CZECHGLOBE OPEN DISPUTATION

INVITATION

"*DeNovo* assembly for high throughput sequencing"

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On **29th August 2014** at **10:30 am** in the large meeting room

of **Global Change Research Centre AS CR, v. v. i.**; Brno, Bělidla 986/4a

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Abstract

The sequencing of single bacterial genomes has become more feasible for research groups or even single researchers due to advances in both sequencing technology as well as algorithmic developments. New developments in technological platforms offer more cost-effective and simplified genomic reconstructions, and new software developments can facilitate this by taking advantage of the specific strength and weaknesses of each platform. Often ignored but equally important is the post-assembly refinement of a genome, that can further decrease genome fragmentation and, given the right technology combination, even recreate a circular, closed genome. Here I want to give an overview of the limitations of current generation sequencing & assembly technologies and what can realistically be achieved in terms of quality and accurate recovery of an assembled genome.

In the second part an overview of common genome annotation and comparison tools is given with examples for Pseudomonas genomes.

The last part will cover Cyanobacterial metagenomic studies in the Arctic, where we described the phylogenetic composition in respect to toxin production & geographical distance.

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