SUBJECT MATH-DEV 2: Population-based model calibration

Background

Novadiscovery evaluates the outcomes of treatments by applying them in silico to a population of virtual patients. Those virtual patients are represented by a vector of descriptors that impact the model behavior. Thus, the same model can behave differently from one patient to the next, similar to real life situations when the outcome of a treatment varies from one individual to the next. Unfortunately, for a lot of those descriptors, their exact value or value distributions are unknown from the onset. Being able to infer those from indirect information such as expected behaviors of our pathophysiological model or observable data points from in vivo or in vitro experiments then becomes a crucial exercise so as to simulate our models on realistic patients. The process of inferring those descriptors distributions is later referred to as calibration. Furthermore, some parameters are unknown but not patient-independent. The co-existence of patient-dependent and patient-independent parameters makes the calibration task more complicated because it requires a hierarchical approach[1] to the inference problem. The goal of this internship is to review existing hierarchical inference methods and to implement and integrate one into the existing calibration platform.

Objective:

Implement and compare several optimization algorithms to try and calibrate unknown descriptor distributions.

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https://doi.org/10.1371/journal.pcbi.1007043
Work Process:
- Literature review
- Prototyping of one or two candidate methods
- Integration into the current platform

Deliverables:
Integration of population-wide calibration into the existing platform

You are
- A team player, a good listener, and an effective communicator. Join a growing multidisciplinary team of enthusiastic innovators
- Curious and proactive with a solid grounding in biology: Particularly in cell biology, molecular biology, and omics, to address real-life clinical issues.
- Autonomous and self-motivated with strong analytical and problem-solving skills: Find innovative solutions to science and engineering problems
- Eager to learn and use mathematical methods for the modeling of biological systems: Simulate virtual diseases and treatments with ODE, PDE, Monte-Carlo Simulations
- Willing to explore and exploit large datasets and virtual populations: Apply machine learning, statistical analysis, and outliers detection
- Responsive and capable of facing time-sensitive challenges: Project management with client-facing opportunities are awaiting you

You will
- Contribute actively to the creation of in silico pathophysiological models
- Impact the development of the company’s simulation platform
- Analyze and exploit large simulation results
- Participate in weekly and monthly project meetings and reporting

Details
- Apply directly on our careers page
- Contact: recruitment@novadiscovery.com
- Type: Internship
- Salary: Competitive
- Start date: Flexible

Technologies & languages:
Distributed Computing (AWS), Docker, Python, Haskell
Duration:
3 months / 6 months

Keywords:
Bayesian Inference, MCMC, Calibration, Optimization, Systems Biology