The SASSIE Portfolio

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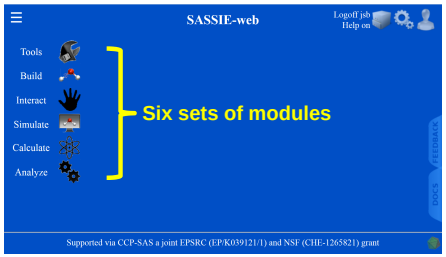
Introduction

Overall, SASSIE is a set of program modules arranged in six groups to perform a full modelling workflow:

- Manipulate experimental SAS and reflectivity data.
- Prepare structures for simulation.
- Carry out the simulations.
- Compare simulations to experiment.



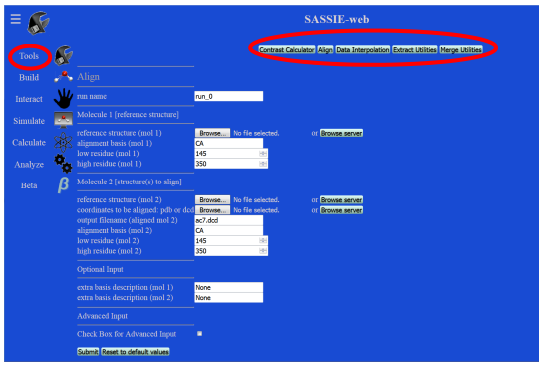
Simulation modules allow access to modern, parallelised engines for all-atom and coarse-grained simulations:

- Molecular dynamics (MD)
- Monte Carlo (MC).

Applicable to a variety of protein, nucleic acid and carbohydrate systems.

Computational tools

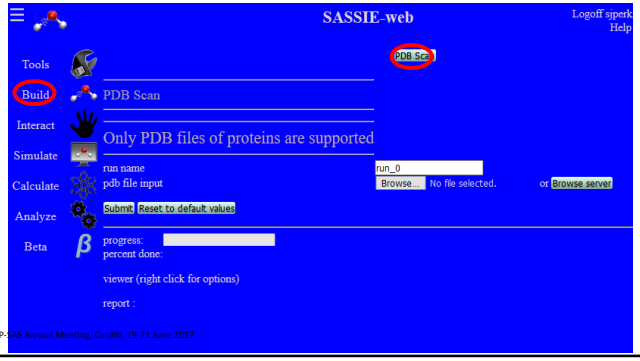
(1) Tools menu - Prepare and manipulate the experimental or structural data.



Computational tools

(2) Build menu – Prepares the starting structure file for simulations

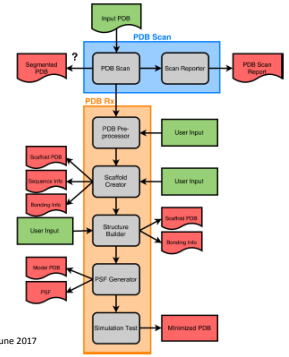
PDB scan – the user supplies a starting PDB file with atomic coordinates and the module and the module reports on the integrity of the coordinates. This deals with a major issue in simulations – namely bugs in the starting structure.



Computational tools

(2) Build menu – Prepares the starting structure file for simulations

PDB Rx – the user supplies a starting PDB file with atomic coordinates and the module attempts to clean up the structure by adding missing atoms, creating loops, reproducing symmetric units, etc. Proteins and nucleic acids are repaired using PyRosetta

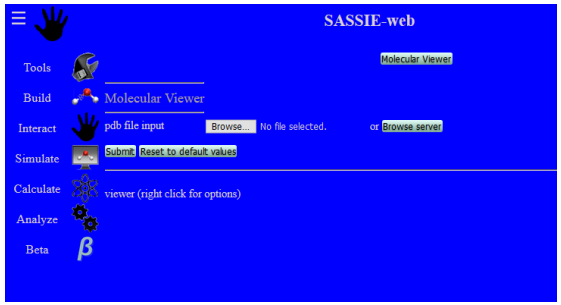


PDB Scan – available now

PDB Rx – in preparation

Computational tools

(3) Interact menu – Enables 3D structures to be viewed – very handy to have



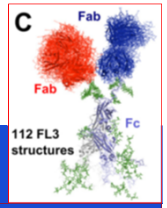
Monte Carlo simulation

(4) Simulate menu – options 1 and 2

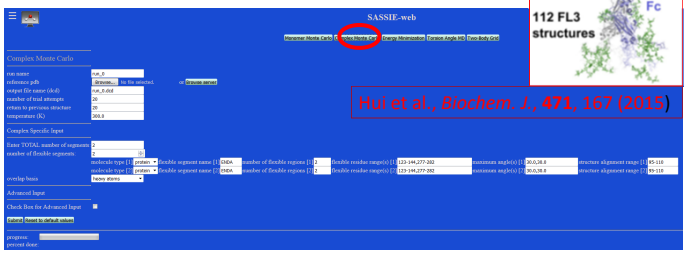
Monte Carlo simulation of proteins and nucleic acids. This is rapid compared to molecular dynamics.

Monomer MC – used for single chains

Complex MC – used for multiple chains



Hui et al., Biochem J., **471**, 157 (2015)

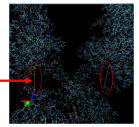


Energy minimisation and molecular dynamics

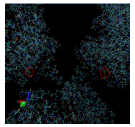
(4) Simulate menu – option 3

Molecular dynamics based on Newton's laws of motion.
Energy minimisation removes locally stressed configuration.
Engine used: NAMD

Disulphide bond



Before



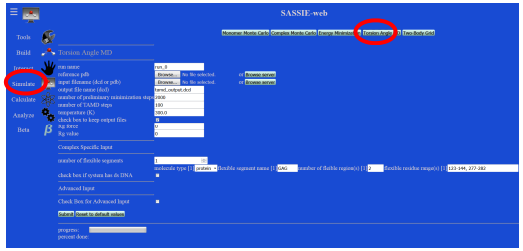
After

Torsional angle molecular dynamics

(4) Simulate menu – option 4

Useful to optimise torsional angles between segments of a polymer using Newton's laws of motion.

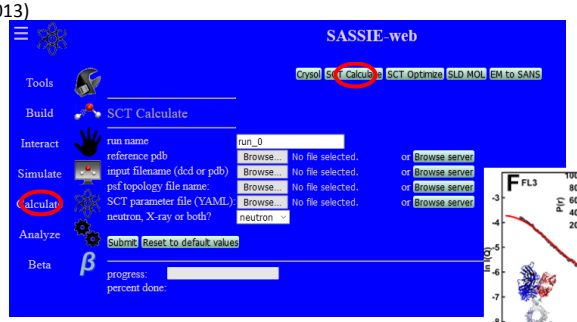
Engine used: CHARMM package



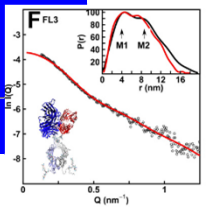
SCT

(5) Calculate menu – option 2

SCT is a coarse-grain SAS calculator to generate scattering curves (Wright & Perkins, 2013)



IgA1



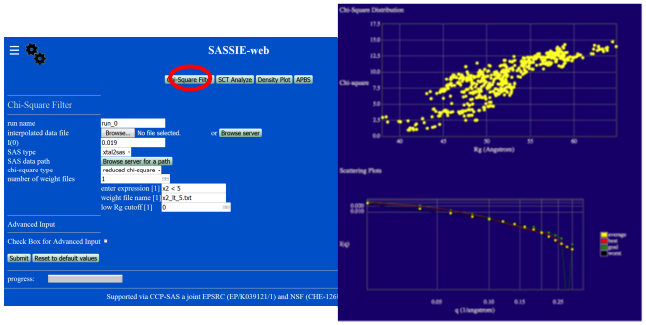
Compare and fit theoretical scattering curves against experimental ones

Hui et al., *Biochem. J.*, **471**, 167 (2015)

Fitting against experimental data

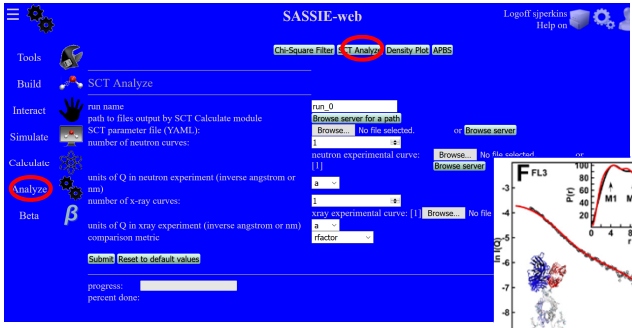
(6) Analyze menu – option 1

Chi-square filter uses this parameter to identify the quality of the curve fit



(6) Analyze menu – option 2

SCT analyze uses the R factor to identify the quality of the curve fit



IgA1

Compare and fit theoretical scattering curves against experimental ones

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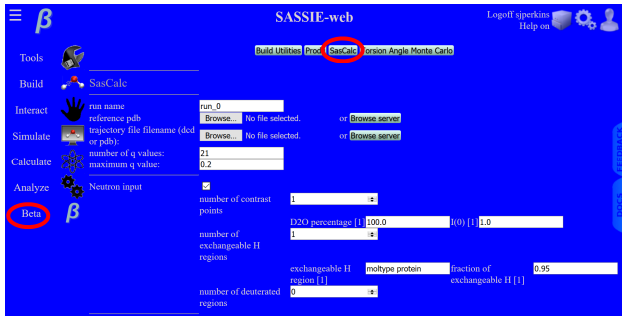
SasCalc

(7) Beta menu – option 3

SasCalc is under development to calculate SAS profiles from ensembles of atomic coordinates



Also "Capriqorn" – an all-atom explicit solvent MD simulations SAS calculator

And "SasCalc-PBC" – see the poster

Acknowledgements

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Engineering and Physical Sciences Research Council

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WHERE DISCOVERIES BEGIN