

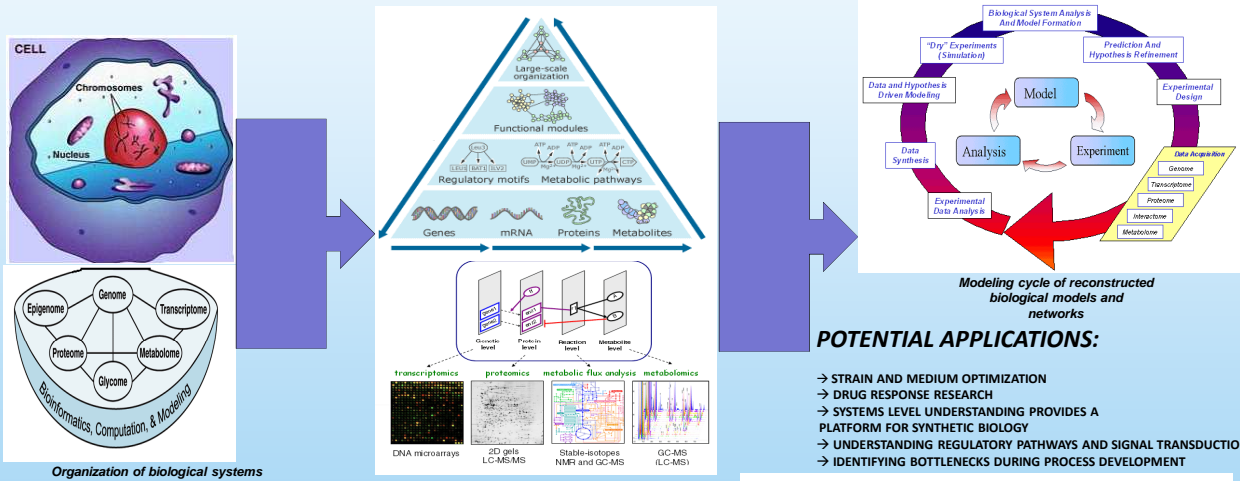
# Reverse Engineering strategies for reconstructing biological networks from omics data

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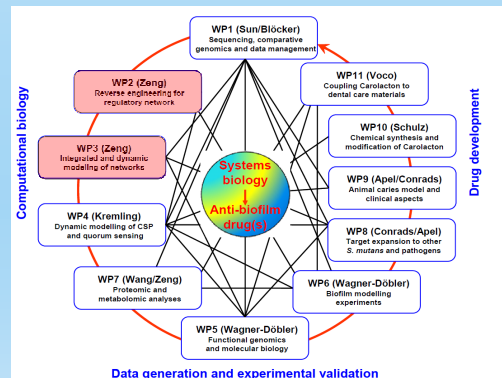
## CONCEPTUALITY:

→ To construct qualitative and quantitative in-silico models (reconstructed networks) of biological systems using integration of omics data (transcriptomics, proteomics, metabolic datasets)

→ Such reconstructed networks can then be used for simulating the behaviour of the biological system to different biochemical conditions such as drug treatment, environmental and genetic perturbations.



**CURRENT APPLICATION AREA: Reverse Engineering the genetic network of the caries causing pathogen *Streptococcus mutans* in response to the biofilm inhibitor Carolacton.** Understanding context-dependent and condition-specific regulatory relationships at the gene level is vital for uncovering the pathogenicity, adaptability and resistance mechanisms of pathogens. Such an understanding could also provide insights into specific mechanisms at the genetic interaction level orchestrated by a foreign molecule or drug. The aim of this work-package of the BioInSys project is to reconstruct the genetic regulatory network of the caries causing dental pathogen *Streptococcus mutans* in response to the biofilm inhibitor Carolacton. Dental plaque is an extremely complex biofilm community in which quorum sensing by intra- and interspecies signalling has been established to play a key role in plaque biofilms. The transcriptomic response of *S. mutans* to Carolacton was measured using microarrays and the data subsequently used for making functional and regulatory inferences from the Carolacton-specific response network. The network was referred from the microarray-based transcriptomic data by using a unique reverse engineering method (Trend Correlation Method) developed by our group. This work comprises the top-down data-centric approach of the BioInSys project's modelling framework which provides the experimental framework with hypotheses for further testing and verification.



### WHAT DO WE OFFER ?

**TREND CORRELATION (TC) METHOD (He and Zeng, 2006. BMC Bioinformatics. 2006, 7:69):**

→ A reverse engineering algorithm designed specifically for inferring the functional and regulatory networks of organisms using dynamic time series biological datasets at the transcriptomic, proteomic and metabolic levels.

→ Most of the reverse engineering methods in the contemporary literature need "equidistant" (periodic) sampling for the biological datasets. The TC method can use both periodic and non-periodic datasets for network inference.

**NEW METHOD IN THE PIPELINE : FOR INFERRING CORRELATIONS IN DIFFERENTIAL TIME WINDOWS**

### WHAT WE ARE LOOKING FOR?

→ Research groups who have a systems-level question in terms of understanding systemic responses of biological systems to a specific stimulus or condition.

→ Do you want make sense of high-dimensional -omics datasets?

→ Groups who would like to study the systemic response using high-quality time-series omic datasets aimed at answering specific biological questions : be it at the transcriptomic, metabolic or proteomic levels.

### Contact

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