Questions and overview

The exam will be in total 10 minutes/person.

You make 10 minutes presentation covering the question.

Remaining 10 minutes: We ask questions across the course-subjects, including your project and assignments

Note: Important to be quantitative. Make sure to refer to key equations.

- Q1: Protein Misfolding Diseases. Similarities and differences.
 - Master equation of the aggregate kinetics (Mechanistic description).
 - 2-step Finky-Watsky (Phenomenological description).
 - Pros and Cons of the Mechanistic vs Phenomenological.
- Q2:Protein quality control. Components of PQC and their function.
 - Negative and positive feedbacks in between PQC and aggregates. How do feedbacks affect kinetics of the aggregate formation. Relate to the models and diseases:
 - Model of the PQC in Aβ kinetics by Krohn et al. JCI 2011
 - Proteasome dynamics in Parkinson by Sneppen et al.
- Q3:Receptor desensitization/adaptation
 - Michaelis-Menten kinetics.
 - Circuits and capabe of adaptation: Negative Feeback and Incoherent Feed-forward loops and the related criteria.
 - Feedback algebra
- Q4 Fold-change detection.
 - Fold-change detection, model of incoherent feed forward loop.
 - What are the adaptation and FCD good for?

- Q5:Excitable media. Heart arrhythmia and pulsatile insulin secretion.
 - Feedbacks and their properties common for excitable media –systems
 - Fitz-Hugh-Nagumo model. Travelling waves.
 - Agent-based model for hearth arrhythmia.
 - Re-entrant circuits.
 - Estimate for the risk of AF.
- Q6: Cortisol dynamics
 - Regulatory network of HPA axis and associated diseases.
 - Model for the dynamics of Cortisol. Mechanism of ultradian oscillations.
 - Model vs. experiments and relevance to diseases
- Q7: Dynamics of the Immune response vs. infection.
 - Models for Resolution of infection, persistent infection and immunopathology
 - Influence of the viral inoculum and initial effector pool sizes
 - Treatment/intervention strategies and how these relate to the modeling results.