P02.726

Feedback Control Strategies for Spatial Navigation Revealed by Dynamic Modelling of Learning in the Morris Water Maze

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The Morris water maze is an experimental procedure in which animals learn to escape swimming in a pool using environmental cues.

Despite its success in neuroscience and psychology for studying spatial learning and memory, the exact mnemonic and navigational demands of the task are not well understood. Here, we provide a mathematical model of rat swimming dynamics on a behavioural level. The model consists of a random walk, a heading change and a feedback control component in which learning is reflected in parameter changes of the feedback mechanism. The simplicity of the model renders it accessible and useful for analysis of experiments in which swimming paths are recorded.

Here, we used the model to analyse an experiment in which rats were trained to find the platform with either three or one extramaze cue. Results indicate that the 3-cues group employs stronger feedback relying only on the actual visual input, whereas the 1-cue group employs weaker feedback relying to some extent on memory. Because the model parameters are linked to neurological processes, identifying different parameter values suggests the activation of different neuronal pathways.

P02.728

Online Suite of Web-tools to Process Stoichiometric Network Analysis: Tools-4-Metatool

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Stoichiometric network analysis (SNA) is a powerful approach to study complex metabolic networks. SNA provides fundamental information on the structure of the network, as it is: the stoichiometric matrix, the convex basis, elementary modes or extreme currents, and enzyme subsets. Metatool is one of the most popular tools to perform SNA. Metatatool output is hard to process and visualize, especially for users who have no experience with this software.

In this communication we present the web-tool called Tools-4-Metatool (t4m) (http://solea.quim.ucm.es/t4m/) as an online platform that analyses, parses, and manipulates files related with Metatool. It has two major options: Analysis and Compare.

Analysis facilitates the visualization of the results of the SNA. This option has five tools:

- MDigraph: that draws bipartite directed graphs of Metatool's metabolic network, its subsets and the subsets' pathways;
- MetaMatrixTXT: visualizes the convex basis and elementary modes of Metatool's output in function of subsets, in vectorial or matrix format;
- CBGraphs: draws bipartite directed graphs of Metatool's convex basis and its pathways;
- EMGraph: draws bipartite directed graphs of Metatool's elementary modes and its pathways;
- SortEModes: orders Metatool's elementery modes that contain a given metabolite (or a list of metabolites) in a certain side of its reaction.

Compare was developed to compare different Metatool's results from two species, using subsets or elementary modes comparison. It is composed by:

- Compara: tool that matches up distinct Metatool's outputs and shows the identical subsets;
- ComparaSub: compares different Metatool's outputs and shows the first output in function of the subsets of the second;
- ComparaEM: compares distinct Metatool's outputs and shows the identical elementary modes.

The suite t4m also include scripts that generate Metatool's input based on COBRA SBML files, Cobra2Metatool, or based on a Metatool's output file that is filtered by a list of convex basis' enzymes, Cbasis2Metatool. Besides, t4m has a script, called CheckMIn, that checks Metatool input file format and its consistency.

All these tools have been tested with several metabolic networks. In this contribution we will present some examples to illustrate the use and t4m possibilities.

P02.730

Metabolic Networks Based Approach for Understanding Structural Organization Principles of Essential Genes

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Misuse of antibiotics had raised the concern of antimicrobial resistant for decades. Thus characterizing sensitive targets in these "super bugs" is an urgent challenge. Essential genes are vital for growth/viable, making them ideal candidate targets of study. Identifying essential gens via genome-scale knockout experiments are resource intensive and are not universally applicable for all species. Here we propose a metabolic network based approach which aims to understand the structural organization principles of essential and non-essential genes from Escherichia coli. Each gene has a corresponding 'damage list' where the overall reactions can be affected by gene knockout. Our analysis indicates that essential genes tend to affect reactions catalyzed by other essential genes. This is also the case for non-essential genes. Besides, two genes with highly correlated damage lists tend to similarly linked to their respective essentiality, i.e. both are essential or non-essential. Our results suggest a complementary strategy to knockout experiments to identify essential genes in a genome.

P02.732

A New Computational Method for Predicting the Evolutionary Patterns of Influenza: A Viruses Using the Time Series Variations of Genetic Information Since 1995

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In this study, we developed a new computational method for predicting the evolutionary changes of influenza A viruses (H1N1 subtype). All the mRNA sequences of neuraminidase (NA) and RNA polymerase (PA) genes of human-origin influenza A viruses isolated from 1995 to 2009 were collected from the Influenza Virus Resource at NCBI. In a calculation step, we counted all the possible codon variations between the two continuous years (time t and t+1) on each codon position, and then, generated the transition matrices (2 X 2) by calculating the transition probabilities of codon variations over time. On the basis of our calculated codon transition matrices, we generated the random sequences by using a method we developed to predict the future sequences. We used various distributions including Normal Distribution in generating random numbers, and three known-sequences such as 1995, 2000, and 2005-isolated sequences were used as seed sequences. In the final step, all the generated sequences were compared with other known sequences by using the blastn program at NCBI, and we analyzed the statistics of resulting sequences such as similarities, isolated years, species name, and gene name. As a result, we found many interesting results in predicting the future sequences of influenza A viruses (H1N1 subtype). All the calculations were performed in the 'Tachyon' supercomputer at KISTI Supercomputing center.