Workshop on CcpNmr analysis V2 software (October Friday 19th)

MOOT-31 in collaboration with QANUC is proposing a workshop on CcpNMR V2 from 11h to 17h on Friday 19th October. The venue will be at the *Institut de Pharmacologie de Sherbrooke*. The exact location and the indications will be provided to the participants registered by email. Please register at mootnmr.org.

The workshop will be separated in three part:

11h-12h30 Part 1

- Creating projects and loading spectra, entering sequences and molecular information, spectrum window navigation, peak picking, initializing HSQCs, finding and linking peaks in related spectra

12h30-13h30 lunch

13h30-15h Part 2

- Sequence specific assignments of proteins chemical shifts from triple-resonance experiments, finding side chain resonances, copying assignments, multiple shift lists

15h-15h30 coffee break

15h30-17h Part 3

- Relaxation, binding titration, preparing figures, exporting files and else...

Departure to the Grand TIMES Hotel for registration at 18h
(It takes, in the worst-case scenario, 20 min to get there)

For installing the CcpNmr software:

The stable release of the CcpNmr suite his available as a pre-compiled Linux or Mac release; you just need to unpack it (e.g. issue the command "tar xvzf analysis2.4.2_*.tgz"; preferably in your program directory). There is also a Windows* release for which you just need to double click on the CcpnmrSetup-build-2.4.2-*.exe file.

*Be aware that the Windows XP/Vista/7 version is slower and more demanding on the CPU than the Unix counterpart.

CcpNmr Analysis 2.4.2
https://www.ccpn.ac.uk/v2-software/downloads/stable

For any help or question concerning the installations, you can contact me at
danny.letourneau@usherbrooke.ca

The complete dataset for the Workshop will be available soon.

Look forward to meet you there!

Dan and Pierre