



Science and  
Technology  
Facilities Council



*Working Group 1 2026*

CCP-EM Group  
1 May 2026  
Online

# CCP-EM WG1: Agenda

1. Welcome to new members
2. Overview of CCP-EM software
3. Training
4. Spring Symposia 2026 / 2027
5. AOB

*Time for questions / comments after each section*



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Medical  
Research  
Council



Research Complex  
at Harwell



University of  
Pittsburgh

Department for  
Science, Innovation  
& Technology

GΦL  
Global Phasing Limited

al.c  
ada lovelace centre

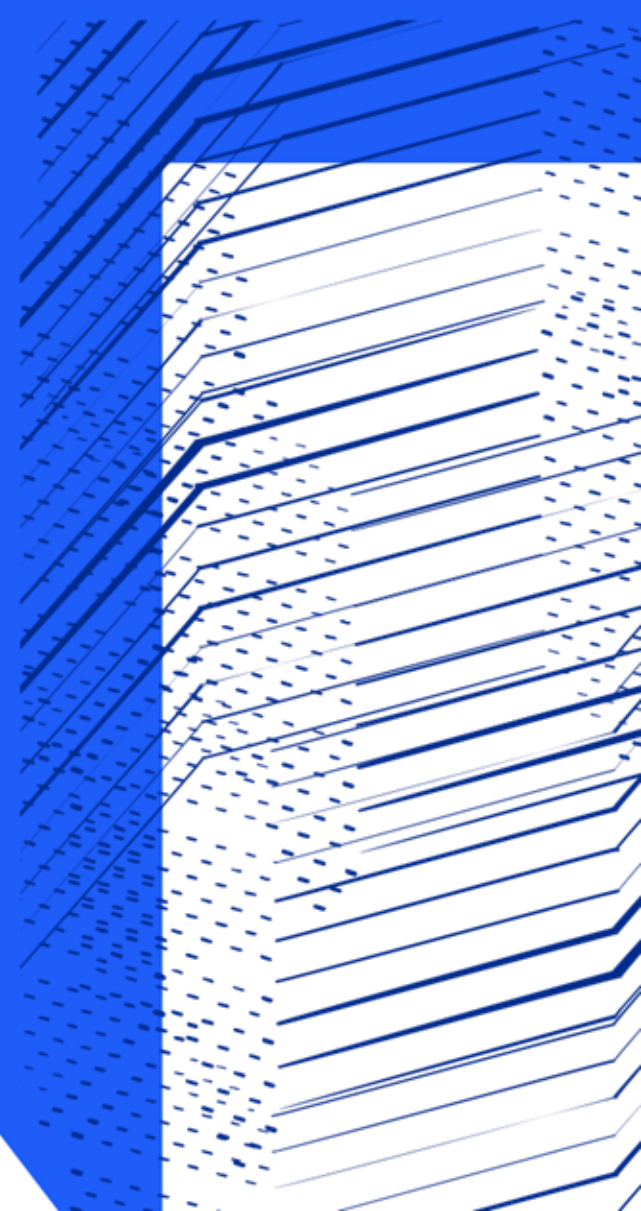
CoSec



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*Welcome to new members*



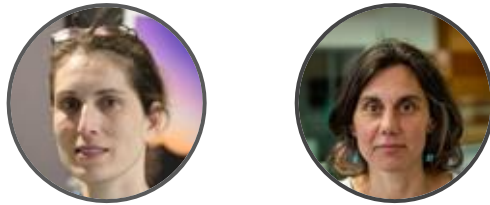
# Welcome to new members

## Executive Group



*Provides day-to-day management, sets policies, and approves new collaborations or software.  
Grant Cols & Chairs.*

## Chair and Deputy



*Provide leadership and represent the project to external stakeholders*

## Working Group 1



*Provide community oversight for the project and helps to set priorities*

[www.ccpem.ac.uk/about/working-groups](http://www.ccpem.ac.uk/about/working-groups)

# Welcome to new members

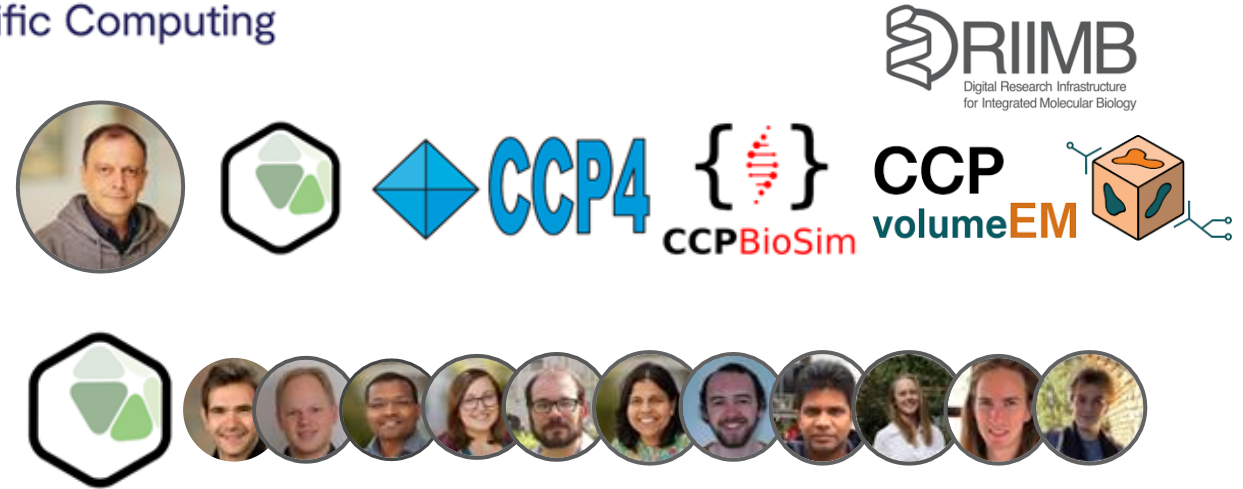
National Laboratories



Scientific Computing



Computational Biology Theme



Electron Microscopy Group



# MRC core grant update



MRC Partnership CCP-EM Core Grant: *“Collaborative Computational Project for cryo electron microscopy (CCP-EM): expanding the reach of cryoEM”*

## **Investigators:**

Tom Burnley (STFC, PI), Martyn Winn (STFC), Maya Topf (LIV/CSSB), Giulia Zanetti (Birkbeck), Sjors Scheres (MRC-LMB), Kyle Morris (EMBL-EBI), Peijun Zhang (Oxford/Diamond), Peter Rosenthal (Crick) and Paula da Fonseca (Glasgow)

## **Project Partners:**

Randy Read (Cambridge), Zach Freyberg (Pittsburgh), Arjen Jakobi (Delft), Ivo Tews (Southampton/CCP4), Geerten Vuister (Leicester/CCPN), Sarah Harris (Sheffield/CCPBioSim), Paul Verkade (Bristol), Dan Rigden (Liverpool), Keitaro Yamashita (Tokyo), Ellen Zhong (Princeton), Dari Kimanius (CZII), Mark Basham (RFI)

# MRC core grant update



Science themes:

- ***In situ* cryo electron tomography**, for the determination of macromolecular structures in their native environment and their role in medically important pathways;
- **High resolution cryoEM with ligand** identification and validation, contributing to rational drug design;
- **Heterogeneous reconstruction** to identify conformational and/or compositional variability;
- **Data/metadata management** to handle the increasing data volumes, and ensure that database entries are well annotated and FAIR.

Submitted: January 2025 | Awarded: June 2025

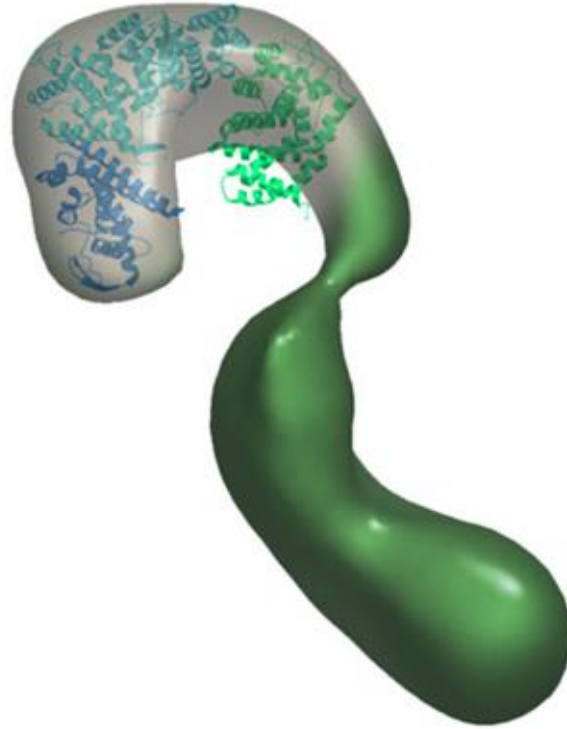
Funding period: March 2026 - February 2031

Funds (£1.8M): Agnel Joseph & Colin Palmer, 0.5 Matt Iadanza, 0.3 Lauren Giles

Activities: Spring Symposium, CCP-EM workshops (SPA/STA/model building), developer meetings, software development and maintenance



# New member questions?



*pdb101.rcsb.org | Nup192*



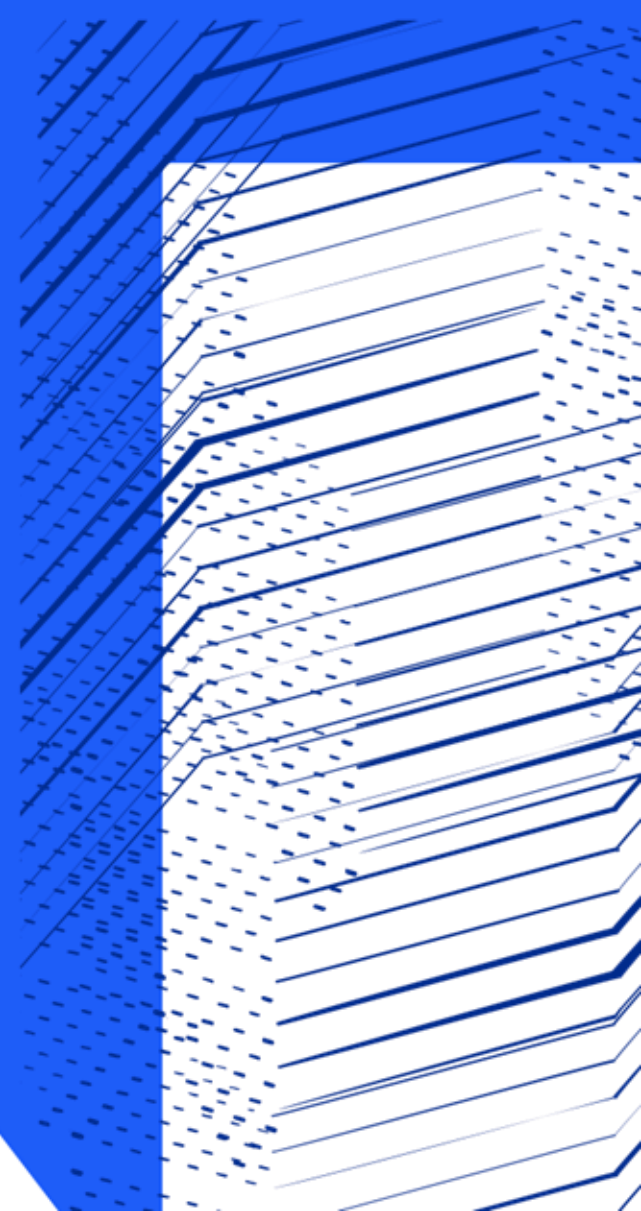
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# CCP-EM

## *Overview of CCP-EM software*

### *Colin Palmer*



# CCP-EM Software Suite: *Doppio*

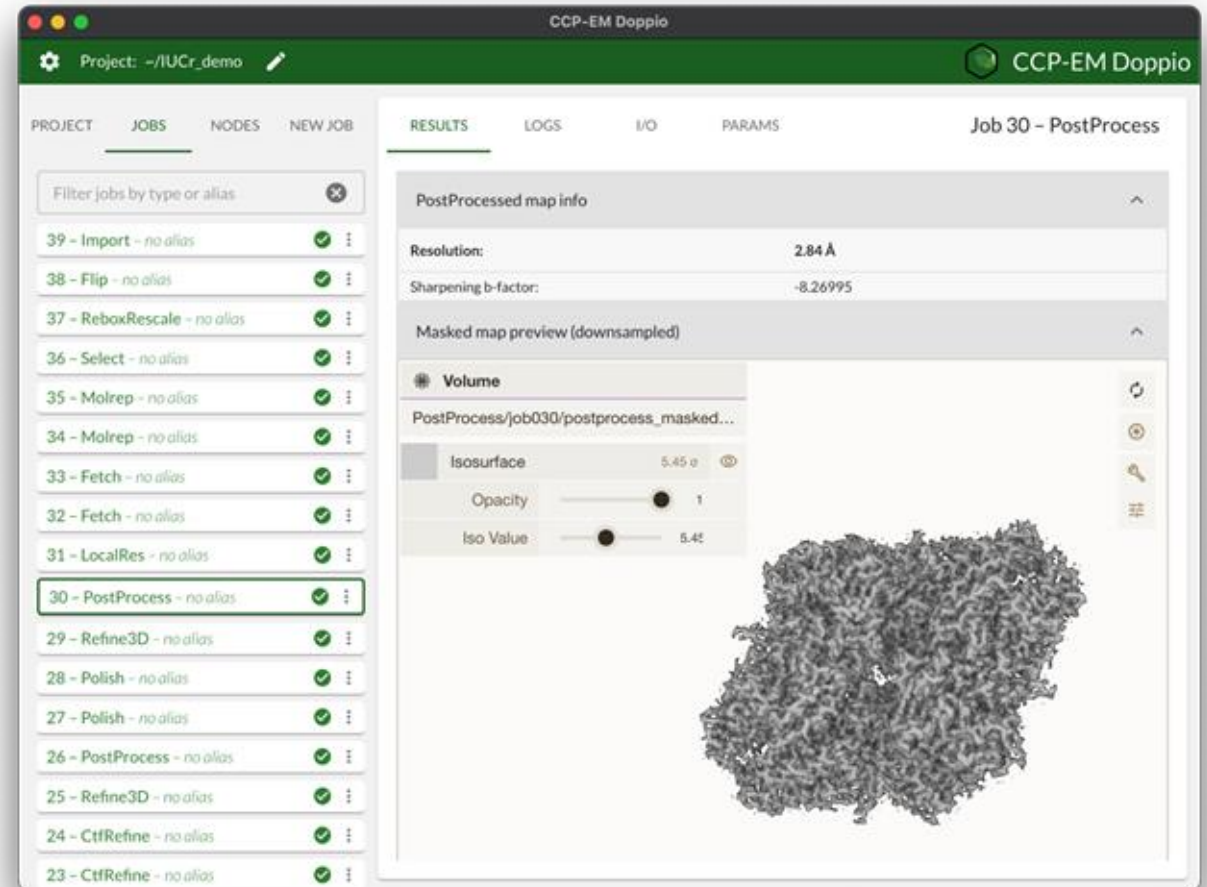
Supports SPA, STA and model building

Local / Remote modes

Linux and Mac

CCP-EM licence, free for academic use, fee for commercial use

Supports: Relion, CCP4, Chimera/X



# CCP-EM Doppio 1.6

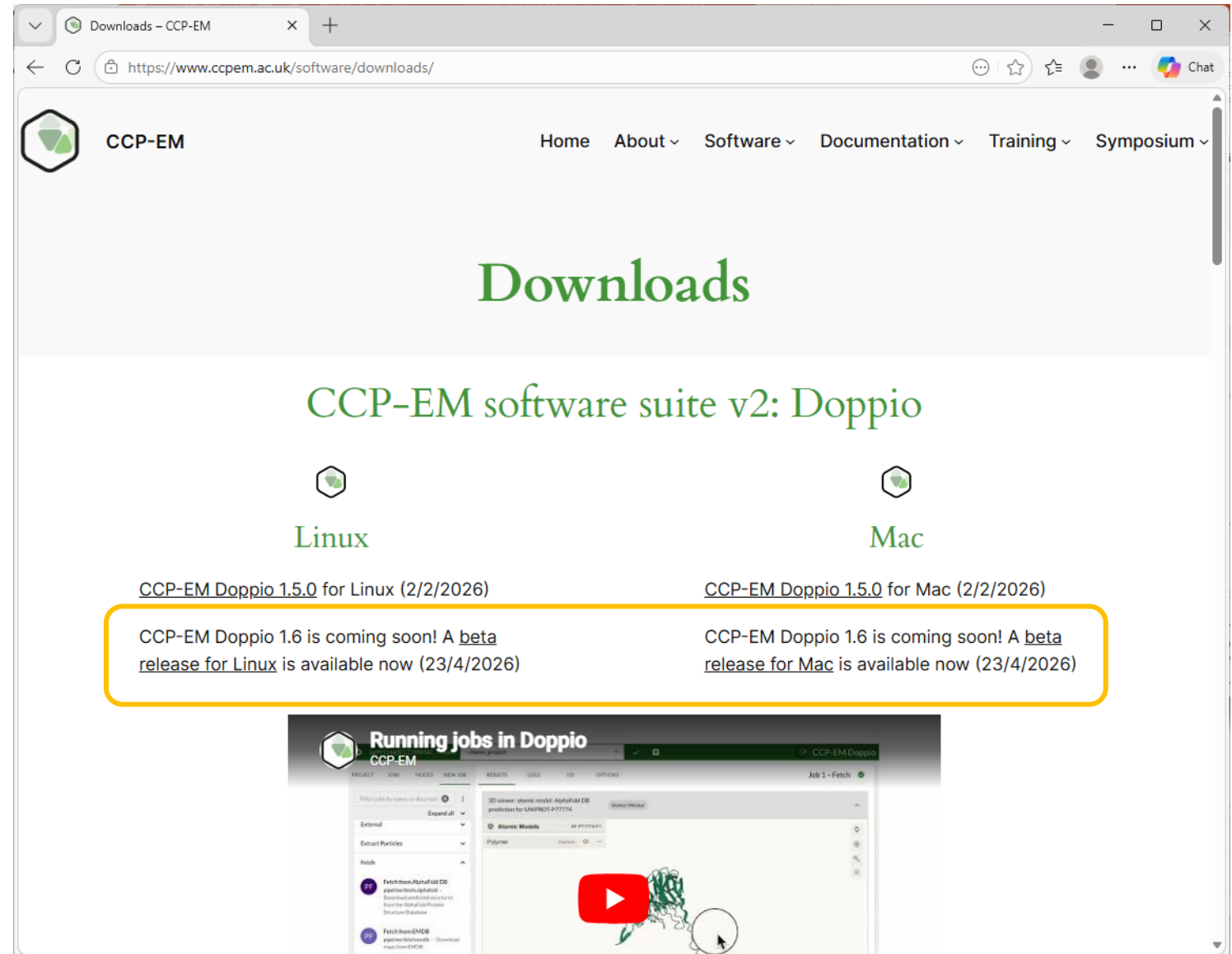
Last year: Doppio 1.3

Now: Doppio 1.6 (beta version)

See Agnel's symposium talk

Main developments:

- Visualisation improvements (Moorhen, Mol\*, particle picker)
- Job continuation and overwriting
- Allow use of multiple projects
- doppio-ssh launcher
- New tools: LTM, DPI score



The screenshot shows the CCP-EM Downloads page. The main heading is "Downloads" in green. Below it, the text "CCP-EM software suite v2: Doppio" is displayed. There are two columns for "Linux" and "Mac". A yellow box highlights the announcement: "CCP-EM Doppio 1.6 is coming soon! A [beta release for Linux](#) is available now (23/4/2026)" and "CCP-EM Doppio 1.6 is coming soon! A [beta release for Mac](#) is available now (23/4/2026)". At the bottom, there is a video player titled "Running jobs in Doppio" showing a 3D molecular model.

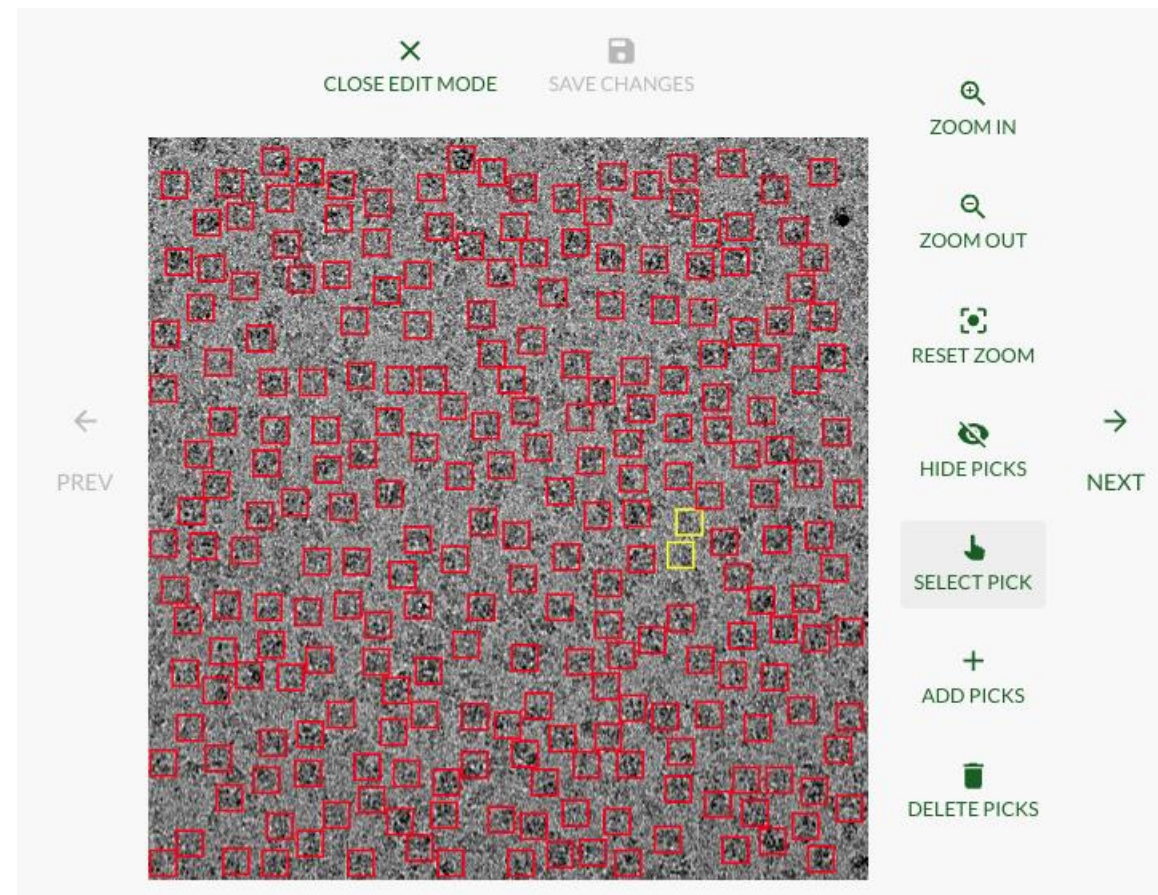
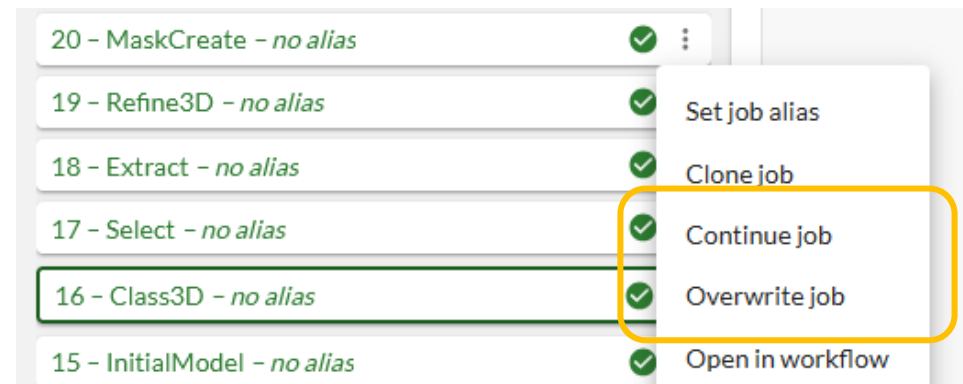
# Doppio UI updates

## Job control

- Job continuation
- Job overwriting

## Particle picking

- View picked coordinates on any image in the data set
- Add / delete picked particles
- Also adds image zoom & pan – plan to separate this to allow use on all image types
- SPA only for now, should adapt easily to STA too



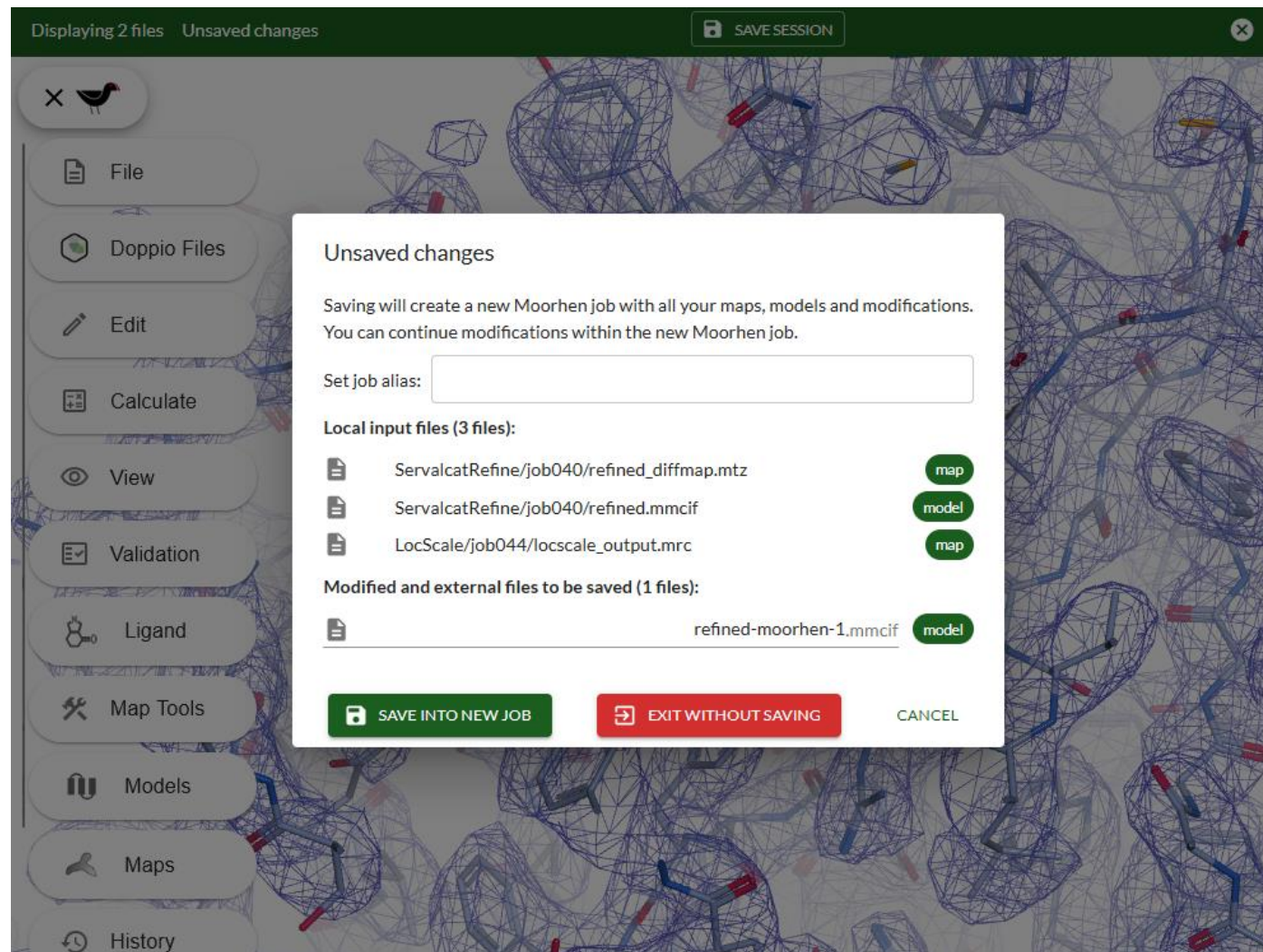
# Doppio UI updates

## Moorhen

- Major rewrite of integration into Doppio
- Better tracking of opened & edited files
- Save, restore and continue sessions
- MTZ and difference map handling



George Coldstream



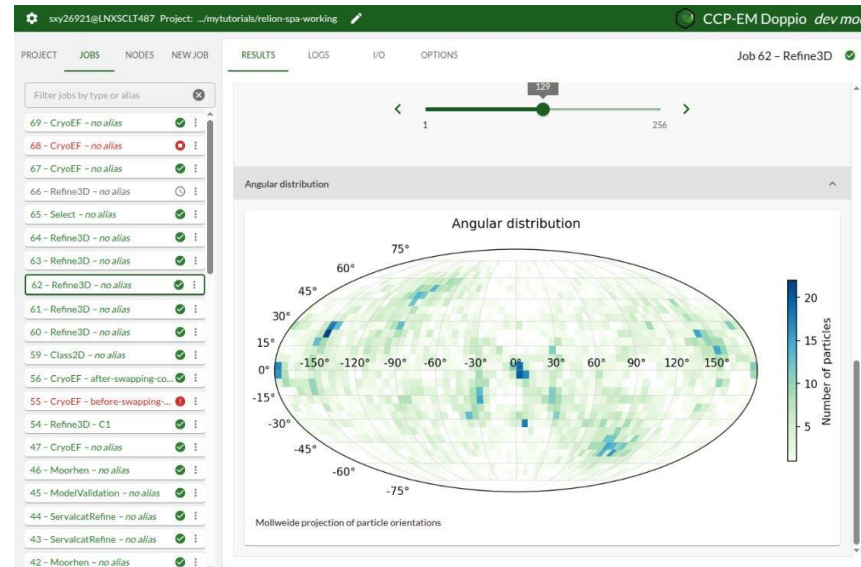
# Doppio UI updates

## Angular distribution plots

- 2D Mollweide projection plots
- 3D “porcupine” plots (RELION bild files)
- So far only in Refine3D job – plan to add to InitialModel and Class3D jobs

## Mol\* upgrades

- New buttons to show / hide individual items (maps, models, porcupine plots) in one click



Job 61 - Refine3D

Open with: CHIMERAX COOT PDF VIEWER RELION DISPLAY TEXT EDITOR UCSF CHIMERA UGLYMOL MOL\*

Inputs to this job:

- Extract/job018/particles.star ParticleGroupMetadata relion
- Class3D/job016/run\_it025\_class002\_box256.mrc DensityMap

Outputs from this job:

- Refine3D/job061/run\_data.star ParticleGroupMetadata relion refine3d
- Refine3D/job061/run\_optimiser.star OptimiserData relion refine3d
- Refine3D/job061/run\_model.star DensityMapMetadata relion refine3d model
- Refine3D/job061/run\_half1\_class001\_unfil.mrc DensityMap relion refine3d halfmap
- Refine3D/job061/run\_half2\_class001\_unfil.mrc DensityMap relion refine3d halfmap
- Refine3D/job061/run\_class001.mrc DensityMap relion refine3d
- Refine3D/job061/run\_class001\_angdist.bild DensityMap relion refine3d angledist



Jola Mirecka

# Doppio back-end updates

## doppio-ssh script

- Easily start Doppio over SSH
- Remote server with GUI in local browser
- Automatic port selection and forwarding
- Works on Linux, Mac and Windows (via WSL or MobaXterm)

## Multiple projects

- Can now run multiple Doppio server instances in different projects simultaneously

```
[16:09] colin@SCLT419 ~/software/doppio/1.6.0b1/install/app
$ ./doppio-ssh b5bj.aip2.isambard

Doppio API token: c6229b8a7f6ac6f101447db38155986340e6d5bc3438994de2f58ae7c0006f5b

INFO: Started server process [78361]
INFO: Waiting for application startup.
INFO: Application startup complete.
INFO: Uvicorn running on http://127.0.0.1:37721 (Press CTRL+C to quit)
INFO: Doppio is now running.

Go to this link in your browser to open Doppio:

file:///home/b5bj/cpalmer.b5bj/.local/share/doppio/doppio-78361-open.html

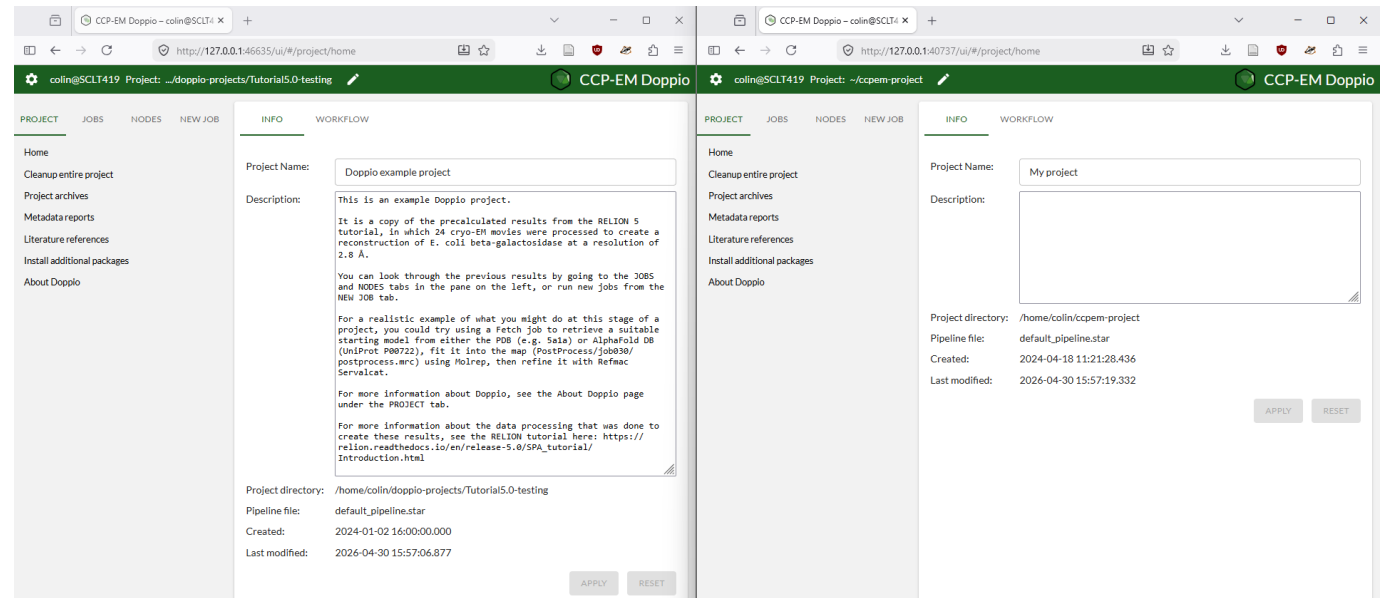
Or you can access Doppio directly using these details:

Server URL: http://127.0.0.1:37721/
Access token: c6229b8a7f6ac6f101447db38155986340e6d5bc3438994de2f58ae7c0006f5b

Press Ctrl+C to quit this Doppio server

Forwarded local port 37721 to remote port 37721

doppio-ssh is opening your browser to navigate to: http://127.0.0.1:37721/
```



# Doppio: new tools

## LTM

- Template matching in tomograms
- Tools for mask and template creation and other related tasks
- Collaboration with Zachary Freyberg

Template Matching

- LC** Create Mask for TM  
Itm.create.mask - Create a mask for template matching using LTM
- LC** Create Template for TM  
Itm.create.template - Create a template for template matching using LTM
- LE** Extract Peaks from LTM Results  
Itm.extract.peaks - Extract peaks from LTM template matching results
- LH** LTM Half-tomogram Local CC Calculation  
Itm.halftomo.localcc - Calculate local cross-correlation map for half-tomogram in LTM
- LT** Template Matching with LTM  
Itm.template.match - Template matching using LTM

## Template Matching with LTM

**RUN** **JOB INFO** **RESET OPTIONS**

Job alias:

----- Main -----

Tomogram file: \*

Template file: \*

Template mask file: \*

Minimum tilt angle (degrees, e.g. -40): \*

Maximum tilt angle (degrees, e.g. 40): \*

Particle diameter (A): \*

Mask type: \*

Angular step (degrees):

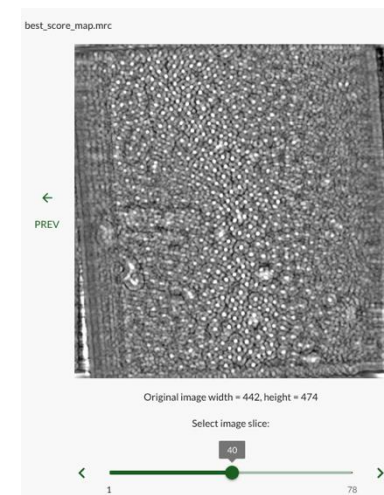
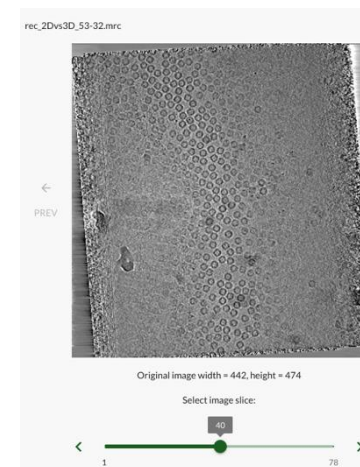
Psi step (degrees):

Chunk size (angles):

Which GPU ID to use (e.g. 0 or 1 etc):



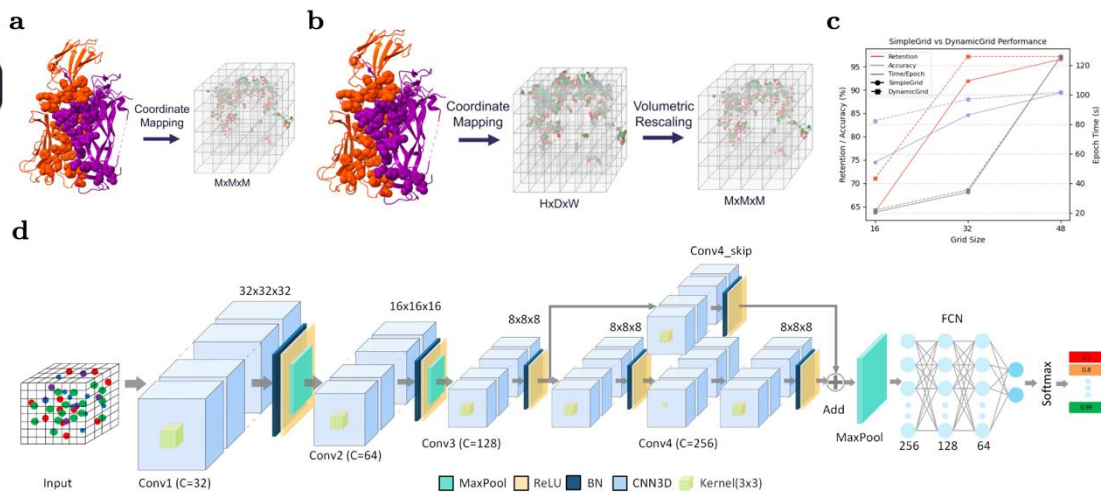
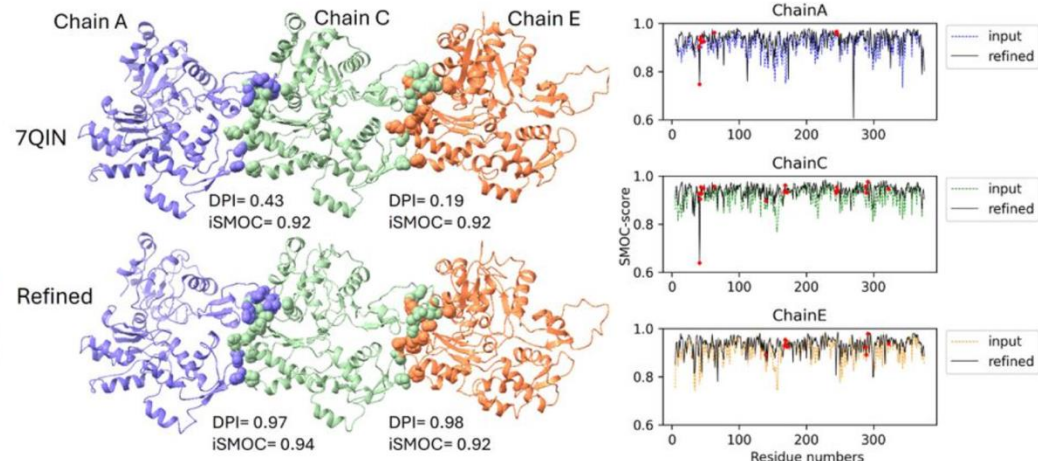
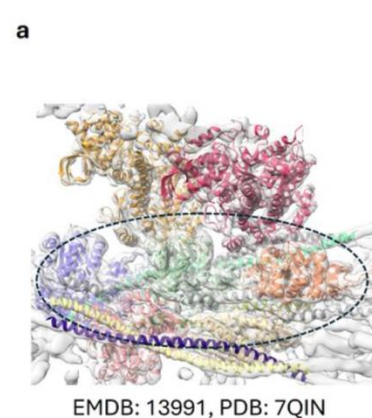
Rangana Warshamanage



# Doppio: new tools

## DPI-score

- Deep learning-based Protein Interface quality score



6.6 Å resolution structure with a homo pentamer of Actin

CCP-EM software suite v2 (Doppio) was used to perform flexible fitting using TEMPy-REFF job, which was followed by Servalcat refinement.

	Submitted structure	Re-refined structure
Actomyosin complex (6.6Å)		
CCC-mask	0.54 (percentile: 49)	0.6 (percentile 57.9)
Average model map FSC	0.76 (percentile: 65)	0.89 (percentile 98.5)
iSMOC (AC, CE)	0.92, 0.92	0.94, 0.92
DPI (AC, CE)	0.43, 0.19	0.97, 0.98



Sony Malhotra

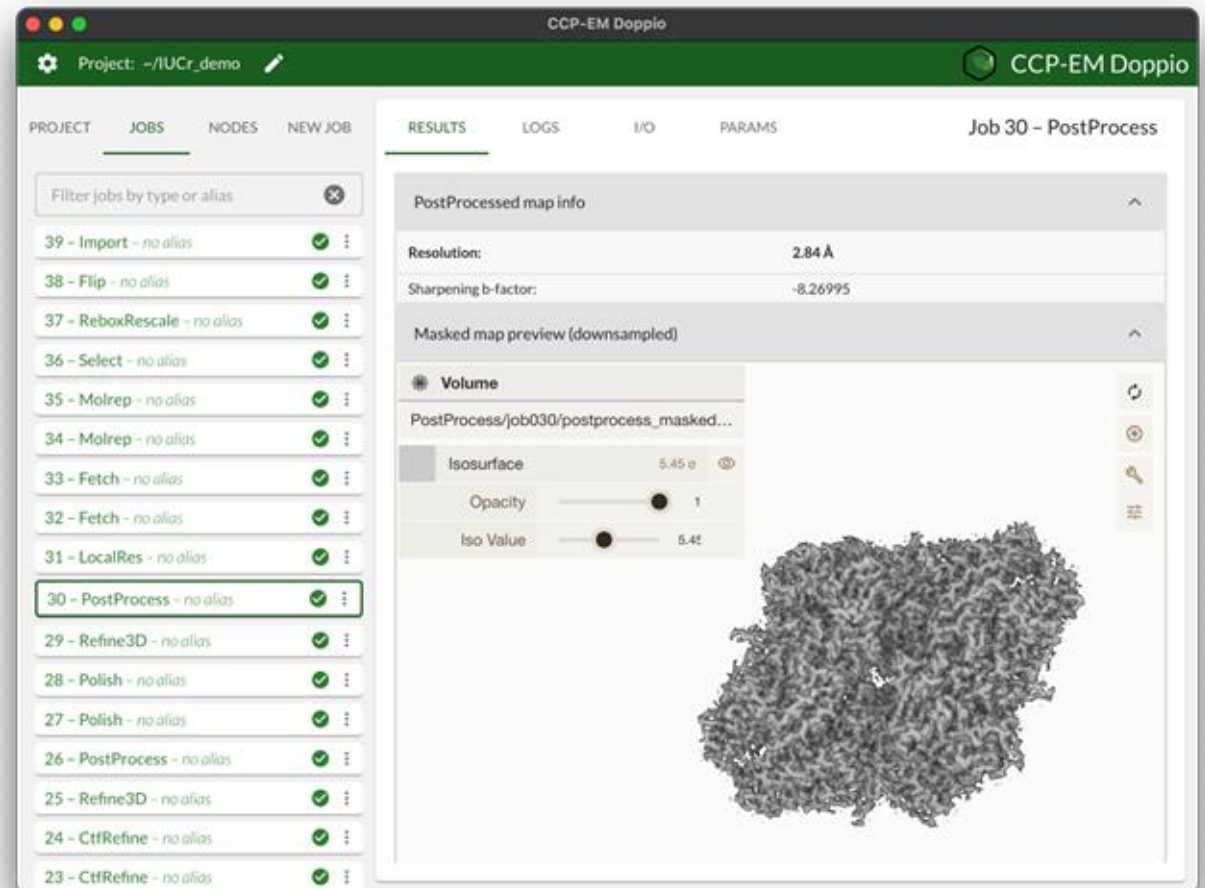


Niraj Bhujel

# Doppio: current developments

Coming soon:

- Automated depositions
- Live on-the-fly processing
- HRA latent space visualisations





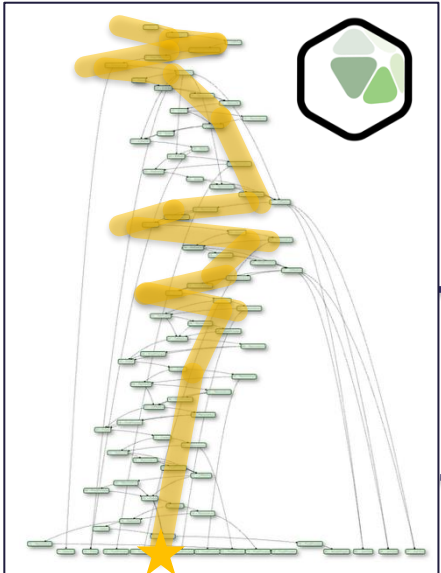
Daniel Hatton

# Coming soon: automated depositions

Chan Zuckerberg Imaging Institute (CZII)



Additional CIF files



CCP-EM Doppio

Prepare OneDep deposition

Job alias:

Main

Main map: PostProcess/job030/postprocess\_masked.mrc

Atomic model: Moorhen/job035/refined\_m\_moorhen.pdb

Halfmaps: Refine3D/job029/run\_half2\_class001\_unfl.mrc  
Refine3D/job029/run\_half1\_class001\_unfl.mrc

Masks: MaskCreate/job020/mask.mrc

Associated sequences: Fetch/job032/P00722.fasta

Additional maps:

Additional deposition data files (mmapcif format):

OneDep deposition ID \* <sup>required</sup> 123ABC



Matt Iadanza



Prepare EMPIAR deposition

Job alias:

Main

Job to create deposition from: \* Refine3D/job025

Deposit raw micrographs (if available)?  Yes  No

Deposit corrected micrographs (if available)?  Yes  No

Deposit particles (if available)?  Yes  No

Deposit polished particles (if available)?  Yes  No



empiar\_depositor



Deborah Harrus



Kyle Morris



# Coming soon: Live processing in Doppio

Collaboration between **CCP-EM** and **eBIC**

eBIC's automated processing pipeline integrated into Doppio. Run automated SPA processing (motion correction to post processing) as micrographs are produced. These automated processing 'recipes' can be customised.

Deployable on GPU workstations, clusters, and HPC. Integrated solution allows for easy deployment with Doppio at Cryo-EM facilities, labs, and industry around the world.

Run experimental jobs while data is processed, continue further processing, or start model building all in Doppio.

Live data dashboard (based on components from eBIC's PATo).

(Later this year) Live tomography processing pipeline in Doppio (motion correction through to alignment, denoising, and segmentation).



George Coldstream



Stephen Riggs



Daniel Hatton

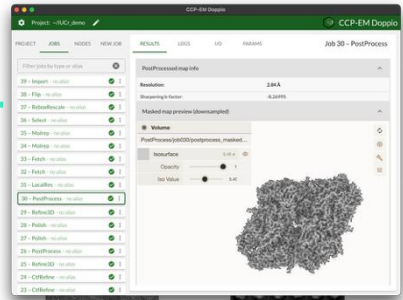
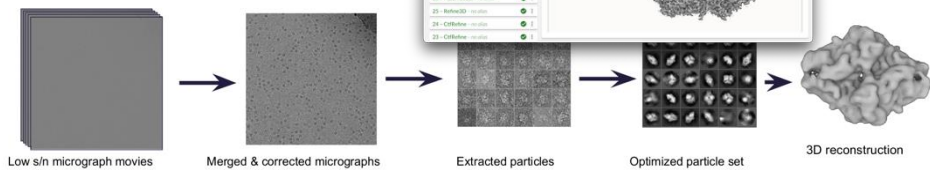


Guilherme De Freitas

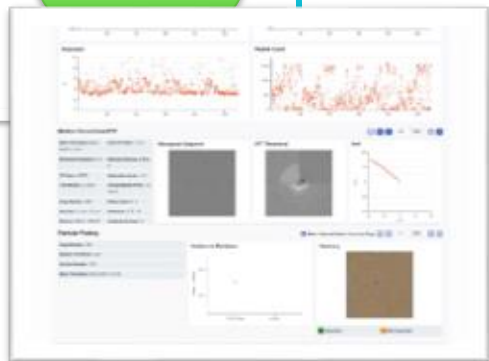
The image displays two screenshots of the Doppio software interface. The top screenshot shows a 'Jobs' list with columns for PROJECT, JOBS, NODES, and NEW JOB. It includes a 'Filter jobs by type or status' section and a 'Selected class average: score = 0.5' section with two circular micrograph images. The bottom screenshot shows a 'Live dashboard' with a table of jobs, a 'Class score distribution' histogram, and a 'Start new live data processing' form with various parameters like 'Micrograph directory to watch', 'Particle diameter (Å)', and 'Voltage (kV)'. The interface is dark-themed with green accents.

GUI

# Doppio-Vivo

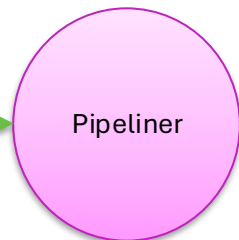
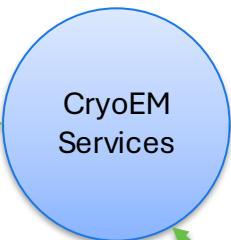
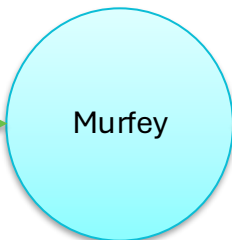


# Doppio

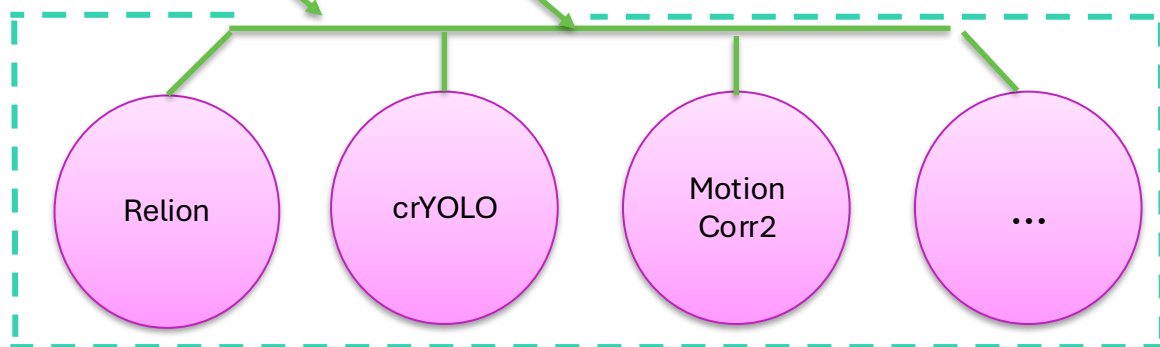
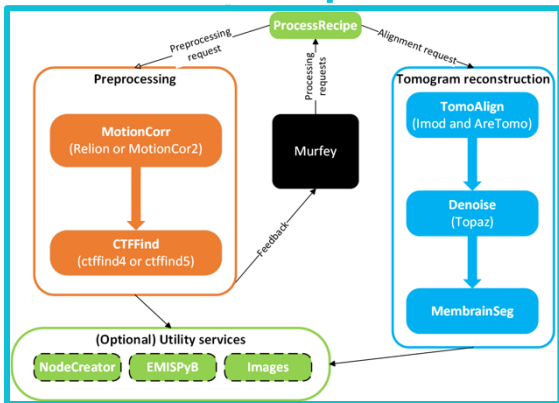


Managers

# eBIC pipeline



Tasks



# Coming soon: latent space visualisation

- Dynamic latent space visualisations for heterogeneous reconstruction algorithms
- Interactive particle and cluster selections
- Utility functions for clustering and dimensionality reduction



Hieu Le

A screenshot of the CCP-EM Doppio software interface. The top bar shows the user 'git95787@Hieu-Le-STFC' and the project path 'Project: ../doppio-project/ccpem-project'. The interface is in 'dev mode'. On the left, there is a 'PROJECT' tab with a list of jobs, including '42 - Select - cryodrgn.select.particles', '41 - Select - no alias', '40 - CryoDRGN - no alias', '39 - Select - no alias', '38 - Select - no alias', '37 - Select - no alias', '36 - Select - no alias', '35 - Select - no alias', '34 - Select - no alias', '33 - CryoDRGN - no alias', '32 - Select - no alias', and '1 - CryoDRGN - no alias'. The main area has tabs for 'RESULTS', 'LOGS', 'I/O', and 'OPTIONS'. Under 'RESULTS', there is a list of analysis options: 'UMAP Embeddings: Scatter and 2D Histogram', 'Embeddings TSNE', 'Embeddings UMAP built in function', 'UMAP 2D Density Heatmap of Latent Space', 'UMAP of latent space with density profiles', 'PCA of latent space with density profiles', 'K-means Centres on PCA of Latent Space', 'K-means Centres on UMAP of Latent Space (Kmeans on Latent)', and 'Training Loss'. Each option has a corresponding 'INTERACTIVE PARTICLES SELECTION' button on the right. A mouse cursor is hovering over the 'UMAP 2D Density Heatmap of Latent Space' option. At the bottom, there is a slider for '0.615'.

# Doppio: development plans

Open for discussion!

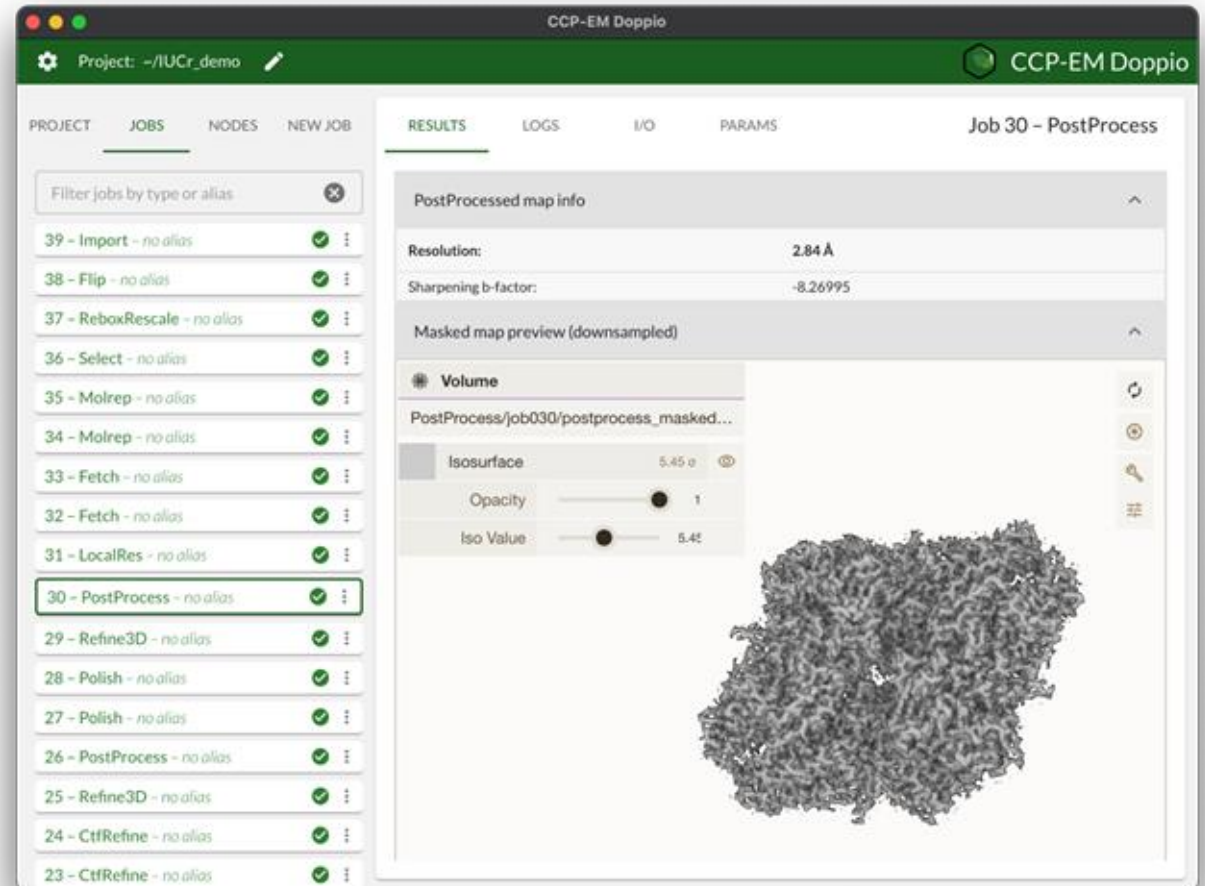
Current goals:

- Full “batteries included” suite, including RELION, em\_placement, Servalcat etc.
- In-browser image selection / exclusion and STA particle picking – remove need for external tools
- Job scheduling (“run this, then that”)

Later:

- More advanced scheduling (sub-jobs, mini pipelines, decision logic)

Also many smaller improvements planned

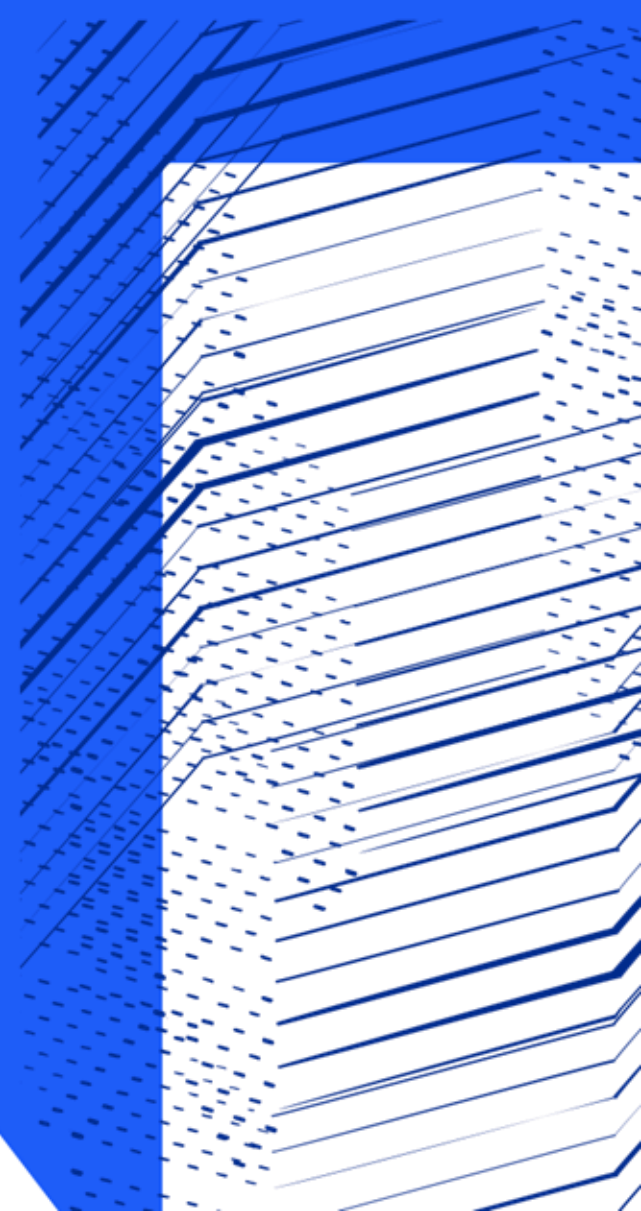




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*Other software developments*





# RELION acceleration

Critical need to speed up SPA for whole community particularly facilities & industry

Initially we target Relion SPA to be 3-5 faster by:

- 1) Relion run time parameterisation is difficult to optimise and not obvious; GPUs often not run optimally
- 2) GPU routines (re)optimised for use with current generation of GPUs
- 3) Improve algorithmic efficiency



**Sjors  
Scheres**



**Gérard  
Bricogne**

# RELION Benchmarking and Profiling

Initial work with Oxford RSE Group and DLS/STRUBI

Benchmarking RELION performance

Profiling of GPU usage and access patterns

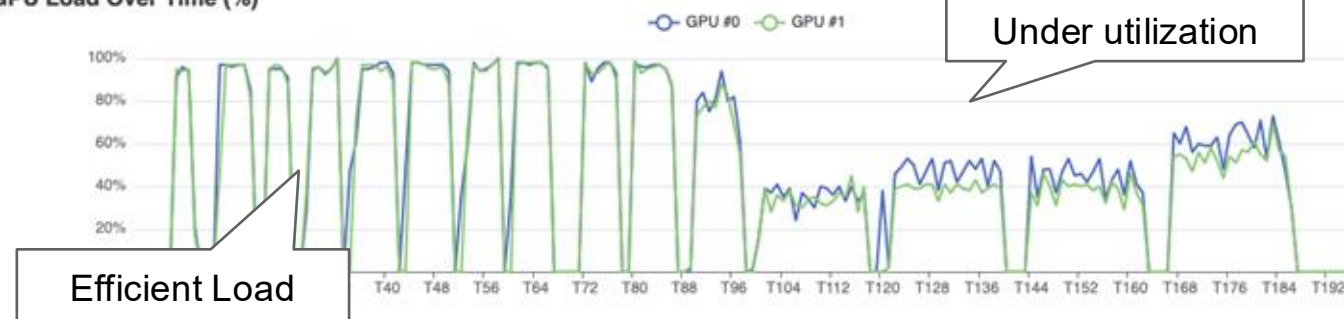
## Relion Benchmarks

Fields in (brackets) represent job parameters

Enter job parameter -- or select key -- Add Column Reset

ID	Project ...	Job name	Type	Node	CPU cores	GPU count	(nr_mpi)	(nr_thre...	(gpu_ids)
1	default	Import	relion.import...	arc-c130	48	0			
2	default	MotionCorr	relion.motion...	htc-g053	48	0	1	12	0
3	default	CtfFind	relion.ctffind...	htc-g053	48	0	6		
4	default	AutoPick	relion.autopic...	htc-g029	20	1	1		0
5	default	Extract	relion.extract	htc-g053	48	0	4		
6	default	Class2D	relion.class2d...	htc-g038	28	1	1	12	0
7	default	Select	relion.select...	htc-c005	96	0			
8	default	InitialModel	relion.initial...	htc-g036	28	1	1	12	0
9	default	Import	relion.import...	arc-c283	48	0			
10	default	MotionCorr	relion.motion...	htc-c005	96	0	1	12	0
11	default	CtfFind	relion.ctffind...	htc-c005	96	0	6		
12	default	AutoPick	relion.autopic...	htc-g038	28	1	1		0

GPU Load Over Time (%)



# RELION acceleration

Working with Xcelerit to speed up relion\_refine (used by Class2D, Class3D, InitialModel and Refine3D jobs)

Main focus on Expectation step – most of the run time for large jobs

Currently approx. 2x speed-up of E-step (varies on different systems and data sets)

Working with Dan Hatton at DLS to start testing on eBIC data collections

Anticipate a further 2 – 3x speed-up should be possible



# Software feedback?

Is there any key functionality missing in Doppio / are you aware of new tools that should be included in the suite?

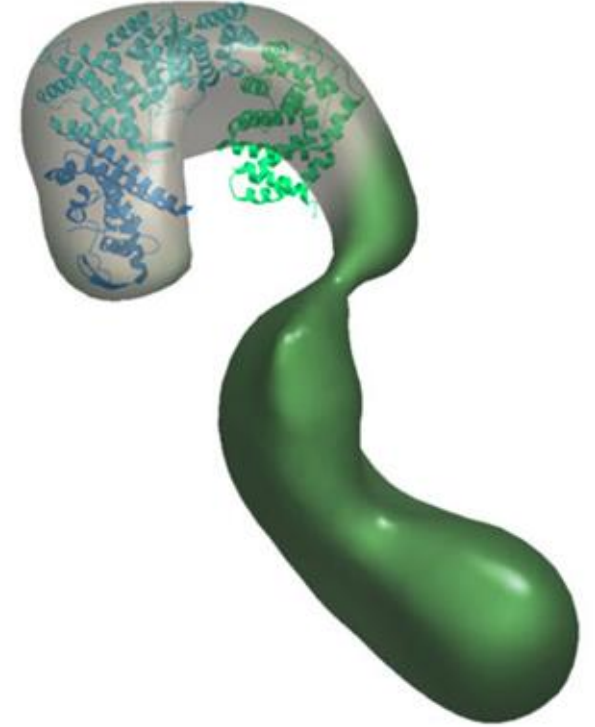
What would help users in your group/facility adopt Doppio for SPA/STA/modelling?

What should be our main focus(es):

- New scientific functionality
- Ease of use
- Ease of install/setup
- Documentation

If you/your group haven't used Doppio - why and what can we do to help?

*We are setting up a CCP-EM Software User Panel, with thanks to TJ Ragan*

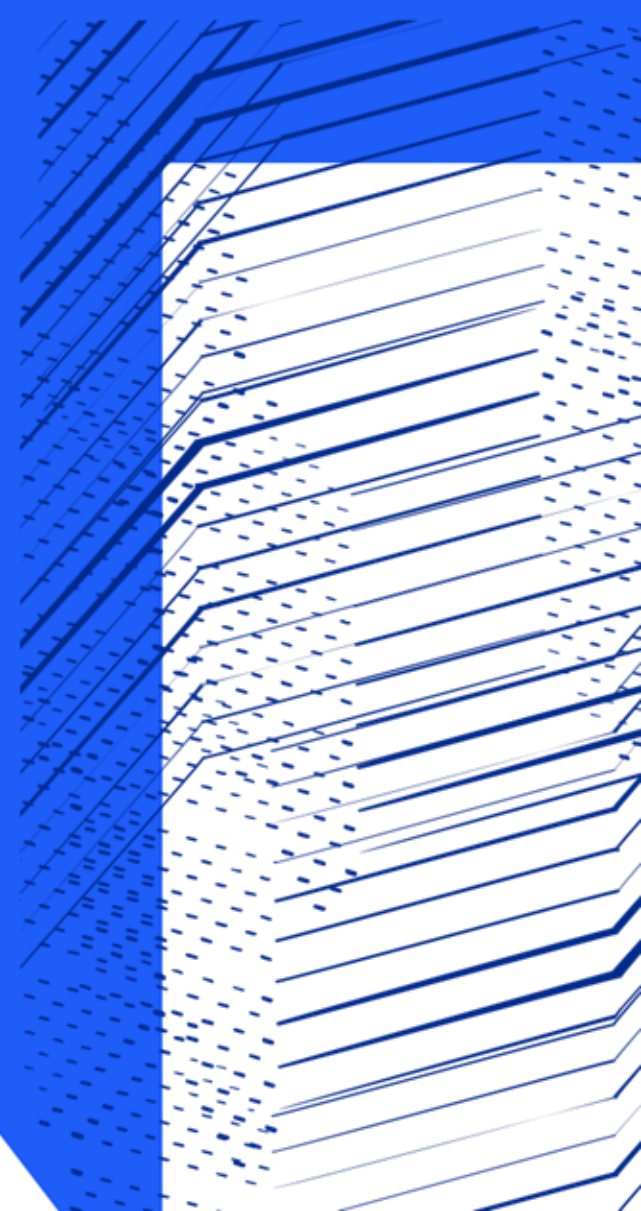




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*Overview of CCP-EM training*



# CCP-EM Workshops 2025-2026

- Structure determination (MX and Cryo-EM). Thailand, July 2025
- Integrative structural biology, Italy, July 2025
- CCP4-BCA summer school. York, August 2025
- Shanghai School. September 2025.
- EMBO Cryo-EM image processing, Birkbeck, Sep 2025
- Icknield workshop, RAL, Oct 2025
- CCP4/CCP-EM School Santiago, Chile, Nov 2025
- Doppio workshop, St Andrews, March 2026
- Model building workshop, India, March 2026
- Central European Workshop 2026, Czechia, April 2026
  
- *UK EM facilities workshop, Warwick, June 2025*
- Doppio road shows around UK: Manchester, Crick, Imperial
  
- **Since 2013 we have led or co-led 55 workshops, teaching over >1,500 researchers**



# CCP-EM Planned Workshops 2026

- International School Crystallography, May 2026
- Dutch cryoEM school, Leiden/Delft, June 2026
- CCP4-APS Chicago, July 2026
- IUCR Calgary, August 2026
- MSCDA cryoEM course, Exeter, Sep 2026
- CAHRA Heterogeneity challenge, Sept 2026
- China National Facility for Protein Science, Sep 2026
- Icknield workshop, Nov 2026
- King Mongkut's, Thailand, Nov 2026

*Please get in touch if you would like us to run a training course at your institute*



# Training using STFC Ada & SC Cloud

Doppio and example data installed on STFC Ada service training system

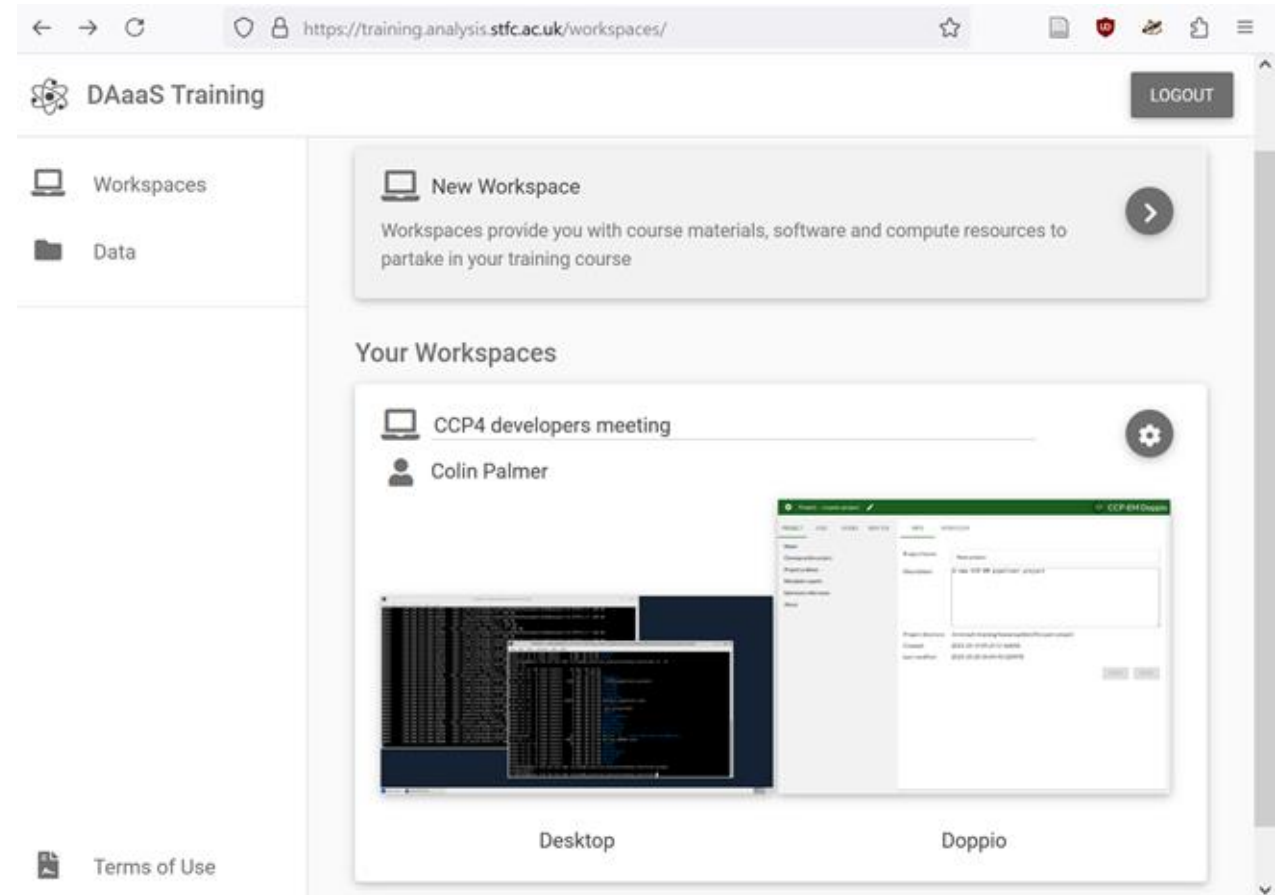
Manages access to virtual machines provided by STFC SC Cloud (inc. GPU)

Simple sign-up/authentication

Doppio app runs in user's local browser – much faster than a remote desktop

Also able to use Dectris Cloud

*Please get in touch if you would like us to run a training course at your institute*



# Heterogeneous reconstruction challenge



## The 2025 Community-Wide Assessment of Cryo-EM Heterogeneous Reconstruction Algorithms (CAHRA)

A community-wide data processing challenge for cryo-electron microscopy.

<http://heterogeneity.notion.site/challenge>

Test performance of HRA algorithms using benchmark data

Determine the SOA of the method and potential for bias/hallucinations

Development and improve metrics for quantifying map and model quality

Challenges focus on:

- *Conformational heterogeneity*
- *Compositional heterogeneity*

*Encourage entries from algorithm developers and wider community*



Ellen Zhong



Ryan Feathers



Pilar Cossio



Sonya Hanson



Tom Burnley



Joel Greer



# CAHRA Timeline and Review Workshop

Datasets released, open for submissions	Nov 1st 2025
Launch Webinar	Nov 14th 2025
Deadline for preliminary submissions	March 14th 2026
<b>Deadline for final submissions</b>	<b>June 1st 2026</b>
<b>Results announced</b>	<b>July 2026</b>
<b>CAHRA Challenge Review Workshop</b>	<b>Sept 16th-18th 2026</b>

- ***Review workshop at RAL/DLS***
- Winner of each challenge will have access to a travel and accommodation bursary to attend the Challenge Review Workshop
- There is also a total of \$10,000 in monetary awards for top-performing methods



Joel Greer



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- 10+ preliminary entries across challenge datasets
- Rankings for preliminary entries now live
- For more details see Joel's What's New Symposium talk

# Training Questions

Should we focus on?

SPA

Tomography

Model building

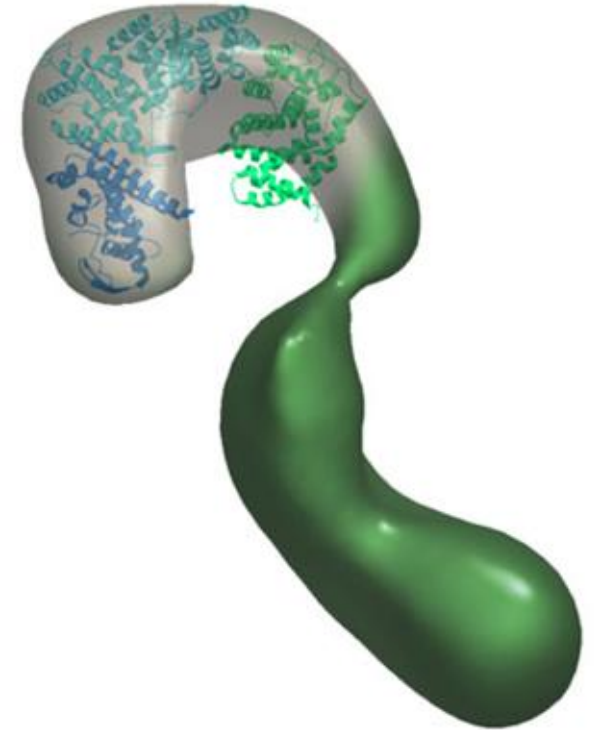
Software development

Should we do more online training?

Should we include more AI based tools in software e.g. trained on code or mailing list?

Are you aware of other training resources we could disseminate?

If you would like us to run a course at your institute please get in touch!

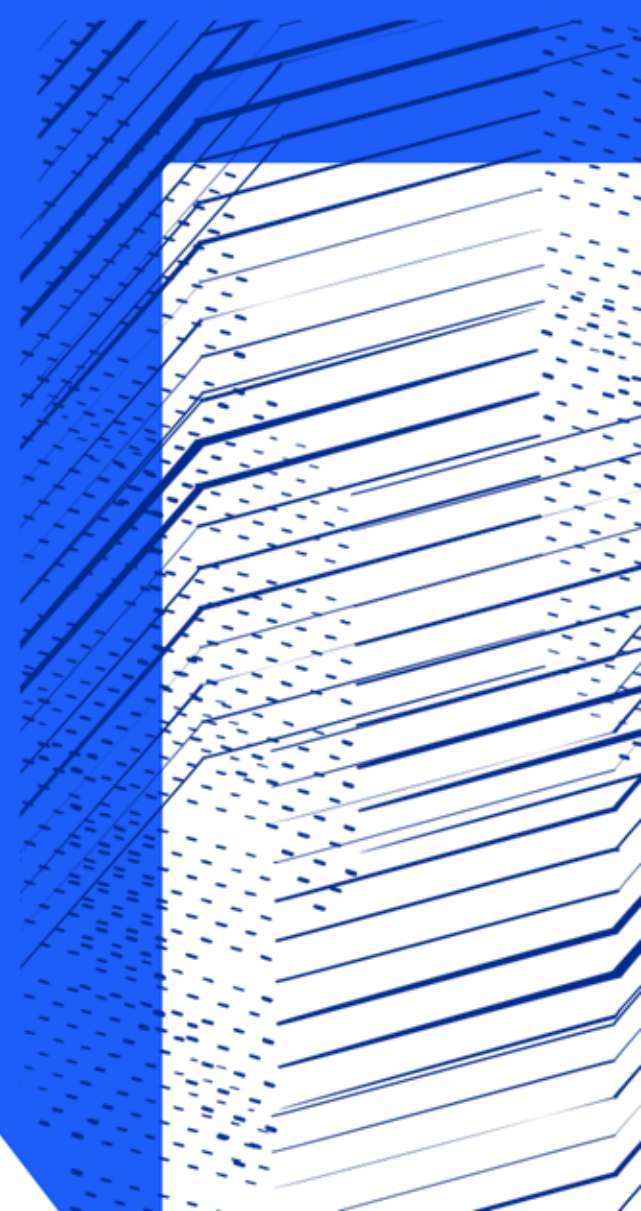




Science and  
Technology  
Facilities Council



*Overview of CCP-EM Spring  
Symposium conference*



# Spring Symposia 2026 / 2027

2026: 12th Ed. EMCC, Nottingham (22-24 April)

Included Diamond **Biological Cryo-Imaging meeting (BCI)** and **Karen Davies Memorial**.

CCP-EM Scientific Organisers **Ana Casanal & Jamie Blaza**

**312 In-person delegates** (16 countries, 4 continents)

**635 virtual delegates** (unique Zoom views, 28 countries, 5 continents)

6 talks from selected abstracts, 100 posters

£35k sponsorship (w/ DLS): 32 bursaries (registration & accommodation) including 2 bursaries for travel expenses

Raw recordings now available, edited YouTube talks to follow

Previous years talks on YouTube





## *Spring Symposium*

Small drop in number of in-person delegates in 2026 – budget constraints?

<b>Edition</b>	<b>Venue</b>	<b>Year</b>	<b>In person</b>	<b>Virtual (unique views)</b>
<b>12</b>	<b>Nottingham EMCC</b>	<b>2026</b>	<b>312</b>	<b>635</b>
<b>11</b>	<b>Nottingham EMCC</b>	<b>2025</b>	<b>375</b>	<b>612</b>
<b>10</b>	<b>Nottingham EMCC</b>	<b>2024</b>	<b>366</b>	<b>833</b>
<b>9</b>	<b>Nottingham EMCC</b>	<b>2023</b>	<b>257</b>	<b>680</b>
<b>8</b>	<b>Nottingham EMCC</b>	<b>2022</b>	<b>150</b>	<b>917</b>
<b>7</b>	<b>Virtual</b>	<b>2021</b>	<b>-</b>	<b>900</b>
<b>6</b>	<b>Virtual</b>	<b>2020</b>	<b>-</b>	<b>2439</b>
<b>5</b>	<b>Nottingham Jubilee</b>	<b>2019</b>	<b>286</b>	<b>?</b>
<b>4</b>	<b>Keele</b>	<b>2018</b>	<b>180</b>	<b>?</b>
<b>3</b>	<b>RAL</b>	<b>2017</b>	<b>215</b>	<b>?</b>
<b>2</b>	<b>RAL</b>	<b>2016</b>	<b>159</b>	<b>?</b>
<b>1</b>	<b>RAL</b>	<b>2015</b>	<b>100</b>	<b>?</b>

# Spring Symposia 2027

2027: EMCC, Nottingham (21-23 April)

Diamond Biological Cryo-Imaging meeting (BCI), 21 April

CCP-EM Spring Symposium, 22-23 April

*Continue in-person / virtual hybrid format*

## introduction



STRUCTURAL  
BIOLOGY

ISSN 2059-7983

This article is part of the Proceedings of the 2024 CCP-EM Spring Symposium.

**Keywords:** cryoEM; electron cryo-microscopy; CCP-EM; Spring Symposium.

## Ten years of the CCP-EM Spring Symposium

**Lauren Giles and Tom Burnley\***

Science and Technology Facilities Council, Research Complex at Harwell, Didcot OX11 0FA, United Kingdom.

\*Correspondence e-mail: tom.burnley@stfc.ac.uk

Here, we describe the first ten years of the CCP-EM Spring Symposium, an annual conference to bring together the cryogenic-sample electron microscopy (cryoEM) community to present and discuss the latest methodological advances and applications. We quantify the growth of the event and provide a detailed breakdown of the demographics of the tenth edition.

### 1. Introduction

*Acta Crystallogr D Struct Biol.* 2025 Dec 1;81(Pt 12):656-659. doi: 10.1107/S2059798325010496.



# Spring Symposia Questions

**Please send nominations for scientific organisers for 2027**

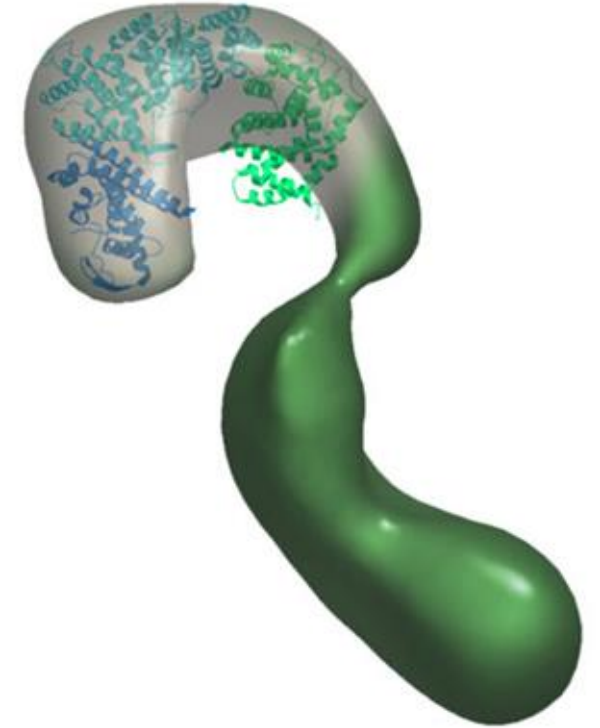
*For specific logistic & scientific feedback please use the feedback form to be sent to delegates soon*

*Posters – too many?*

*How/should we include 100 posters?*

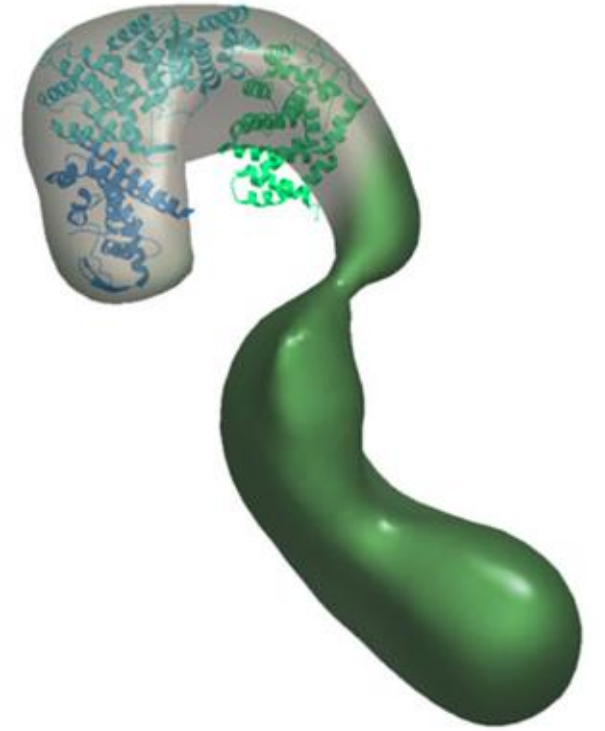
*Reason for drop in in person delegates in 2026?*

*Sponsorship – too commercial or good for industry and helps ECRs?*



[pdb101.rcsb.org](http://pdb101.rcsb.org) | Nup192

# Any other business?



Website & Downloads: [www.ccpem.ac.uk](http://www.ccpem.ac.uk)

Mailing list: [www.jiscmail.ac.uk/ccpem](http://www.jiscmail.ac.uk/ccpem)

Bluesky: [ccpem.bsky.social](https://ccpem.bsky.social)

Email: [ccpem@stfc.ac.uk](mailto:ccpem@stfc.ac.uk)

CCP-EM Core Team

CCP-EM Commercial License Holders

CCP4 Core Team

CCP-EM Collaborators

STFC Business & Innovation

CCP-EM Users

MRC Core funding

<https://heterogeneity.notion.site/challenge>

