

**Oberseminar Theoretische Informatik**  
Sommersemester 2006

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## **Simple and Fast Alignment of Metabolic Pathways by Exploiting Local Dissimilarity**

Mo, 03.07.2006 um 14 Uhr (s.t.) im SR 226 (Carl-Zeiß-Str. 3, 2. Stock).

An important bioinformatics tool for analyzing metabolic pathways is being able to do a homology search, that is, for a given “pattern” network one tries to find occurrences of similar (sub)networks within a set of “host” networks. Recently, Pinter et al. [Bioinformatics, 2005] proposed to solve this computationally hard problem by restricting it to the polynomial-time solvable case where both the pattern and host network are trees. This restriction, however, severely limits the applicability of the algorithm. Here we show that it can be circumvented by exploiting the “local dissimilarity property” of metabolic networks, that is, the neighbors of a node generally are mutually very different in their functionality. This yields a fast and simple algorithm for homology searches among metabolic pathways; for a testbed of pathways extracted from the BioCyc database, we show that it is faster than the implementation of Pinter et al., yet being applicable to general networks. Furthermore, we point out how the concept of local dissimilarity can be exploited for the alignment of other types of biological networks.

Internetseite der Veranstaltung:

<http://theinf1.informatik.uni-jena.de/teaching/ss06/oberseminar-ss06>