs in complex microbial communities

Thomas Y. Michaelsen, Liping Hao, Jakob Brandt, Søren M. Karst, Rasmus H. Kirkegaard and Mads Albertsen

Albertsen Lab, Center for Microbial Communities, Aalborg University, Denmark



Introduction

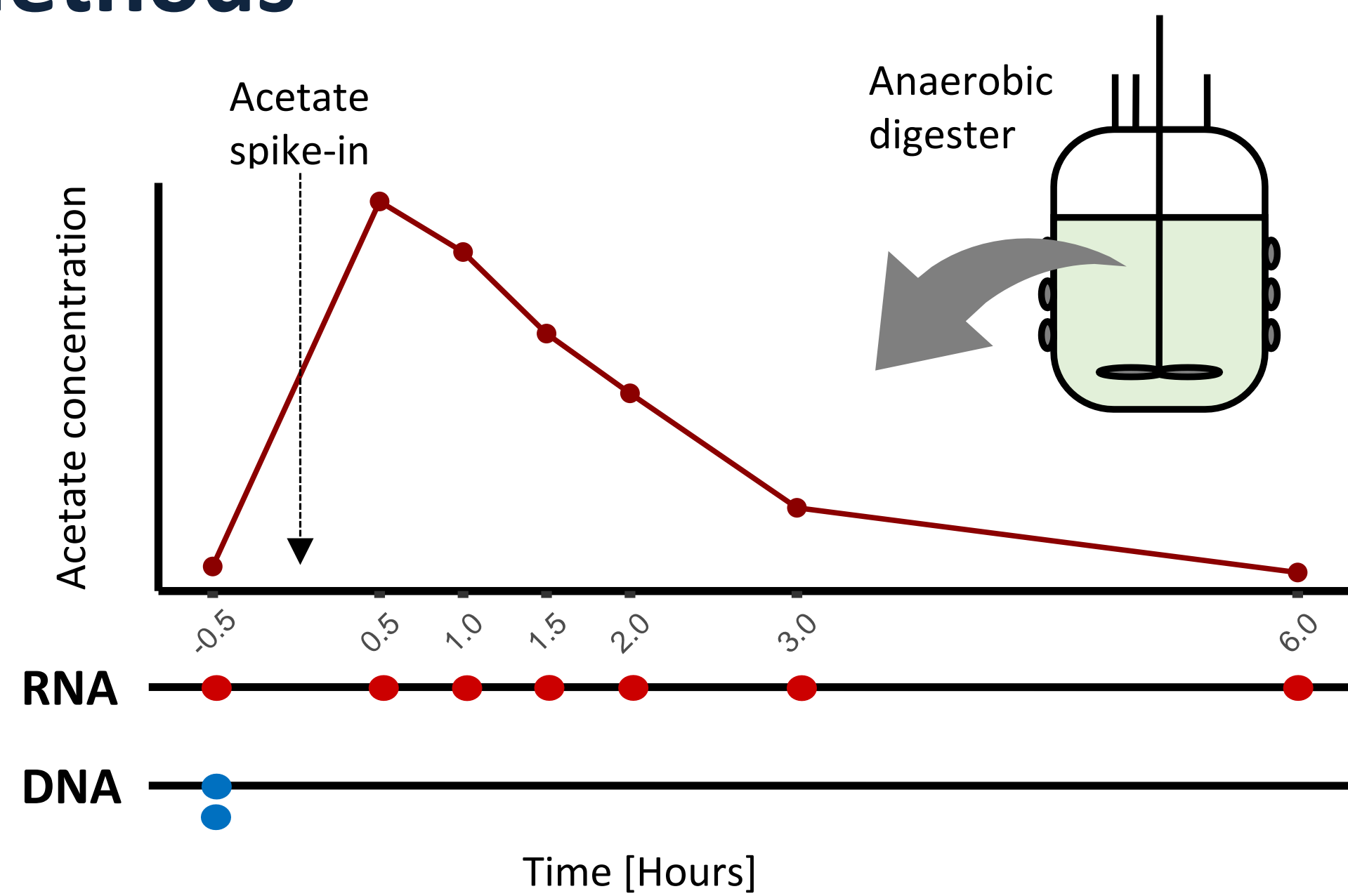
Advancements in high-throughput sequencing have led to an increasing amount of time series studies, investigating the temporal variation of microbial communities across multiple environments. However, the integration of this vast amount of data with high-quality metagenome-assembled genomes (MAGs) are lagging behind. We introduce a simple, quantitative framework linking MAGs to functional response and food webs.

Objective

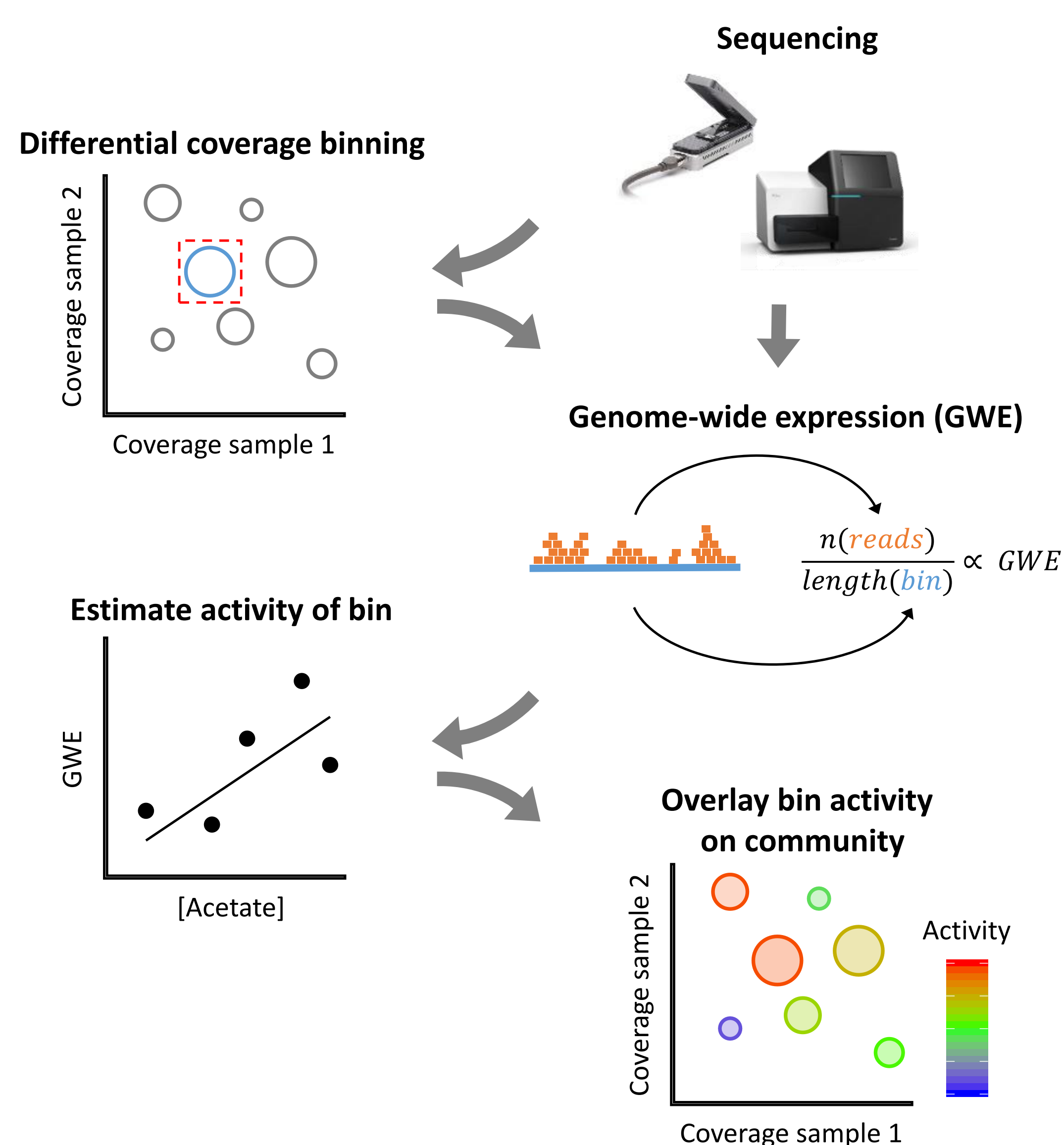
Develop a genome-centric approach to characterize and quantify the activity of a complex microbial community using metatranscriptomics.

- Characterize genome-wide expression patterns
- Identify reactive species in complex samples
- Identify key biological pathways

Methods



Experimental design | A continuous stirred tank reactor was inoculated with sludge from an anaerobic digester. After a starvation period the reactor was stimulated with an acetate spike-in. Metagenomes for differential coverage binning were obtained before spike-in and transcriptomes for genome-wide expression were sampled in a regular interval up to six hours after stimulation.

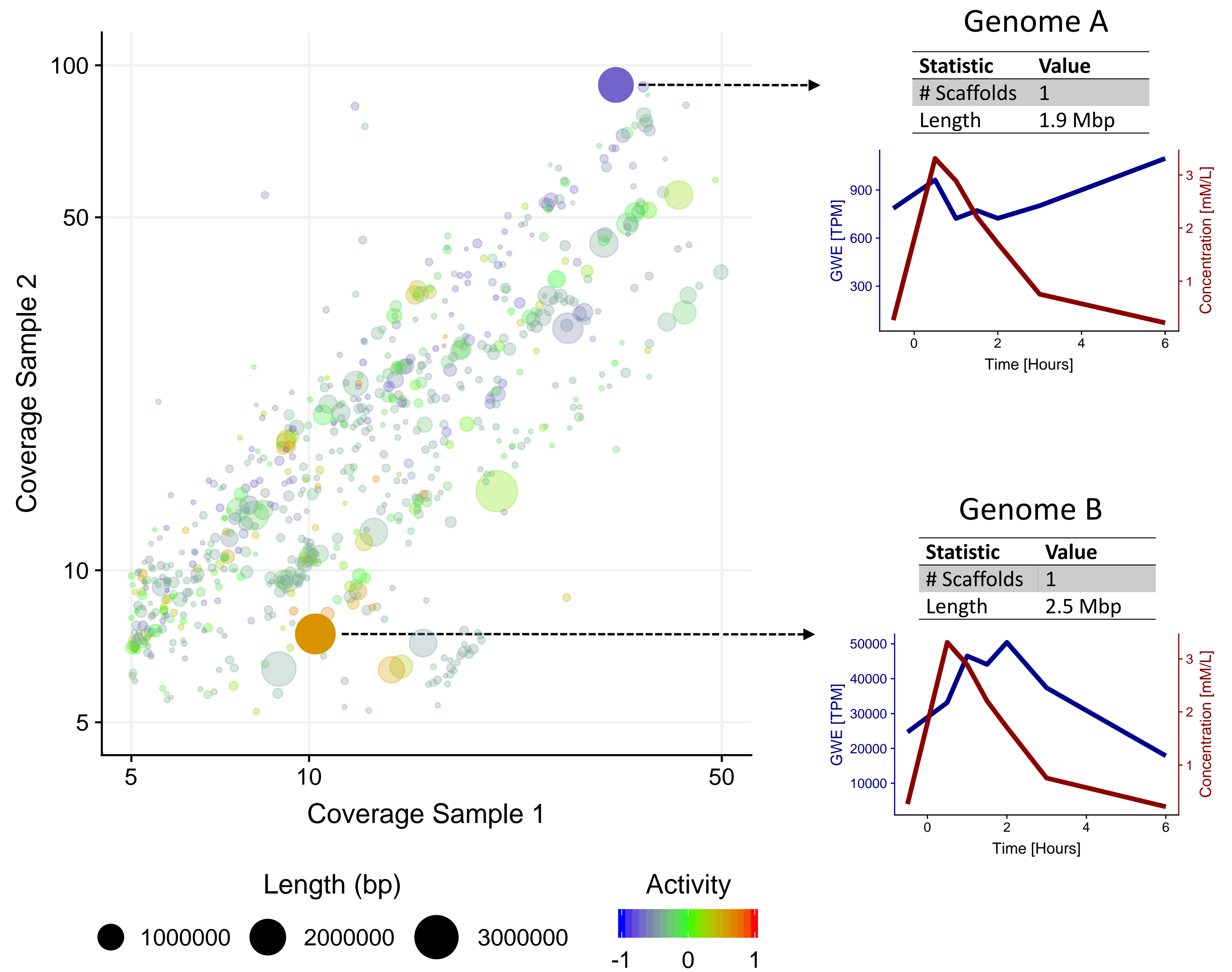


Genome-wide expression analysis | DNA samples were illumina paired-end sequenced and mapped to a Nanopore-only assembly for differential coverage binning. RNA samples were illumina single-read sequenced and mapped directly to assembled bins to estimate genome-wide expression (GWE). The GWE were associated to the concentration of acetate measured at same timepoint by cross-correlation analysis with a lag-time of one. Finally, the activity of each bin, measured as the strength of cross-correlation, were overlaid on the differential coverage plot to identify responders to acetate.

Conclusion

Overlaying transcriptomics data on high quality metagenomes enable fast detection of reactive members in a microbial community.

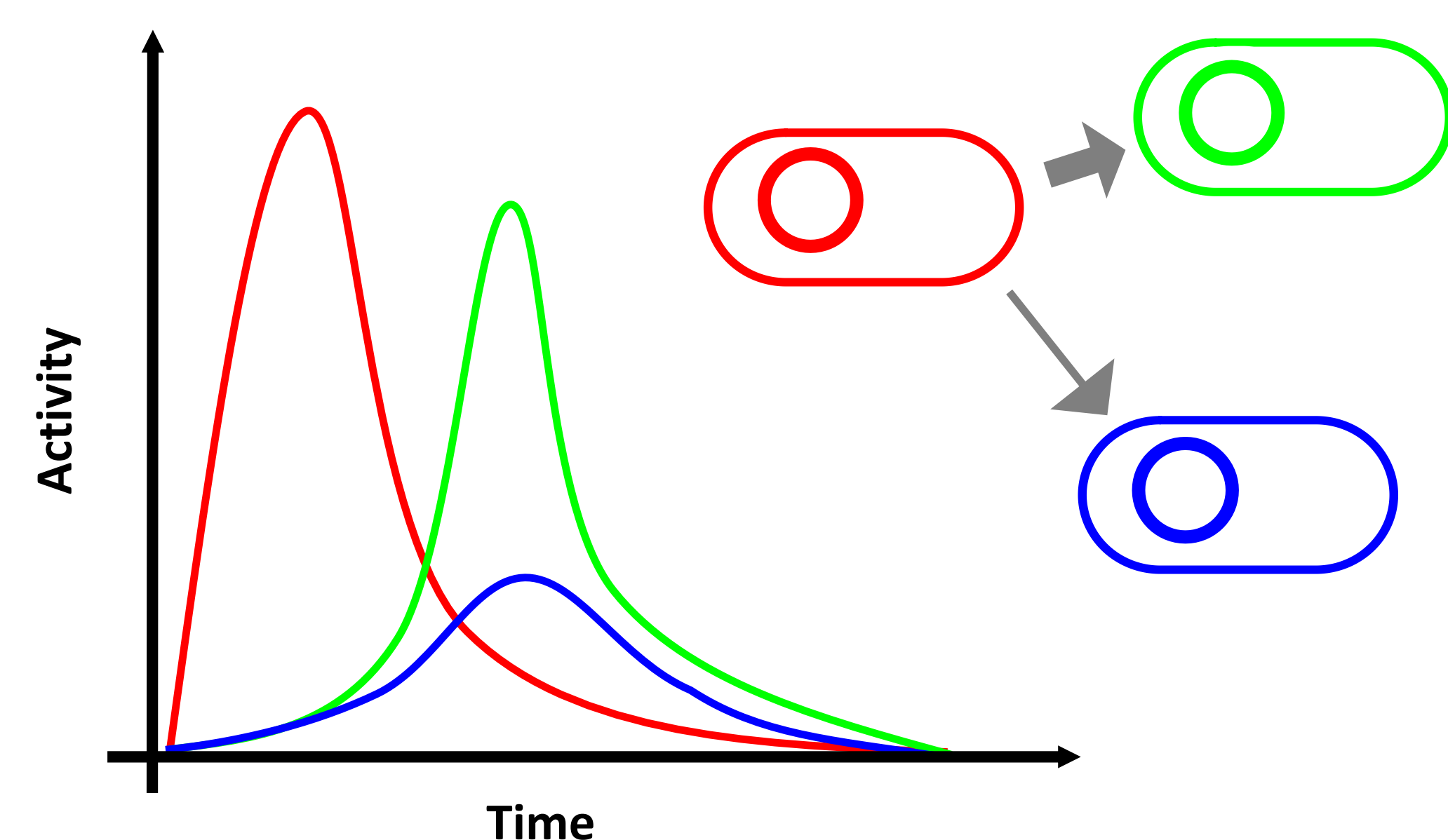
Genome-wide response to acetate



Targeting active members in the community | The leftmost plot shows the differential coverage of two metagenome samples taken half an hour before acetate spike-in. Each point represents a scaffold scaled by size to the length of the scaffold and coloured by the strength of the activity associated with acetate. Transparency are added for visual guidance only. Details of two highlighted bins are shown in the top-right and bottom- windows. Within each window the genome-wide expression (GWE) are plotted against acetate concentration across time, along with essential statistics of the draft genome.

Perspectives

In-depth analysis of targeted draft genomes using time series and correlation network analysis will enable the reconstruction of food webs and interrogate causal drivers for shifts in bacterial activity to identify novel keystone species. In addition, detection of genome-wide patterns as gene clusters and key driver genes will map out the biological functionality and potential of individual community members.



Want to try it out for yourself?

- [mmgenome2](https://github.com/KasperSkytte/mmgenome2) – github.com/KasperSkytte/mmgenome2
- [mmtravis](https://github.com/TYMichaelsen/mmtravis) – github.com/TYMichaelsen/mmtravis

