Automating NMR workflows: Introduction to python programming

Satellite event for course Biomolecular NMR (13-17 Oct 2014)

Description

To work efficiently and reliably with the large amount and complexity of data that typically need to be analysed in (structural) bioinformatics, automation of workflows is a must. In some cases it is possible to find existing software packages to achieve your goal. However, often no suitable package is available for your specific tasks and development of your own piece of software is needed.

Fortunately these days you can find programming platforms with a simple syntax and which require minimal knowledge about computer technology. Python is a programming language that is perfectly suitable for scientific programming: It is simple to learn, but powerful enough even for complicated tasks.

The 2-day course will get you started with python programming and result in a fully functional script for a real life application in Biological NMR: The conversion from CYANA distance restraints to XPLOR distance restraints. It consists of short lectures that introduce you to basic python programming concepts, followed by long practical sessions to get you familiar with all the theoretical topics covered in the lectures. To illustrate the learned techniques they are directly applied to build the CYANA to XPLOR conversion script in the practicals.

Date & Place: 11-12 Oct 2014, Swedish NMR Centre, University of Gothenburg

Registration: by e-mail to Dr. Chris Spronk (chris.spronk ‘at’ spronknmr.eu). The course is free for students and academic researchers.

Lecturers and trainers

- Chris Spronk
- Maxim Mayzel
- Vladislav Orekhov

How to prepare

To be most efficient in the course, it is important that you read the course information document carefully, and make sure you understand the goal of the course.

Reviews on this course

Read the reviews of previous participants here: course reviews