SUBJECT BIOMOD 2: Development and optimization of a physiologically based pharmacokinetic drug module

Novadiscovery is a pioneer in the emerging field of in silico medicine based in Lyon (France). Working with an innovative company in its scale-up phase is an entirely different experience than working for a large established company. You will be assigned a great number of responsibilities and work in a dynamic environment with strongly motivated people who will help you fast-climb a steep learning curve. For more information visit www.novadiscovery.com.

Keywords: PBPK, pharmacokinetics, Systems Biology, Biomodeling

Background:
The biological models developed at Nova are composed of several submodels, each accounting for a given biological phenomenon. Among these submodels, each project always includes a treatment submodel to account for drug disposition. More precisely we use physiologically based pharmacokinetic (PBPK) mechanistic models. However, a version of such a submodel with a modular architecture is a current critical need to allow for re-usability between projects in order to prevent high time re-implementation costs of PBPK models in each project.

Previous works established a first version of such a PBPK module, currently limited to simple perfusion- or permeability-limited small molecules and antibodies. Although this first version is already functional at the cost of several adaptations to fit with each project specificities, this module needs to be further developed by:

- Review and revision of the internal documentation on PBPK modeling
- Assessment of the module credibility and robustness by confronting the module with literature data
- Implementation of currently missing mechanisms such as elimination pathways or subcutaneous administration, as well as refinement of existing mechanisms, such as the blood-brain barrier
- Extension of the module to new contexts of use such as other populations (pediatric, non-human, pathological status)

Objective:
The main objective of this internship will be to work on one of the aforementioned aspects to improve the current module through the implementation of selected new module features and an associated literature review.

**Deliverables:**
- Literature review and model documentation in Jinkō knowledge platform on one or several reference treatments
- Calibration and validation of treatment submodels derived from the module using data extracted from the literature
- [Optional] Addition of new features in the module through a literature review and an update of the Computational Model (CM) in the Jinkō simwork platform

**References:**
To be provided based on the drug candidate chosen

**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**
- **Type**: Internship
- **Salary**: Competitive
- **Start date**: Flexible

**Technologies and languages**
We are looking for people who know some of the following or are eager to learn and work with them:
- Unix environment
- Programming languages (Haskell, NodeJS, TypeScript, Nix)
- Statistical/scientific computing (R, RStudio)
- Big data (NoSQL, Spark, Parquet)
- Markup languages (Markdown, LaTeX)
- Miscellaneous (Git, bash, zsh, RDF, SPARQL, Elasticsearch)