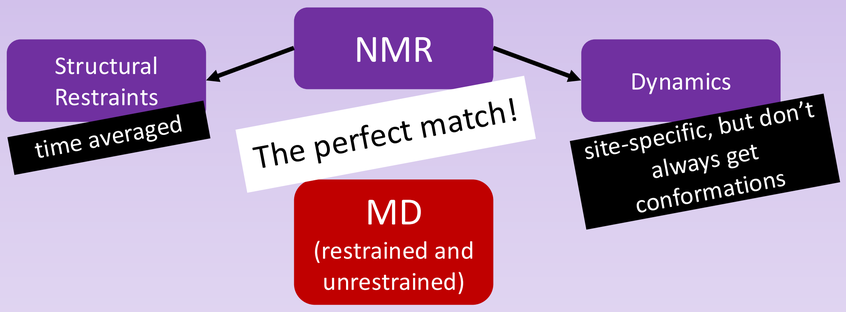
DRIIMB: Digital Research Infrastructure for Integrative Molecular Biology

DRIIMB is the Digital Research Infrastructure for Integrated Molecular Biology project, a collaboration between the structural biology based Collaborative Computational Projects CCPBioSim, CCP-EM, CCPN and CCP4, funded by STFC. Through the DRIIMB consortium, we aim to understand the role of dynamics in biomolecular mechanisms and function. To facilitate this, we are deriving data models to represent the dynamic states, developing data exchanges between CCPs and removing bottlenecks to make better use of the DRI computing environment.

CCPN

Combining experimental NMR data with MD Simulations



- Enabling **easy MD calculation setup** for NMR spectroscopists **from within CcpNmr Analysis** with or without experimental restraints.
- Comparing **site specific information** on **dynamic time scales from NMR data** with **conformations from MD simulations** to understand dynamic processes.

CCPBioSim

Biomolecular Simulation and Integrative Modelling

- Develops workflows for **molecular dynamics simulations of biomolecules**.
- Enables **integration of experimental restraints** from techniques such as NMR, Cryo-EM and crystallography into simulations.
- Generates and analyse **structural ensembles** that capture biomolecular conformational variability.
- Provides tools for **trajectory analysis, ensemble modelling and comparison with experimental observables**.

DRIIMB objectives

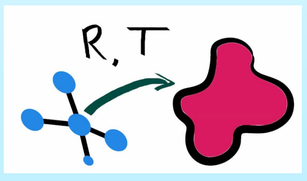
- **Develop interoperable data models**
- **Enable data exchange between CCP platforms**
- **Integrate experimental and simulation workflows**
- **Facilitate access to digital research infrastructure**
- **Support FAIR and reproducible structural biology workflows**

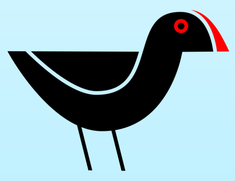
Simulations generate dynamic structural ensembles that complement experimental data and help reveal biomolecular mechanisms and functional dynamics.

CCP4

Macromolecular Crystallography

CCP4 supports **processing** of diffraction data, **structure determination** and **model refinement**.





- A new ligand-fitting algorithm suitable for GPU acceleration
- Robust entropy-based scoring enables automatic ligand cocktail fitting
- Integrated as a task in CCP4 Cloud

- Using **Moorhen** to visualise and process **heterogeneous data** for macromolecule model refinement
- Integrate formats and expertise **across CCPs** to support structural analysis for **integrated data** from crystallography, cryo-EM, NMR, and SAXS

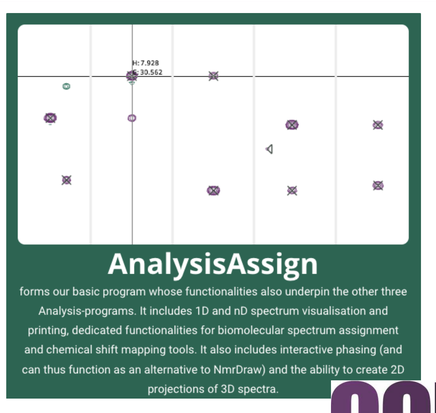
CCP-EM

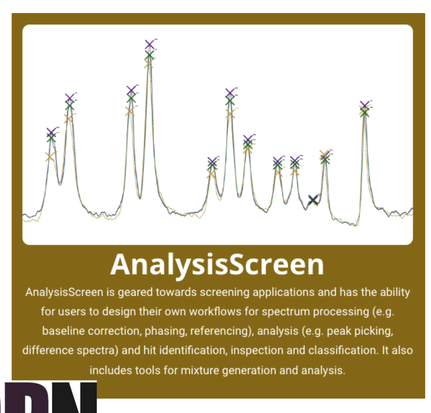
Cryo-EM Data Integration and Structural States

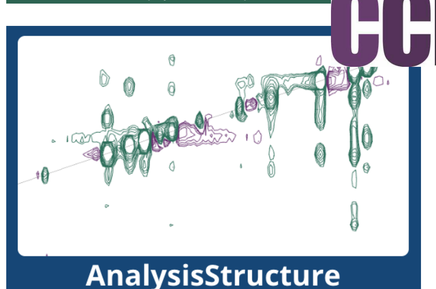
Cryo-EM structural information is integrated with modelling and simulation tools to provide structural states of biomolecular complexes and assemblies.

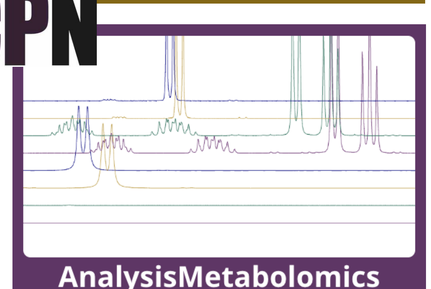
- Using model systems, describe biomolecular datasets as multi-conformational (**crystallography**), multi-state (**cryo-EM**), ensemble models (**NMR**) enabling links between methods
- Support methods for **map–model fitting and structural interpretation**.
- Enable transformations between coordinates, maps, and models.
- Implement **heterogenous reconstruction algorithms (HRA)** and launch a **community challenge** to validate HRA performance using **MD** based ground truth and metrics.

CCPN





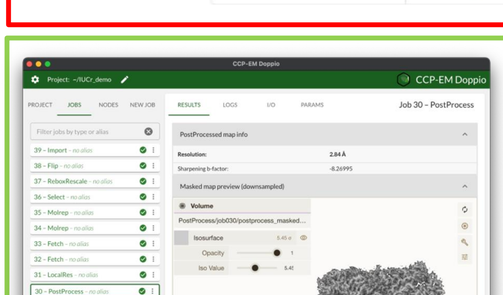




CCPBioSim

Application	CI / Quality	Package
aiida-amber	ci passing; coverage 57%; docs passing	pypi v2.2.0; status stable; python 3.11
aiida-gromacs	ci passing; coverage 78%; docs passing	pypi v2.2.1; status stable; python 3.11
CodeEntropy	CI; coverage 100%; docs passing	pypi v2.1.1; status stable; python 3.12 | 3.13 | 3.14

CCP-EM



Integrated *Doppio* software suite for cryo-EM data processing including:

- Single particle analysis
- Sub-tomogram averaging
- Atomic model building

Community support and software training

CCP4

DRIIMB connects experimental structural biology data with computational modelling to produce dynamic biomolecular ensembles and enable integrative structural analysis.

Integrative Biomolecular Modelling Workflow

Experimental data
NMR | Cryo-EM |X-ray

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Standardized Data models

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DRIIMB Data Integration

↓

Molecular Simulations

↓

Structural ensembles

↓

Understanding biomolecular dynamics