Bringing higher end computational tools to the bench scientist to accelerate the discovery process.

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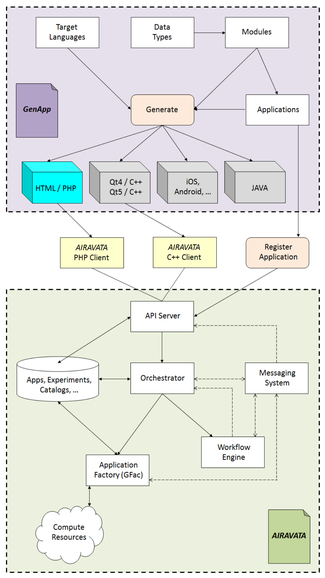
The Problem
A typical bench scientist synthesis, purifies and characterizes samples, collects the scattering data, and interprets the results, often using simplistic models. It is rare that the same individual also has the skills to use advanced atomistic simulation software for example. Furthermore, the cost of developing, deploying and supporting computational tools for a large pool of end users is prohibitive and significantly limits what can be realistically provided. This provides a bottleneck in the discovery process between collecting data and their interpretation.

A Solution?
The CCP-SAS consortium was initiated as a UK/US jointly funded SI2 project. CCP-SAS's initial goals were to build a web-based GUI front-end coupled to a high-performance back-end and to develop advanced analysis modules and new simulation methods. These goals were designed to increase the accessibility of advanced atomistic modeling of scattering data by novice users. The web/HPC framework developed, ***GenApp***, which has led to its own newly funded project, also allows the support of legacy "dark" code as well as helping smaller projects be more accessible. The ***SASSIE*** workflow has been built into that framework. Along with the development of new modeling tools, this workflow has enabled the study of an increasing range of mostly biological macromolecules, while more general soft matter problems remains a work in progress as does the eventual goal of integrating the results from multiple techniques including coarse grain and atomistic simulations into a single optimization problem. Here we briefly outline the current status of the project and its hopes going forward.



GenApp

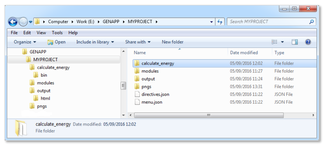
GenApp is an open extensible multi-target application generation tool for the simple and rapid deployment of multi-scale scientific codes.

An application is defined as a collection of executable modules which are then presented through a common user interface. This provides a powerful paradigm to combine both existing and new codes to perform novel workflows, or to develop new applications.

The addition of a module in *GenApp* is simple, and only requires the writing of a short JSON wrapper (a module) to detail the input and output, and the editing of two JSON files, one to specify where the module should appear in the applications menu system (*menu.json*), and the other to specify how the application itself is to be presented (*directives.json*). The modules themselves can be written in any supported language, independent of the choice of the target GUI implementation. Separating the scientific code from the GUI in this way not only facilitates the linking of component modules into larger workflows and applications, but also reduces the burden in supporting legacy codes.

Module executables either run locally (most GUI applications) or, if web-based, on a web server or other resource configured within *Apache Airavata*.

GenApp facilitates the creation of applications as web servers or gateways. This includes remote file management and the execution and management of lengthy non-interactive jobs. The latter capability, provided through integration with *Apache Airavata*, allows *GenApp* applications to harness a range of high-performance computing resources including local clusters, supercomputers, national grids, academic and commercial clouds. Instances of *GenApp* web applications have been tested on XSEDE and AWS.

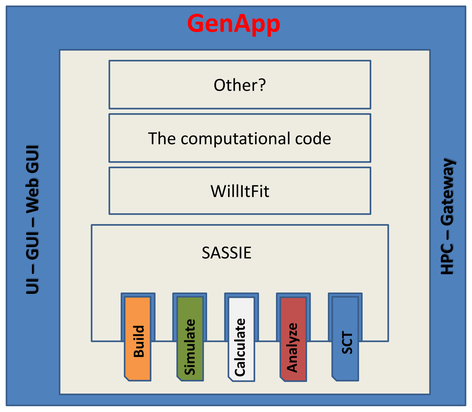



```
# directives.json
# here generating instances of the application "calculate_energy" in
# three separate languages

{
  "title"          : "CALCULATE ENERGY",
  "application"    : "calculate_energy",
  "footer"         : "Powered by GenApp",
  "footersize"     : "50px",
  "version"        : "1.0",
  "languages"      : [ "html5", "qt4", "java" ],
  "executable_path" :
                     {
                       "html5" : "MYPROJECT/calculate_energy/bin",
                       "qt4"   : "MYPROJECT/calculate_energy/bin",
                       "java"  : "MYPROJECT/calculate_energy/bin"
                     }
# for more directives see
# http://gw105.iu.xsede.org/genapp/wiki/docs_directives
}
```

```
# menu.json
# providing each instance of the application "calculate_energy" with
# two menu options (to calculate the energy with Einstein's formula or
# with Planck's formula)

{
# "header" : "MY PROJECT",
    "menu" : [
        {
            "id"     : "calculate_energy",
            "label"  : "Calculate Energy",
            "icon"   : "MYPROJECT/pngs/myproject.png",
            "help"   : "calculate_energy help text",
            "modules" : [
                {
                    "id"    : "einstein",
                    "label" : "Einstein"
                },
                {
                    "id"    : "planck",
                    "label" : "Planck"
                }
            ]
        }
    ]
# for more menu options see
# http://gw105.iu.xsede.org/genapp/wiki/docs_menu
}
```


Reference
Brookes, E.H., Anjum, N., Curtis, J.E., Marru, S., Singh, R. & Pierce, M. The GenApp framework integrated with Airavata for managed compute resource submissions. *Concurrency Comput. Pract. Exper.* (2015), **27**, 4292–4303.

The *GenApp* part of the project is clearly useful for generating a wide-range of scientific applications far beyond the scope covered by the CCP-SAS project and represents the largest "broader impact" to date coming out of this project and is currently the focus of a newly funded project. Interested parties should contact:
genapp-devel@biochem.uthscsa.edu



SOME STATISTICS

- Over a dozen tutorials/workshops around the globe
- Users from 33 countries
- Over 50 publications attributed to CCP-SAS to date
- Over 30,000 jobs run

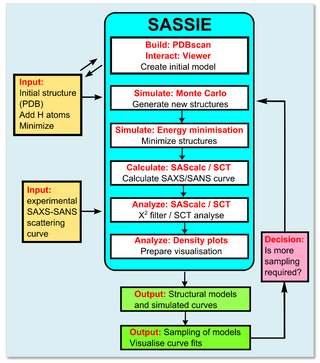
SASSIE-Web

The aim of *SASSIE-Web* is to allow experimentalists (especially novice end users) to construct modelling workflows from a set of sophisticated simulation and analysis modules and run them transparently on centrally-maintained HPC resources using nothing more than a web browser.

The provision of a web interface avoids the need for end users to install and maintain large complex software on their own machines, and remote execution accelerates the computationally expensive steps of the modelling process.

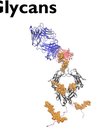
The *SASSIE-Web* menu organizes the analysis workflow in six sets of *GenApp* modules:

- **Tools**: which includes utilities to predict scattering length densities, interpolate experimental data files when required, and extract or merge macromolecular structures;
- **Build**: which includes utilities to check and correct PDB-formatted coordinate files;
- **Interact**: which provides the JSmol molecular viewer for interactive display of a specified structure;
- **Simulate**: which provides MC/MD programs to create representative ensembles of trial structures for testing against the data;
- **Calculate**: which provides a range of scattering curve calculators;
- **Analyze**: which identifies the simulated structures that best-fit the experimental scattering data and provides for their visualisation as envelopes.



Science

Antibody + Glycans

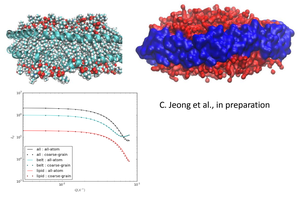


G K Hui *et al.*, Biochem. J. (2015), DOI: 10.1042/BJ20150612

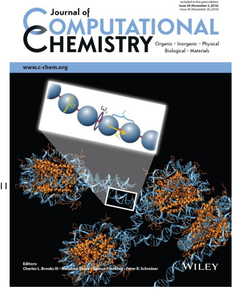
Hfq + RNA

Y Peng *et al.*, *PNAS* (2014), DOI: 10.1073/pnas.1410114111

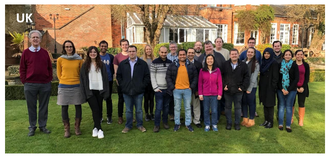
Polymer + Nanodisc

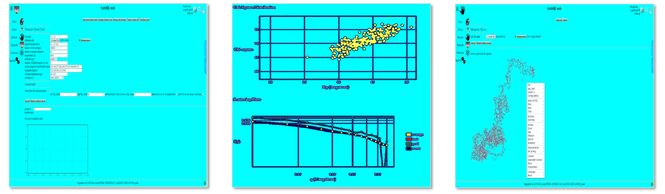


C. Jeong et al., in preparation

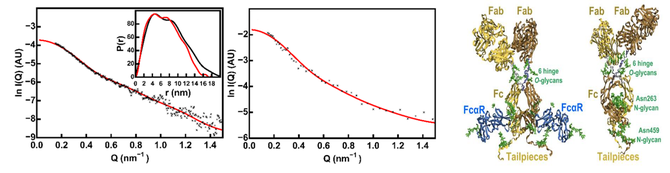


Workshops





(Above) *Screen shots from a SASSIE-Web session: (L-R) Setting up a molecular MC simulation to sample torsion angles; assessing the best-fit structures that are consistent with the experimental scattering data; visualising the structure of the HIV-1 Gag protein in JSmol.* ***(Below)*** *Results from SASSIE modelling: (L-R) Comparing the computed scattering from the best-fit structure with the experimental SAXS & SANS data; the resulting structure of IgA1 (Perkins et al., 2016)*



The modular design of the *SASSIE* framework not only gives the user the freedom to employ any combination of existing modules but also allows them to plug-in new modules and import coordinate models generated with other packages (eg, *AMBER*) at any stage of the workflow. This architecture makes *SASSIE-Web* an attractive option for other end users to contribute their codes. For example, the *Capriqorn* software - to calculate scattering curves from molecular simulations with explicit water models - is currently being integrated into the *SASSIE* framework (Köfinger & Hummer, 2013). And the *WillItFit* (Pedersen *et al.*, 2013) and *QuaFit* (Spinozzi & Beltramini, 2012) packages have already been deployed for 'alpha' testing as web applications hosted on our CCP-SAS server. Anyone interested in contributing other relevant applications should contact: joseph.curtis@nist.gov

Onward towards the FUTURE: current status, aims and aspirations

At the end of this joint SI2/CCP funding the project now enters its most vulnerable phase. As we go forward, the process of extending the computational tools and frameworks to support ever broader ranges of materials, in particular general soft matter problems, will be a big challenge, due to the comparatively infinite complexity of these problems, as will the need to have better integrative modeling of data from a variety of techniques. More importantly, the process of community building, of connecting people and projects, and of fostering contributions to existing tools and infrastructures, needs to accelerate and, to these ends, a variety of efforts to build collaborations are under way. In the US GenApp has secured independent funding while in the UK the Perkins group has received a grant to extend tools to better support carbohydrate modelling. CCP renewal efforts are underway in the UK and in particular a project especially focusing on the more general soft matter piece is being prepared. At the same time, other members of the broader consortium are looking to fostering broader collaborations and inter group discussion and building collaborative partnerships. Once such current activity is supporting a European COST action aimed at building a collaborative network of people around the globe working on integrative modeling of data. Further action through community driven groups such as canSAS are also envisioned. Meanwhile it is a hopeful sign that most of the partners continue to be interested in participating in discussions beyond the end of the current "glue" funding and have expressed interest in having another annual joint international meeting and have submitted a number of abstracts on CCP-SAS as well as results from the utilization thereof to the Triennial SAS meeting in October of 2018.. Finally work remains to be done on developing a robust and inclusive governing (and support) model for long term sustainability.

References
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