Putting it all together: Fully automated NMR spectrometer, web-based analysis, and spectral simulation with 2D/3D structure correlation for first-year organic chemistry

Robert M. Hanson

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http://www.stolaf.edu/people/hansonr

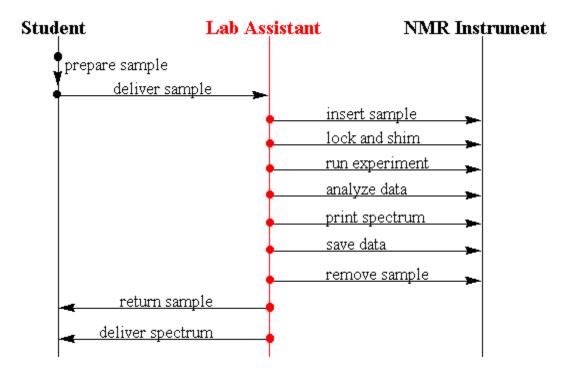
SMASH 2019/NMReData symposium, Sept. 26, 2019

Part I: The instrument and interface Part II: Analysis involving JSME, JSpecView, NIH/chemical resolver, and nmrDB

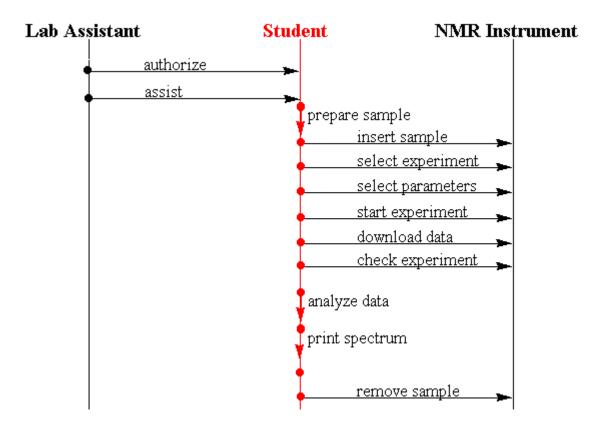
Instrumentation: Bruker 400 MHz Avance III spectrometer with 120-position BACS autosampler, BSMS-2, GRASP II SmartProbe



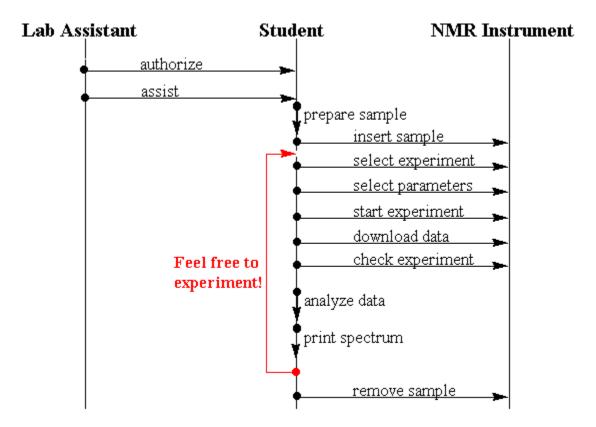
The OLD way...



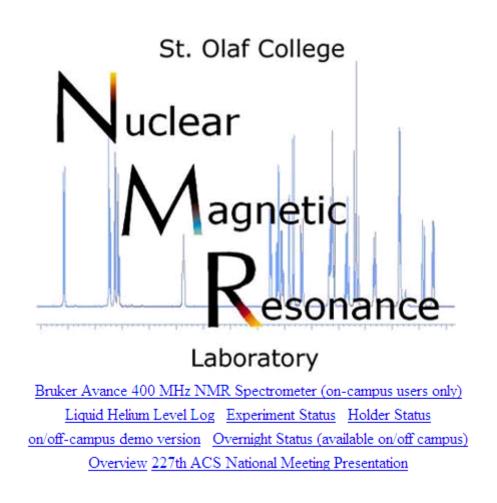
...and the new way...



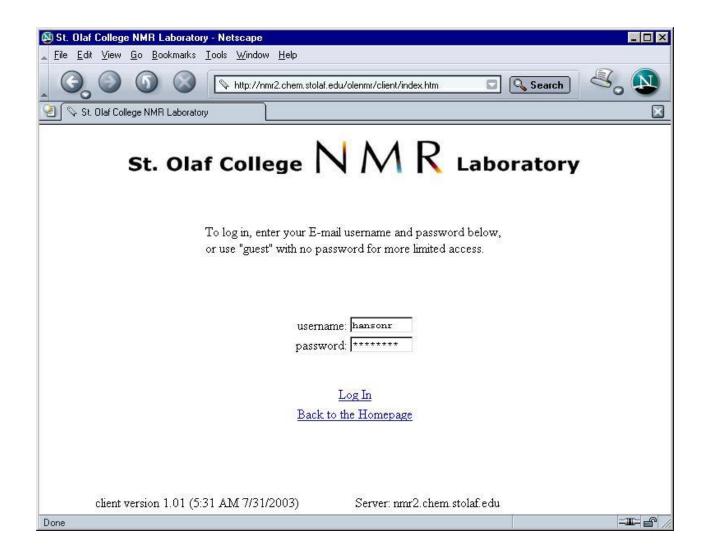
...with a twist!



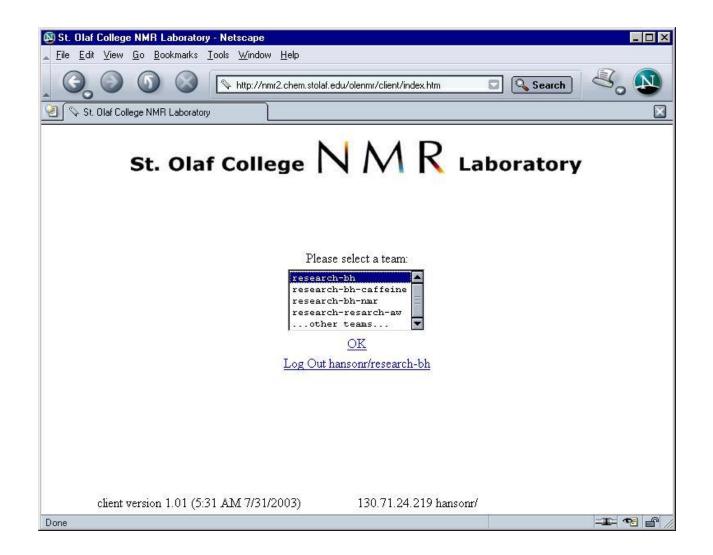
https://chemapps.stolaf.edu/nmr



Implementation involves "standard" St. Olaf login...



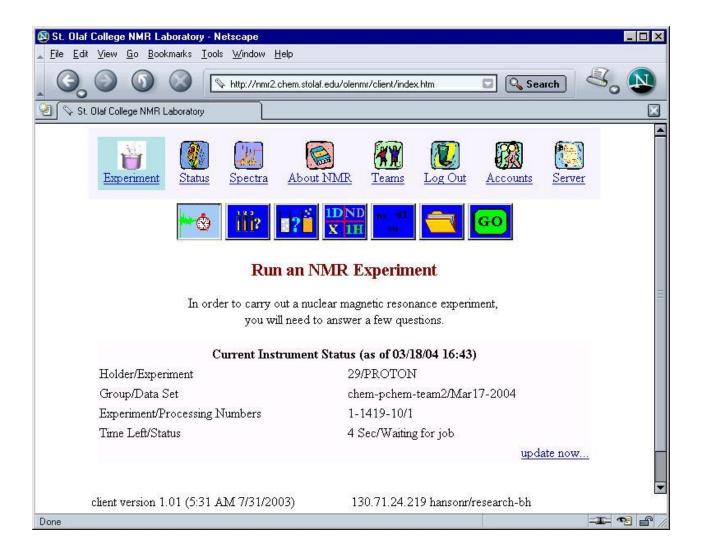
Each user is a member of one or more IconNMR "teams"...



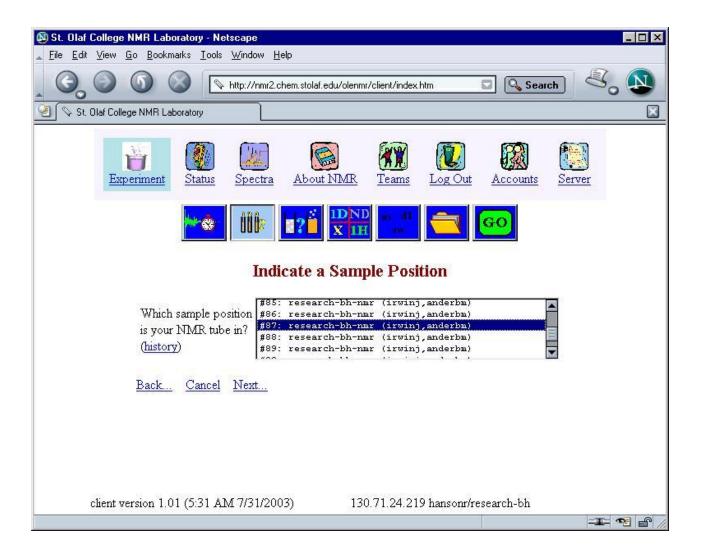
For this simulation we will run an experiment...



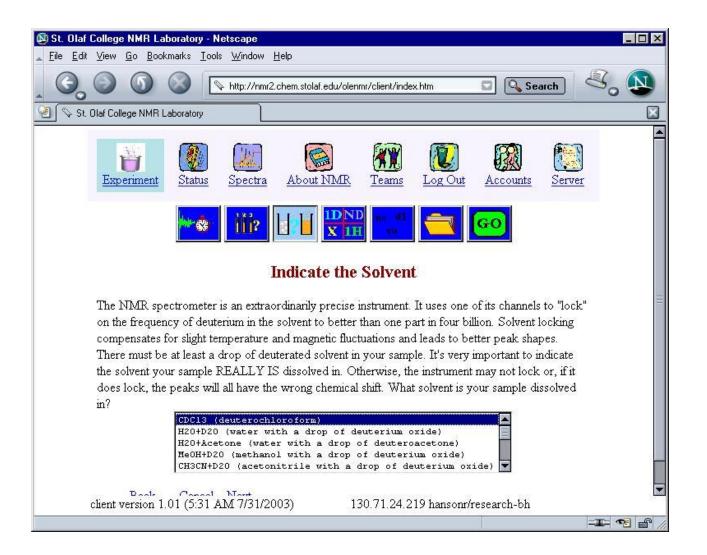
Initially we see a "current status" screen...



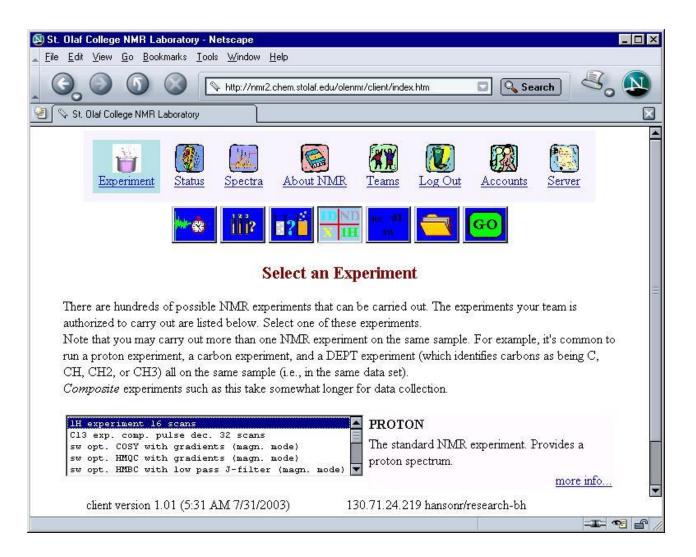
One or more sample positions will have been assigned to the team...



Solvent options are automatically loaded from the Bruker database...



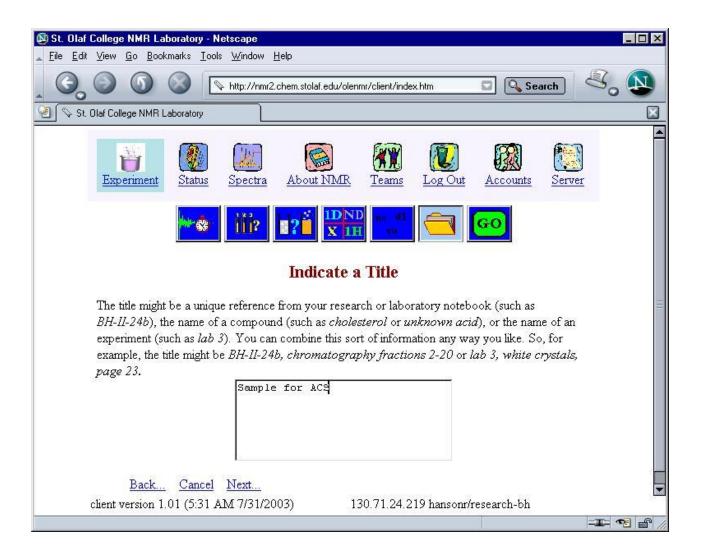
Experiments are drawn from an OleNMR database...



Permissions are experiment-based, not user-based...



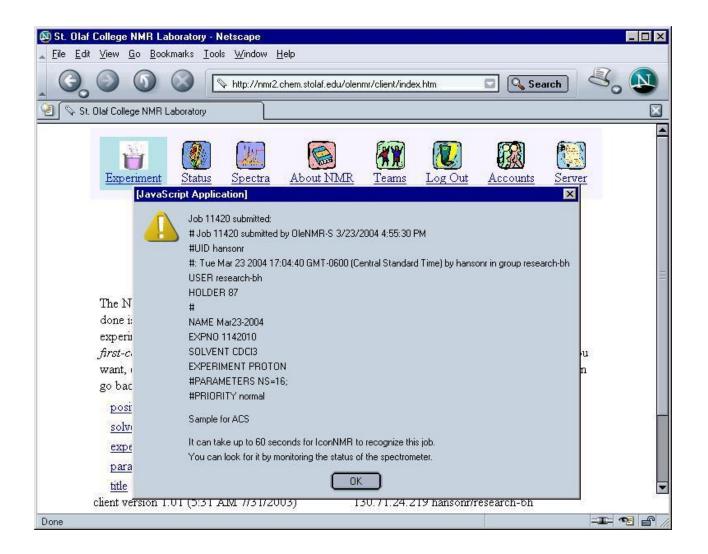
A little instruction to guide novices is on each panel...



We designed a "fair queue" that prevents monopolization...



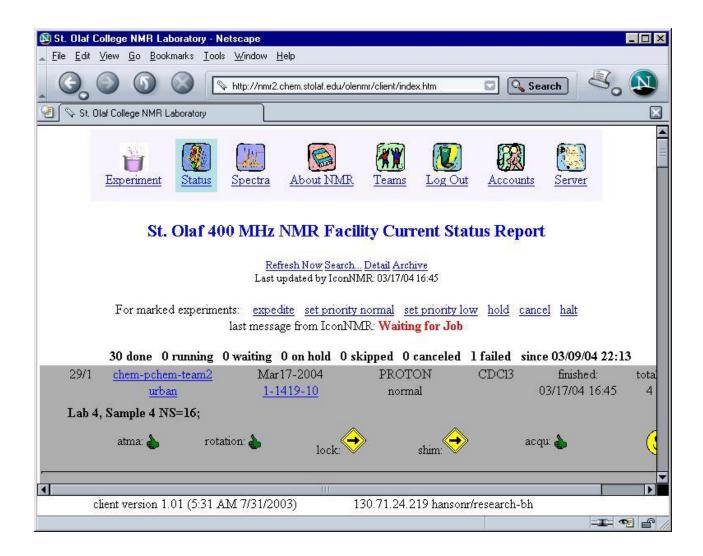
A message from the server indicates successful job submission...



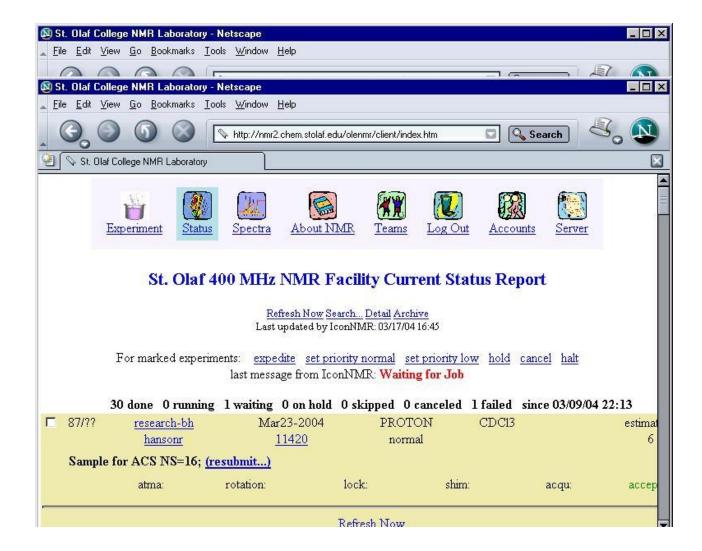
OK, the experiment is submitted; now we will view status...



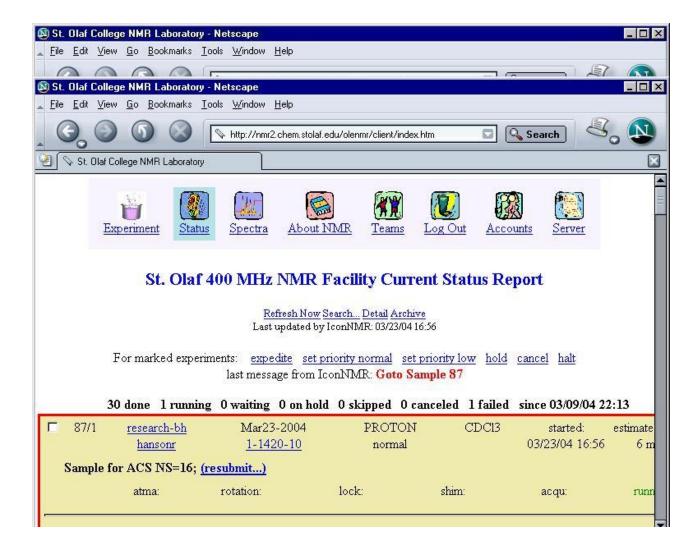
This is a running list of active and pending jobs...



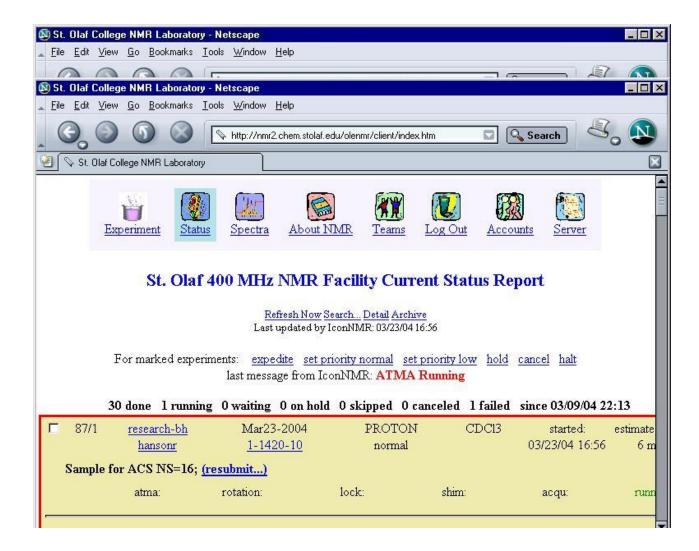
Within one minute our job shows up...



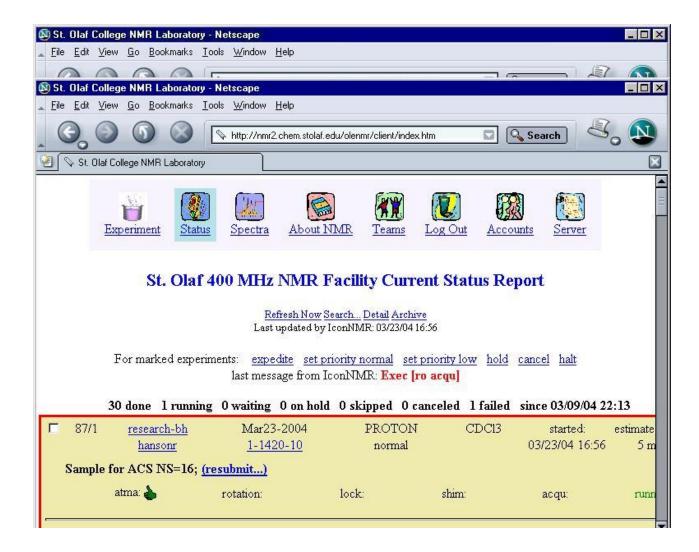
The "last message" indicates that our job is active. The robot is working...



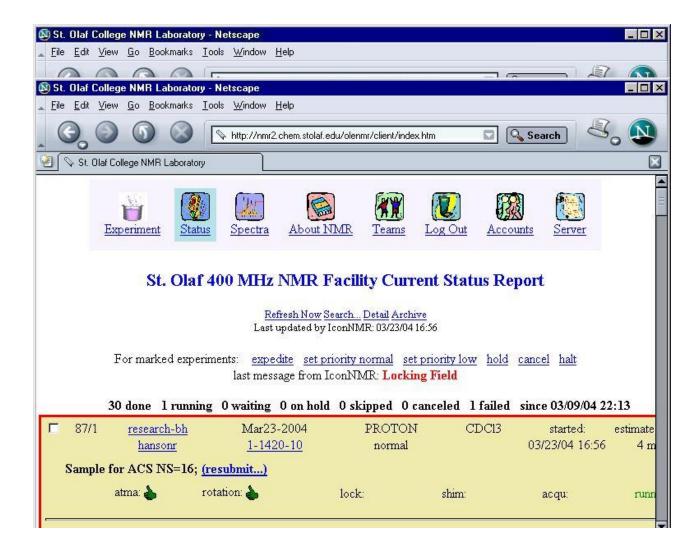
Automatic Tuning and Matching is taking care of solvent changes...



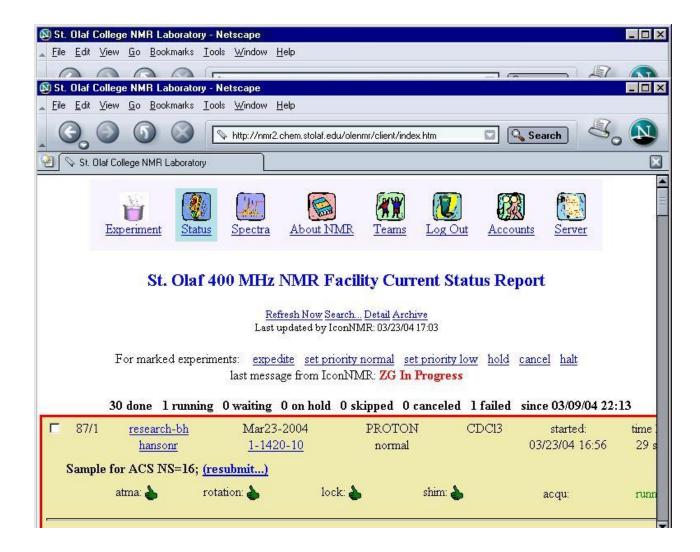
The sample is starting to rotate...



the field is locked and shimmed using deuterium gradient shimming...



ZG stands for "zero go"; the NMR experiment is now running...



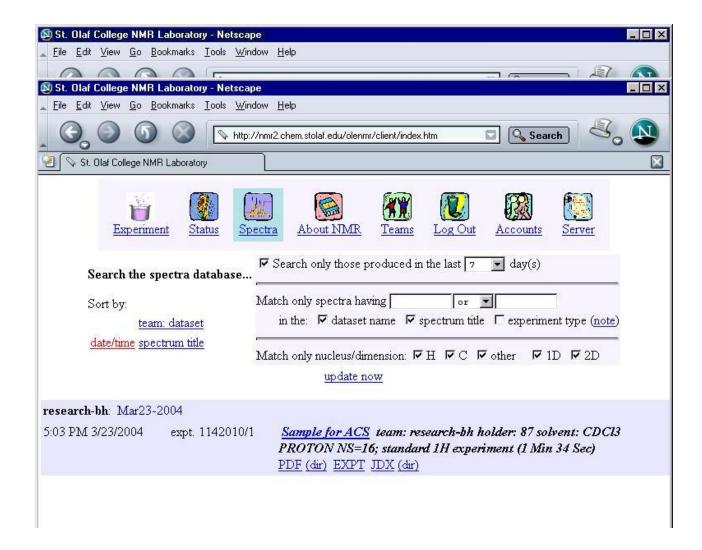
Thumbs-up and a happy-face indicates all is well...

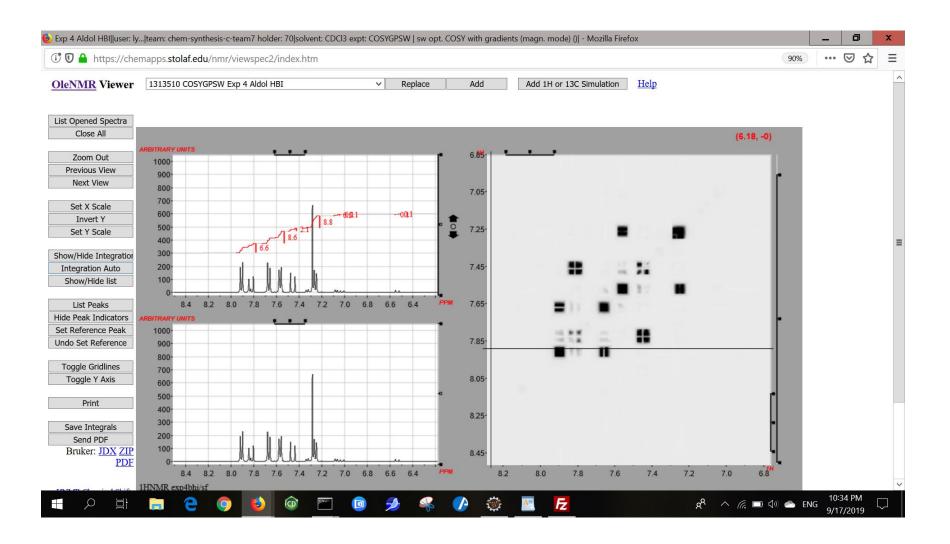


Back to the main interface, we select "view spectra"...

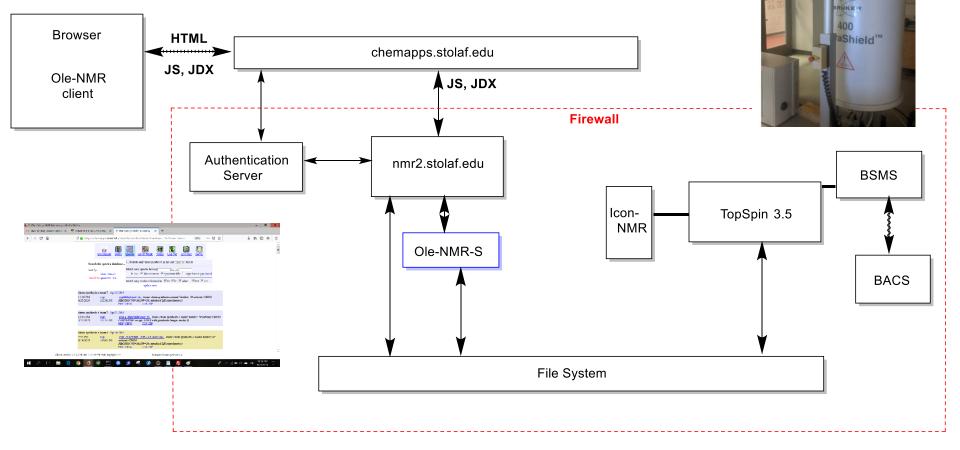


There are many options for selecting specific experiments...



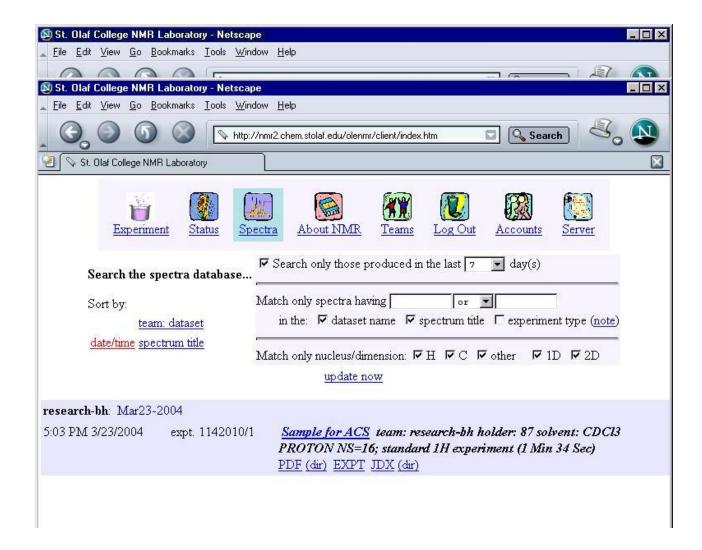


Ole-NMR/TopSpin Overall Schematic



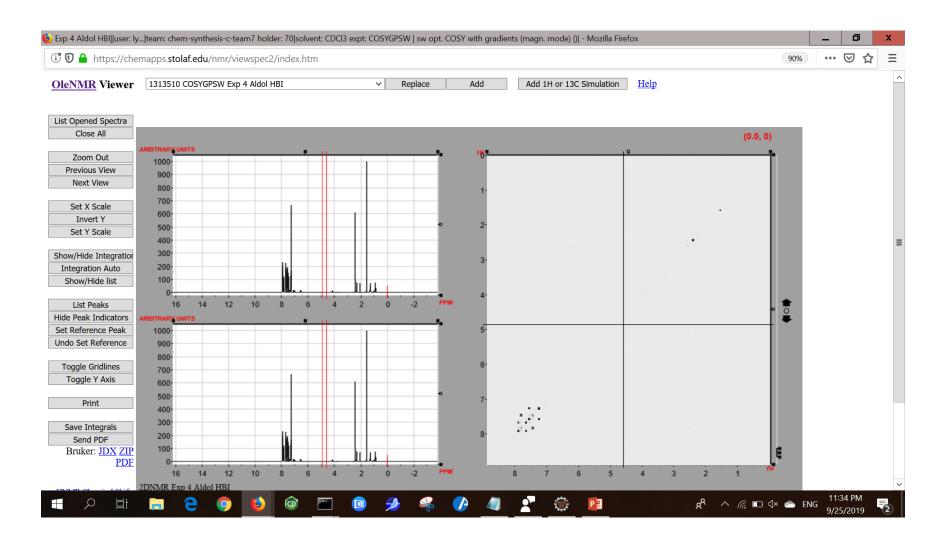
Part I: The instrument and interface Part II: Analysis Involving JSME, JSpecView, NIH/Chemical Resolver, and nmrDB

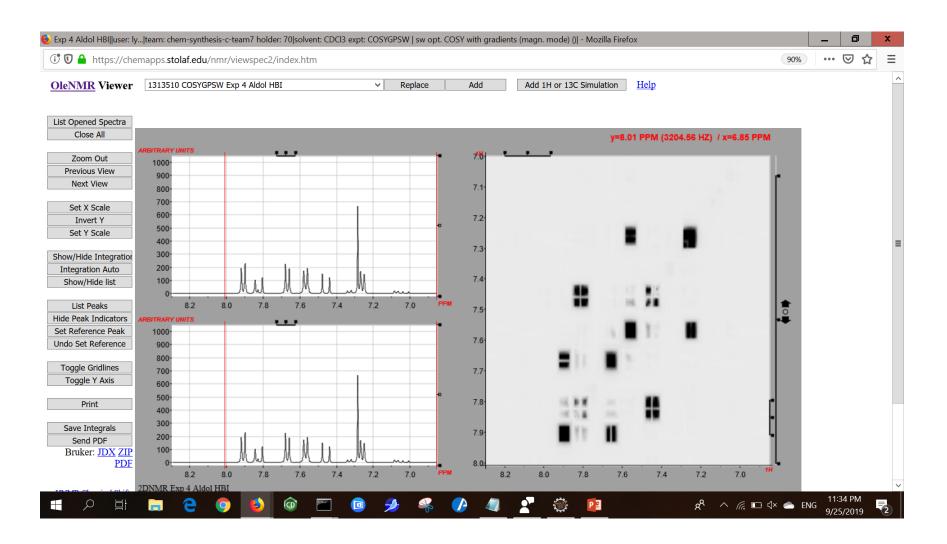
There are many options for selecting specific experiments...

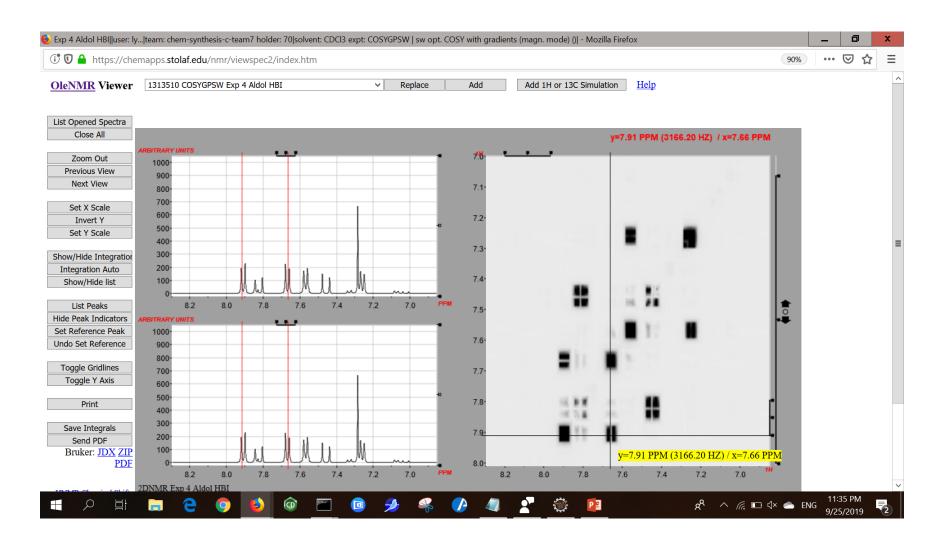


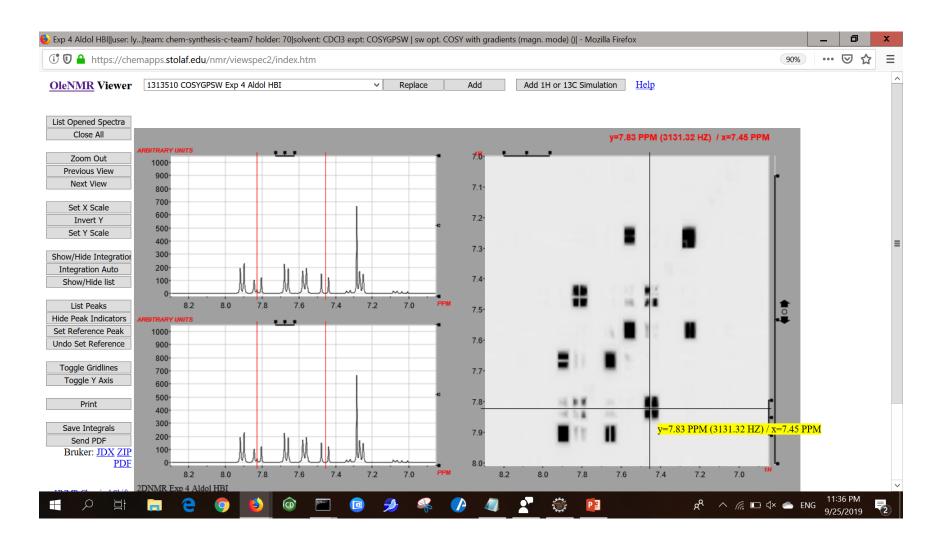
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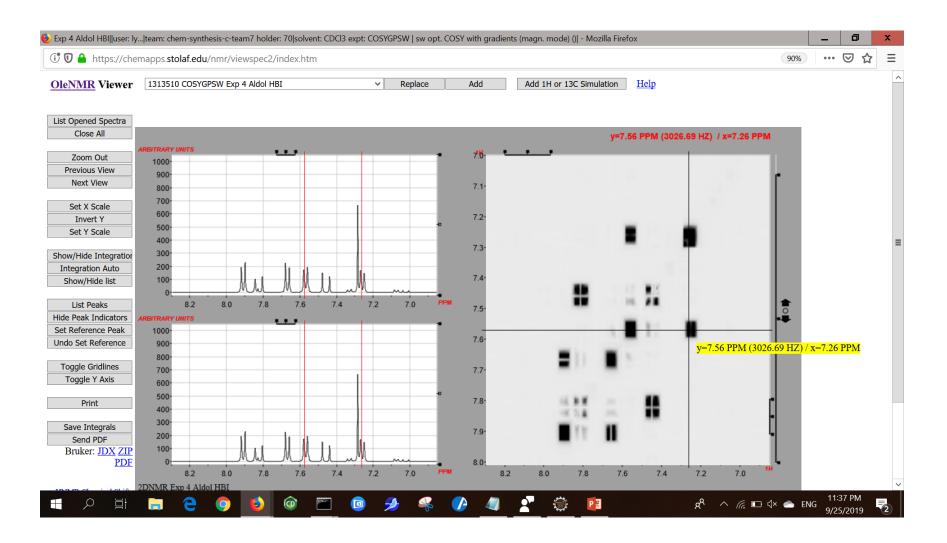
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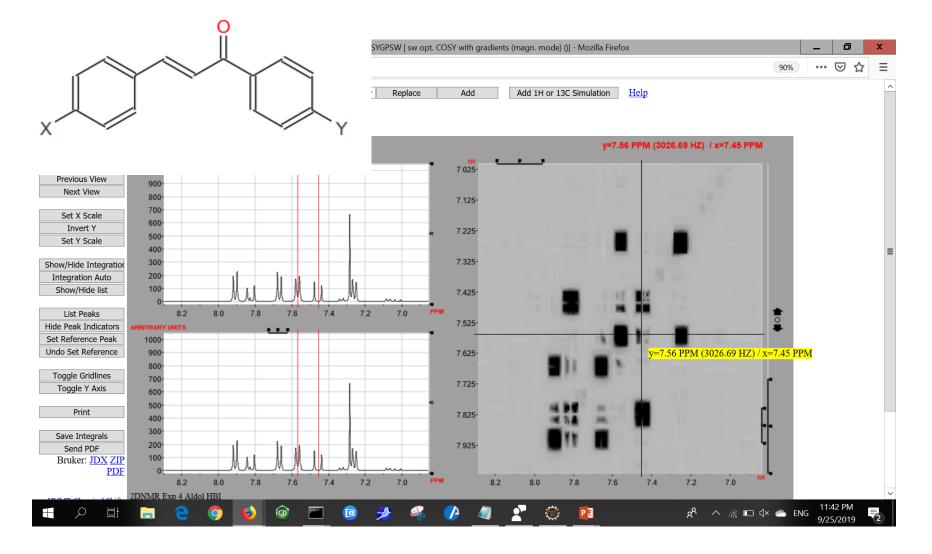








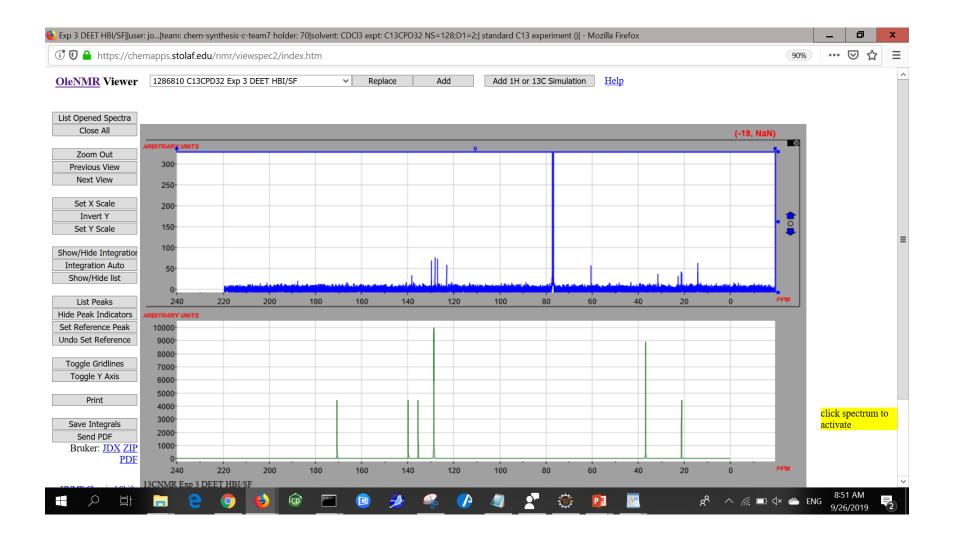


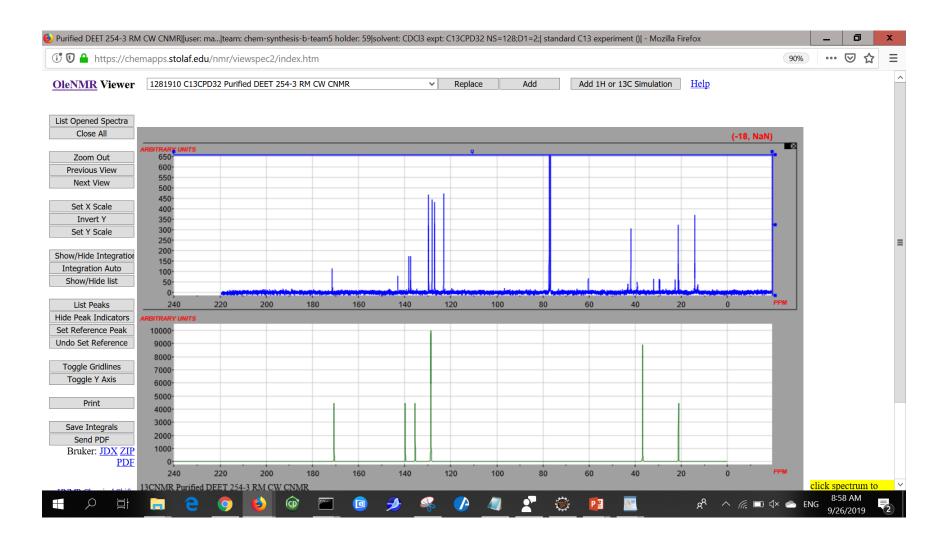


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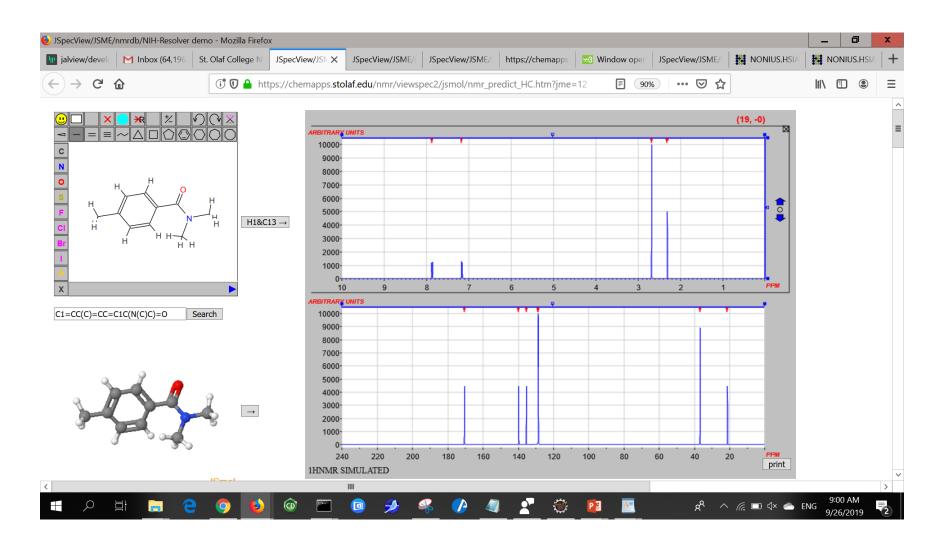
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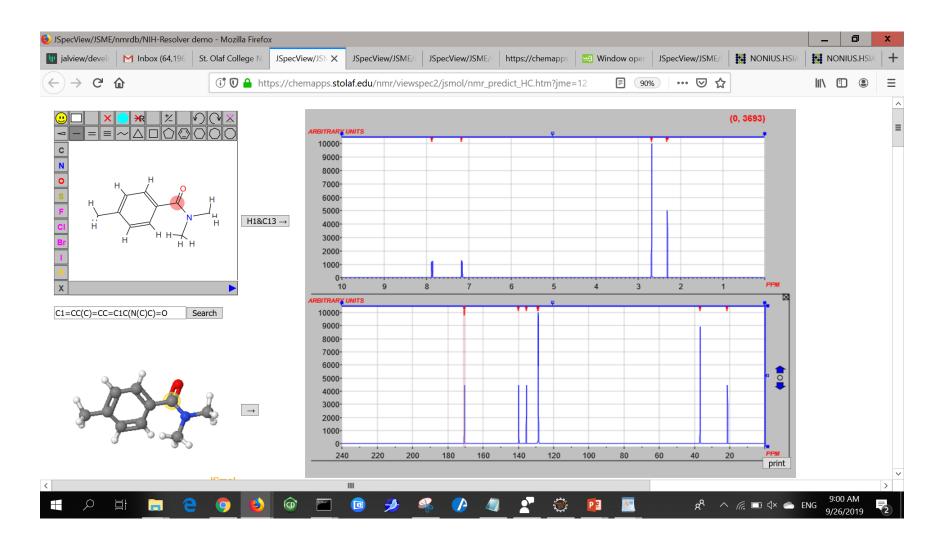
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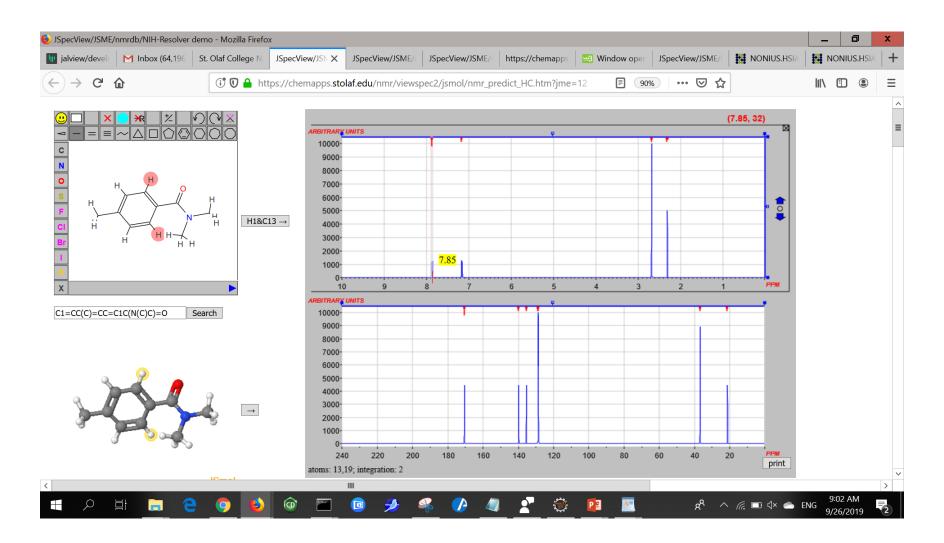




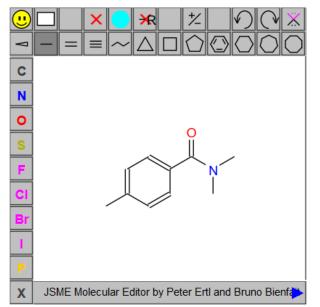
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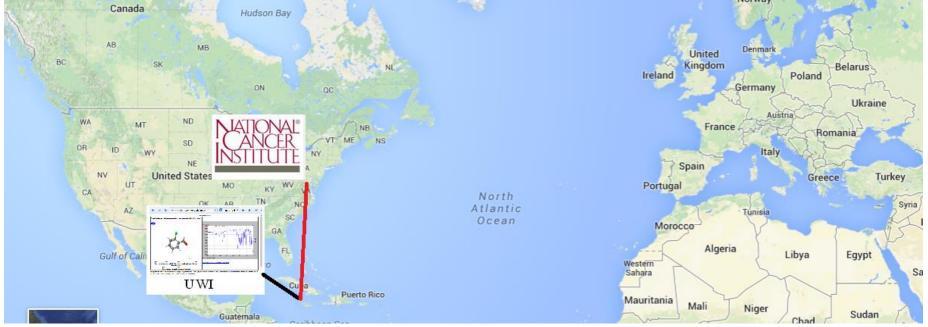


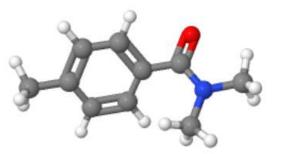




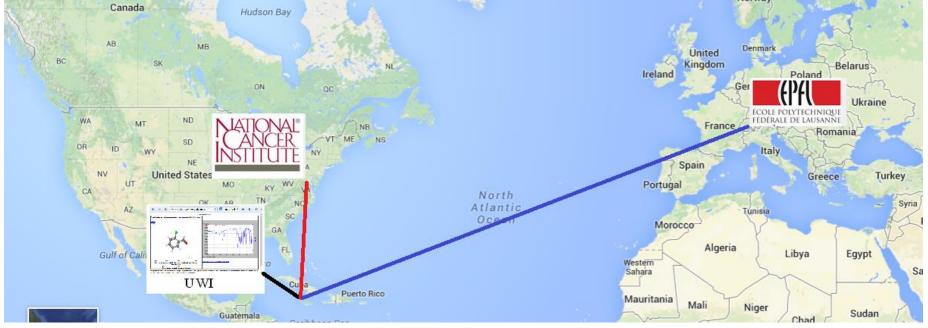


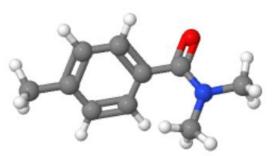


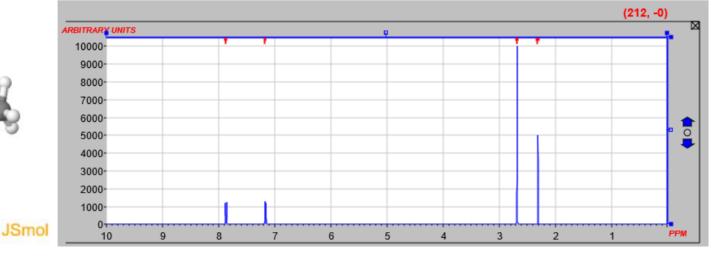


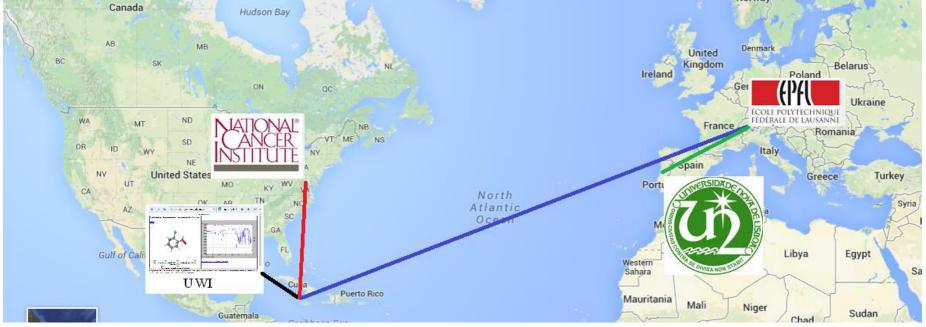


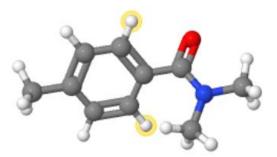
JSmol













JSmol

Acknowledgments...

• St. Olaf College

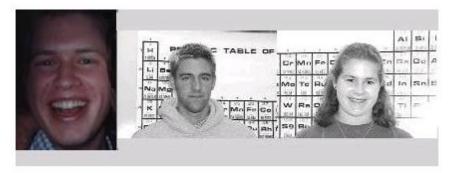


- Peter Ertl, Novartis
- Robert Lancashire, UWI-Mona
- Clemens Anklin, Bruker



Thanks to the students who really made this possible.

(Can you tell they had fun?)



Mike Purnell, Gregg Sydow, and Stephanie Skladzien



Jared Irwin

Bryan Anderson