Lead Scientist Quantitative Systems Pharmacology

Bio-LogX, recently founded by BioNTech R&D Austria's leadership team, is a VC-backed translation & innovation engine based at the Vienna BioCenter. We develop drug candidates from animal to clinical proof of concept – always with the ambition to transform the standard of care. We are agnostic about the therapeutic area but focus on protein modalities: antibodies, other binders, enzymes, fusions, engagers, degraders, agonists, antagonists.

As Lead Scientist Quantitative Systems Pharmacology at Bio-LogX you will join our research team in our lab in Vienna and help us bring next generation drugs from the bench into the clinic.

Your main responsibilities will be.

- Develop and apply mechanistic, multiscale, and translational mathematical/ computational models to support biologics research and early development, including target biology, tissue distribution, pharmacokinetics, pharmacodynamics, biomarkers, and efficacy/safety relationships.
- Survey and synthesize scientific literature and experimental data to identify and implement the most relevant biological processes, mechanistic assumptions, parameters, and datasets for model development.
- Build, calibrate, and refine reduced and more detailed models as needed to evaluate biological hypotheses, molecular trade-offs (e.g. the influence of binding affinities on tissue penetration in bispecifics), and translational questions, using internal and external datasets for parameterization, qualification, sensitivity analysis, uncertainty quantification, and scenario testing.
- Develop reproducible model code, documentation, and version-controlled workflows using modern scientific computing and QSP toolsets (e.g. MATLAB and SimBiology, Julia, Python, R; optionally NONMEM, Monolix, Phoenix NLME, Berkeley Madonna, COPASI, gPROMS, or SBML-compatible environments).
- Contribute to modern computational workflows by structuring models and data in ways that support downstream integration with machine-learning and AI-enabled approaches, for example through interoperable model objects, reproducible data pipelines, API-friendly interfaces, and reduced or surrogate modeling layers that enable efficient evaluation in broader computational discovery environments.
- Translate simulation outputs into clear, actionable recommendations for discovery, translational, DMPK/PKPD, protein engineering, and project teams.

- Collaborate effectively across computational and experimental functions, and communicate modeling strategy, assumptions, results, and limitations to interdisciplinary stakeholders at different levels of quantitative expertise.

What you have to offer.

- PhD in systems pharmacology, systems biology, computational biology, biomedical engineering, pharmacometrics, applied mathematics, or a related quantitative life-science field, with a strong scientific record of publications, presentations, or impactful project contributions;
- 3+ years of postdoctoral experience in disease modeling, QSP, mechanistic PK/PD, systems biology, or related quantitative modeling in biotech, pharma, or a strong academic setting.
- Strong proficiency in differential-equation–based modeling and the ability to independently build, analyze, qualify, and communicate mechanistic models in support of scientific decision-making.
- Experience with quantitative methods such as parameter estimation, sensitivity and uncertainty analysis, model reduction, and integration of in vitro, ex vivo, and in vivo translational data into QSP or mechanistic PK/PD models.
- Hands-on experience with current QSP and scientific-computing tools such as MATLAB (ideally including SimBiology), Julia, Python, and/or R; familiarity with additional platforms such as NONMEM, Monolix, Phoenix NLME, Berkeley Madonna, COPASI, gPROMS, or SBML-based workflows is a plus.
- Familiarity with AI/ML methods that can complement mechanistic modeling, such as supervised learning, surrogate or emulator models, Bayesian optimization, active learning, probabilistic modeling, and practical experience with common Python ML libraries (e.g. scikit-learn, PyTorch, TensorFlow, JAX, or PyMC) in the context of scientific problems.
- Demonstrated ability to collaborate effectively across computational and experimental disciplines, communicate complex ideas to diverse stakeholders, and help identify the most informative experiments to strengthen model confidence and reduce key uncertainties.
- Experience in drug discovery and/or development, especially in biologics, immunology, oncology, fibrosis, or related therapeutic areas is a plus.
- Comfortable in a fast-paced environment and able embrace change, while working to produce key deliverables in accordance with project timelines.

- Excellent communication skills: ability to productively engage with wet-lab scientists with low proficiency in QSP, and to translate your results into practicable recommendations for the team.
- Proactive, self-motivated team player with strong interpersonal skills, appropriate sense of urgency and the ability to work independently.
- Proficiency in English (written and spoken).

Benefits for you.

- Take responsibility for a key research field within Bio-LogX.
- Lead and develop a team of highly skilled bio-informaticians, scientists and researchers.
- Pioneer new methods and processes to industrialize key research techniques.
- Be part of a highly motivated, multinational and fun team that believes protein based modalities can become next-generation medicines for patients.
- A **competitive compensation package that reflects the qualifications and seniority of the candidate** and may include further, e.g. performance-based, incentives. *Due to legal requirements, we are required to state that the minimum salary for this job is a monthly salary of EUR 5.500,-- gross.*