Interactive Visual Support for Metagenomic Contig Binning

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Biogas is becoming increasingly important as a sustainable alternative for conventional energy sources. A good understanding of the biological aspects is crucial to optimize the production.

A mix of bacteria is responsible for digesting the biological material and producing the gas. To control the production process it is required to understand which species are in the mix and what their function is. For this, biologists look at the DNA of the species found in a biogas tank.

Shotgun sequencing methods, result in many small fragments of DNA, belonging to the various species. Multiple samples are taken over time.

Assembly software is used to reconstruct longer sequences of DNA material, called contigs. The confidence of each contig varies, depending on the quality and availability of suitable reads for a given contig

Contigs are binned in groups that are likely to belong the same species.

Contigs in a single bin are then passed again into assembly software to obtain longer sequences of DNA.

Visual Analytics Support

Automated analysis

- Tetranucleotide frequencies are calculated and analyzed.
- Different clustering techniques.
- Principal Component Analysis and Correspondence analysis for statistical summaries of the data.
- Analytical back-end based on R, existing analytical methods.

Interactive Visualization

- Appropriate visualization techniques for multivariate data and statistical summaries.
- Interaction for selection and filtering, to get overview and details on demand.
- Various color modes to enhance visibility of different patterns.

Future Directions and Challenges

- Visualization of uncertainty data, reflecting the uncertainty of the provenance of DNA sequences.
- Contig aggregation and bundling to reduce overdraw.
- Integration and evaluation of contemporary automatic binning approaches.
- User evaluation using subject matter experts.

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