Concept Course Systems Biology, Exam 10.8.2009
113pt, 100pt = 6
If you find any mistakes or omissions, please report them in the www.vebis.ch message board. Thanks

Sauer:

- 4 key challenges of systems biology which distinguishes it from normal biology research (hint: "use computer models" is not a key challenge) 4P
- Name 2 system-level properties discussed in the concept course, and describe why they are systems-level properties 4P
- You want to measure intracellular metabolites of some cells. Describe the most likely problems at each step, the consequences arising from these problems and possible solutions. ?P
- You want to compare the fluxes through the pentose phosphate pathway of normal and H2O2-challenged yeast cells with 13C-analysis. A) Describe the experiment ("feed labeled glucose" is not enough) B) Which metabolites would you measure and why? C) Why would it be easier to use protein-bound amino acids, and what would be the limitation?

Heinemann:

- FBA is a method for analyzing otherwise underdetermined metabolic systems. A) What is the key assumption of FBA? B) ???
- In gene chip analysis, distance measures are commonly used. Describe the fundamental difference between the two types of distance measures used.
- You want to measure the behavior of yeast(?) cells on addition of large amounts of glucose. You want to simulate this behavior using a model before doing the experiment. A) What model would you search the Internet (sic!) for? B) What does this model describe? C) Why would you want to simulate the behavior before doing the experiment?
- What is the fundamental difference between protein-protein / protein-DNA networks and genetic interaction networks?
- Bayesian networks are becoming increasingly popular to study biological systems. Someone wants to study a regulatory network with several well-known feedback loops with a Bayesian network. What would you suggest to him and why?
- Biological networks exhibit many properties. For example, they have a small-world architecture, and they are modular. One property is that network motifs have been found. A) Give an example of a network motif. B) Suppose a great number of motifs has been determined. How can this be used in network analysis in systems biology?

Stoffel:

- a) What are miRNA's? How are they different from siRNA? b) Describe experiments you would do to find target genes of a miRNA.

Wolfrum:

- Describe the principles underlying 454 sequencing technology and their advantages and disadvantages relative to classical sequencing methods.

Aebersold:

- You want to analyze a set of 100 proteins, which are estimated to have between 100 and 500'000 copies per cell, with proteomics methods. Describe 2 MS technologies you would consider to use, and highlight advantages and limitation of each technique for your problem.

- Your PhD project is to determine a protein complex network by affinity purification, you will start with 10 known network nodes. a) Describe how you would map out the network (bullet points). b) A protein kinase is found associated with 2 different complexes in the network. What could be the functional implications of this? c) Describe experiments to check your hypotheses.

Domon:

- a) How do you want to determine which proteins are phosphorylated in a yeast cell? b) How do you determine the position of the phosphorylation? c) How would you determine the stoichiometry of the phosphorylations? d) Propose a system to find out differences between 2 cell types.

Pelkmans:

- Computer-based image analysis can extract confidently single cell features (....) Name three advantages of single-cell multi-feature measurements as compared to population-averaged single feature measurements. Think of (.....).
- Cell behavior is influenced by population context. Describe how population context influences cell behavior and virus infection.
- P-bodies are RNA-protein aggregates (...). Unstimulated cells do not form P-bodies, but you find in literature that arsenic induces P-body formation. You have an antibody XYZ1 which localizes to P-body bound protein ABC. You find that on unstimulated cells, you have a cytosolic distribution, whereas on arsenic-stimulated cells, you have a ???? distribution. A) How would you design an assay for monitoring P-body formation? B) How would you use supervised machine learning methods to distinguish P-body containing cells from cells without P bodies? C) ???

Hafen:

- Describe advantages and limitations of genetic screens (e.g. ey-FLP) in Drosophila for systems approaches.
- In the lecture, we discussed a paper describing a different method of systems level genetic analysis in Drosophila. a) How is this method different from the classical genetic screens described in the lecture? b) Describe why this method is more relevant to systems biology than the classical genetic screens we discussed? c) What technical advances are necessary to use this system more widely in multicellular organisms?