SUBJECT STAT 3: Responders identification and biomarkers selection

Background:
Novadiscovery’s *in silico* approach is used to simulate clinical trials, in order to predict the efficacy of a drug, and to help biotechs and pharmaceutical companies in the selection of the best treatment responders, that is to say the patients among whom the treatment efficacy would be optimal. The objective of this identification approach is to select the combination(s) of patient descriptors (model parameters) and baseline variable values and/or interactions linked to the highest treatment efficacy predicted by the Computational Model.

Objective:

Notes:
- Define criteria to classify patients as responders
- Use the sensitivity analysis approach already implemented in the Jinko platform to identify responders characteristics
- Get familiar with other statistical methods to identify responders currently in use at Nova (Jinko-stats (inhouse R library)) but not yet integrated into Jinko.ia platform (inhouse modeling and simulation platform)
- Benchmark and compare the methods and define the way to combine results (cross selection between methods)
- Analyze algorithms implemented in Jinko-stats, identify required features then work on the migration to Jinko.

Work Process:
- Get acquainted with the statistical approaches already in use
- Discovery of the Jinko platform architecture and features
Integration of the statistical methods in Jinko
Work with both Jinko devs (dev math, core, front), biomodelers and the data-analytics teams
Contribute in drafting related documentation

Deliverables:
- Documentation: how to, methodology notes, SOP
- A fully integrated statistical toolbox to be used by statisticians and biomodelers

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:
Haskell / Python / R / git
References & topics of interest:
- Regression shrinkage and selection via the lasso: a retrospective
- The Variable Selection Problem
- Variable selection using Random Forests
- Fractional factorial design
- Variance-based sensitivity analysis

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<thead>
<tr>
<th>Duration</th>
<th>Keywords</th>
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<tbody>
<tr>
<td>3 or 6 months</td>
<td>Biostatistics, Mathematics, integration, variable selection</td>
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