Feedback on a comparative metatranscriptomic analysis

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Feedback on a metatranscriptomic analysis

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Context

The progress of next generation sequencing favors the development of more comprehensive ecosystem studies thanks to metatranscriptomic approaches. These latter can indeed provide access to functional information at a good analysis depth. Through a study of anaerobic digesters treating wastewater contaminated by an anionic surfactant (namely the linear alkylbenzene sulfonate, LAS), we developed a bioinformatics pipeline to perform RNAseq analysis of the metatranscriptomics data.

Data

The samples originated from distinct biological reactors:
- fed with synthetic medium (UASB_Control)
- fed with synthetic medium + LAS (UASB_SL)
- fed with real laundry wastewater (UASB_LW)

These samples were sequenced in duplicates with Illumina HiSeq platform (2 x 100bp ; ~20M reads/sample )

Tools and workflow

Metrics

Results

- Percentages of LAS removal (~50%) were similar among the three reactors.
- Rarefaction analysis revealed that two million reads were sufficient to access to the main functional capacity.
- In the first step of LAS biodegradation pathway, fumarate reductase subunit C was detected and taxonomically assigned to the genus Syntrophobacter.
- In the second step, many enzymes related to beta-oxidation were expressed preferentially in UASB_SL and UASB_LW. They were taxonomically related to Smithella, Acinetobacter and Syntrophorhabdus.
- Finally, the adenylylsulfate reductase, taxonomically related to Desulfovibrio and Desulfomonile, was observed in the desulfonation step with the highest relative abundance in UASB_LW.

Conclusions

- This study enabled detecting active genes likely involved in each step of LAS biodegradation and exploring the microbial active core related to LAS degradation (Delforno et al., 2019).
- Based on this positive experience, we developed a snakemake pipeline including all this features for use in future metatranscriptomic projects.