Insilico Biotechnology is a market-leading company providing predictive solutions for the Bioeconomy. An interdisciplinary team of experts offers mechanistic models, customized software, and a high performance computing platform for the simulation of living cells. For world-leading pharma and biotech companies Insilico’s technology lowers time, risk and costs of development processes. Founded in 2001, Insilico is a privately held company based in Stuttgart.

To strengthen our young and dynamic research and development team in Stuttgart, we are looking for a master student that will complete a

Master Thesis regarding a New Pathway Analysis Algorithm applied to Large-Scale Metabolic Networks (f/m)  (Reference number 17MT2)

Key responsibilities (note abstract on next page):
- Design, implementation and test of a new method for computing elementary modes
- Technical documentation

Your qualifications:
- Successfully completed bachelor’s degree in Biotechnology, Biochemical Engineering, Biosystems Engineering, Bioinformatics, or comparable
- Basic knowledge in modelling and simulation
- Good written and oral command of German and English is essential

What we offer:
- Personal and professional development in an expanding, internationally operating company at the interface of information technology and biotechnology
- Open and flexible working environment with flat hierarchies
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Start: as soon as possible
Location: Stuttgart
Duration: 6 months
Schedule: full-time

We are looking forward to receiving your complete application documents per e-mail, stating reference number 17MT2. Please include an overview of your academic records and your earliest possible date of entry.

E-Mail address for application documents: career@insilico-biotechnology.com
Your contact person for enquiries by phone: Dirk Rathfelder | +49 711 460 594-19
Abstract of Master’s Thesis

Elementary modes are the smallest sub-networks that allow a metabolic reconstruction network to function in steady state. Elementary modes can be used to (i) understand cellular objectives for the overall metabolic network, (ii) to verify network functionality and (iii) to design new pathways for existing or new products. Furthermore, elementary mode analysis takes into account irreversibility of individual reaction steps and thus allows for prioritizing promising and thermodynamically feasible routes. Computing all elementary modes for a given network, however, most often runs into a combinatorial diversity that impedes the practical application for many relevant cases. In this master thesis, a new method for computing elementary modes is designed, implemented and tested by constraining the solution space to given substrates and/or products. IBM® CPLEX optimizer, an advanced tool for convex analysis will be applied for solving the task. In addition, the work will capitalize on given genome-based networks for *E. coli* and a high-performance computing infrastructure.