# EAGER: Collaborative 3D Materials Science Research in the Cloud

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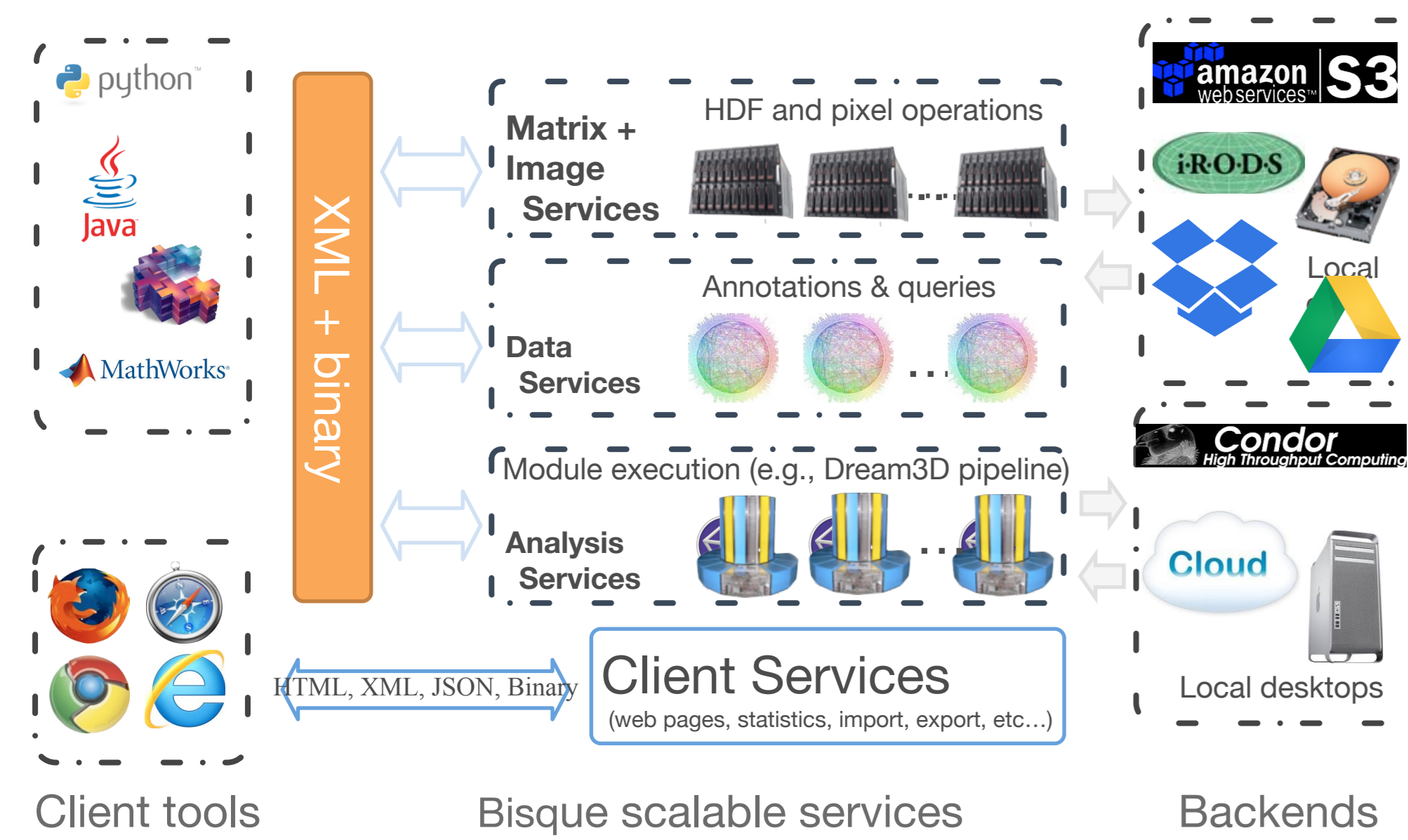
## BisQue Overview



Client tools — Bisque scalable services — Backends

- BisQue (Bio Semantic Query User Environment) is a cloud-based analysis platform developed in the Center for Bio-Image Informatics at UCSB [KVI2010]

- Allows management, analysis, and sharing of images and metadata for large-scale problems

- Images and metadata are organized as a network of trees of data items to handle any type of data organization
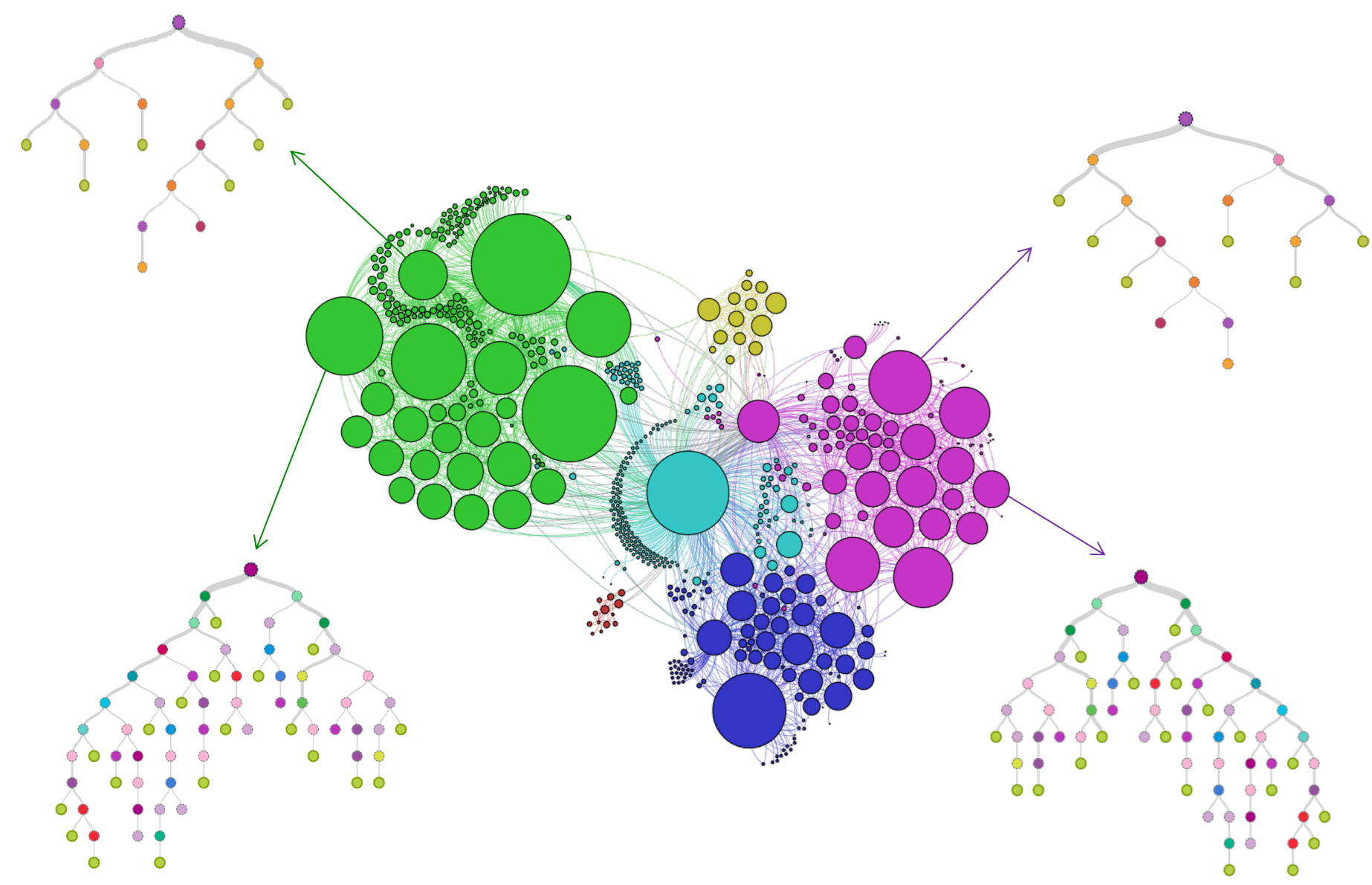


- Images, metadata, and links can be queried via a flexible and scalable query system

- BisQue's module system allows integration of analysis tasks over images and metadata that can be automatically scaled across compute grids

- Provenance is tracked by linking inputs and outputs of time-stamped analysis runs
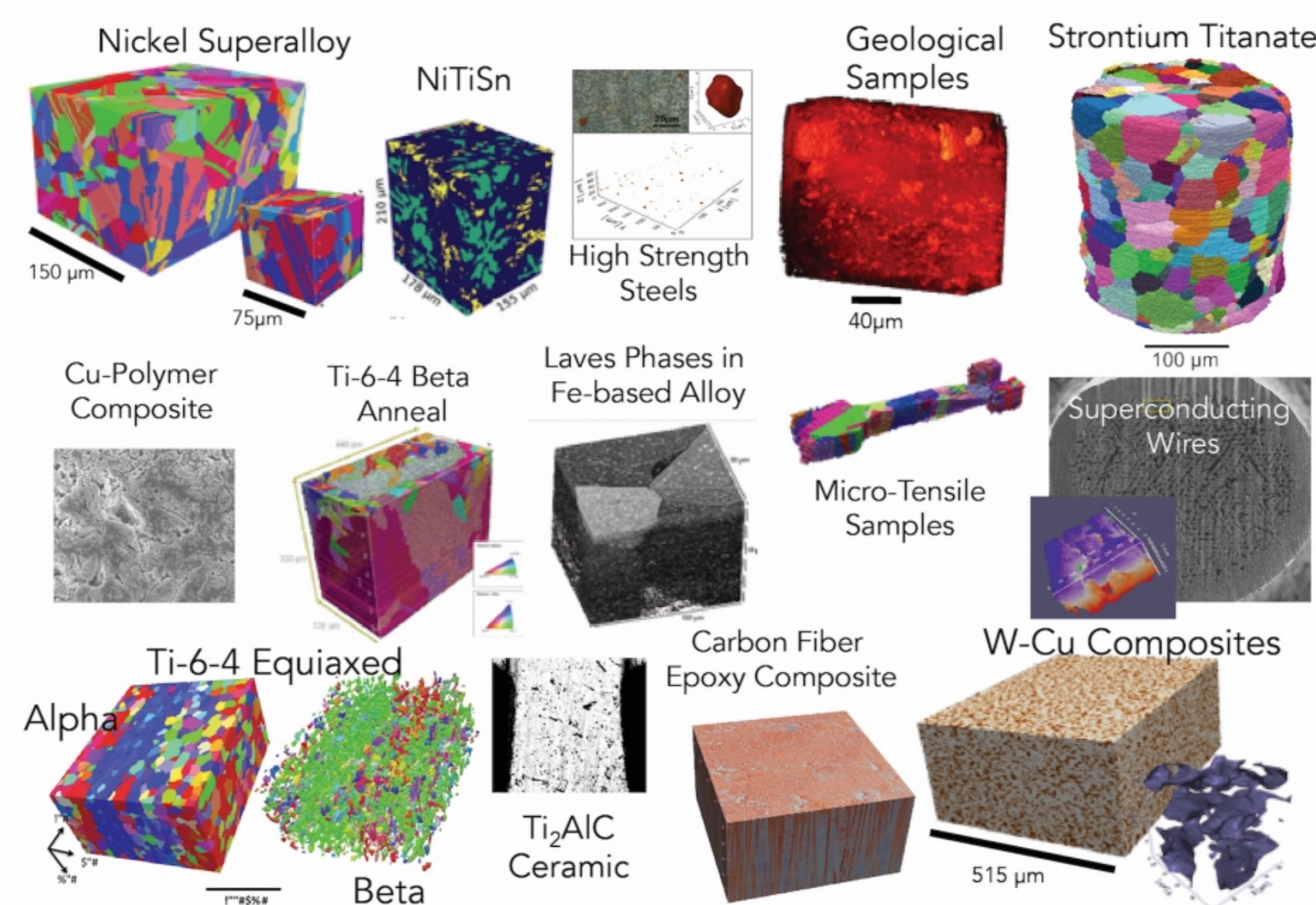
- Support for many life science image and video formats

- More information on BisQue:
  `http://bioimage.ucsb.edu/bisque`
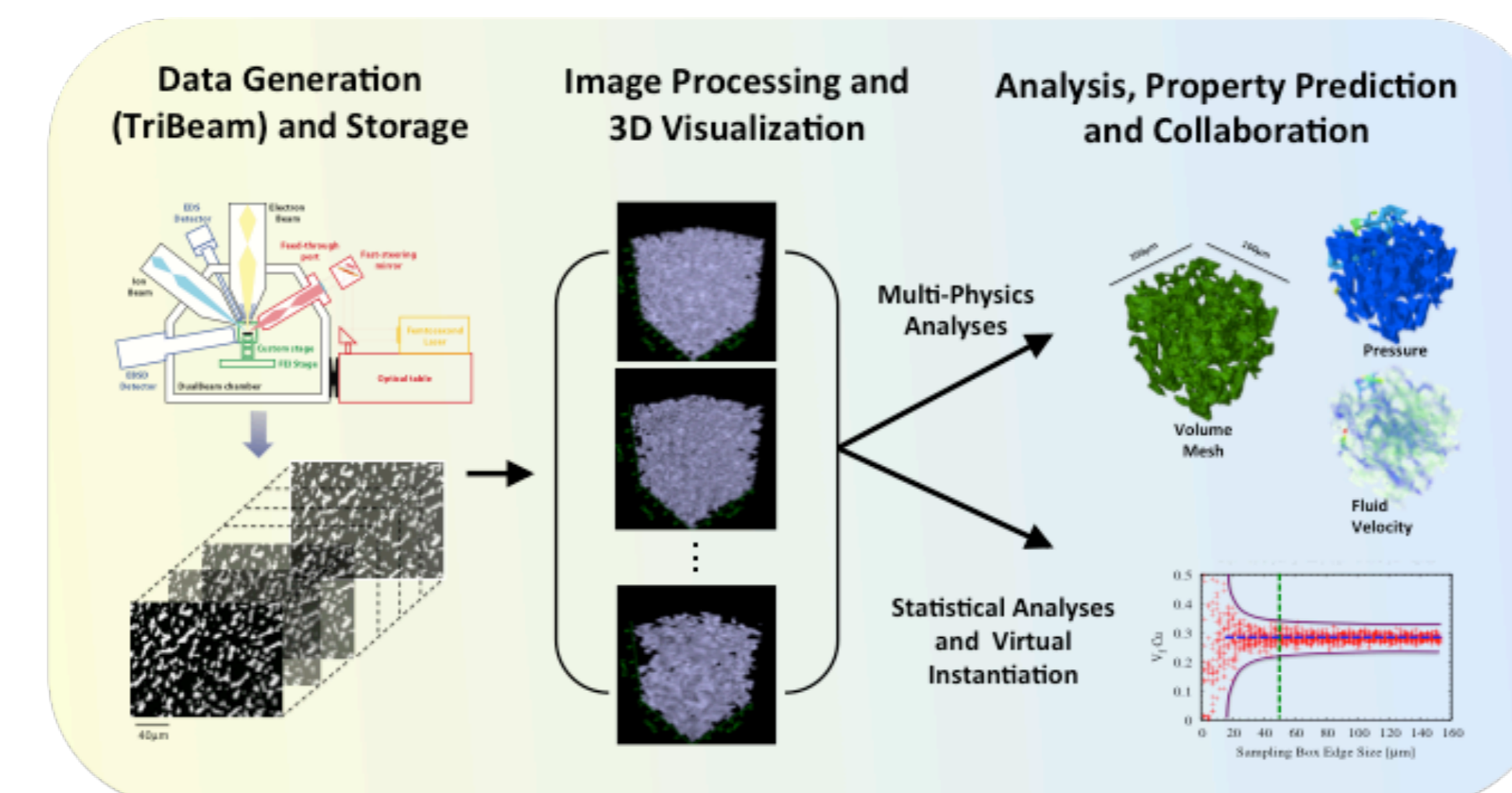
## Materials Science Research at UCSB

- Novel TriBeam tomography platform developed by the Pollock Research Group at UCSB
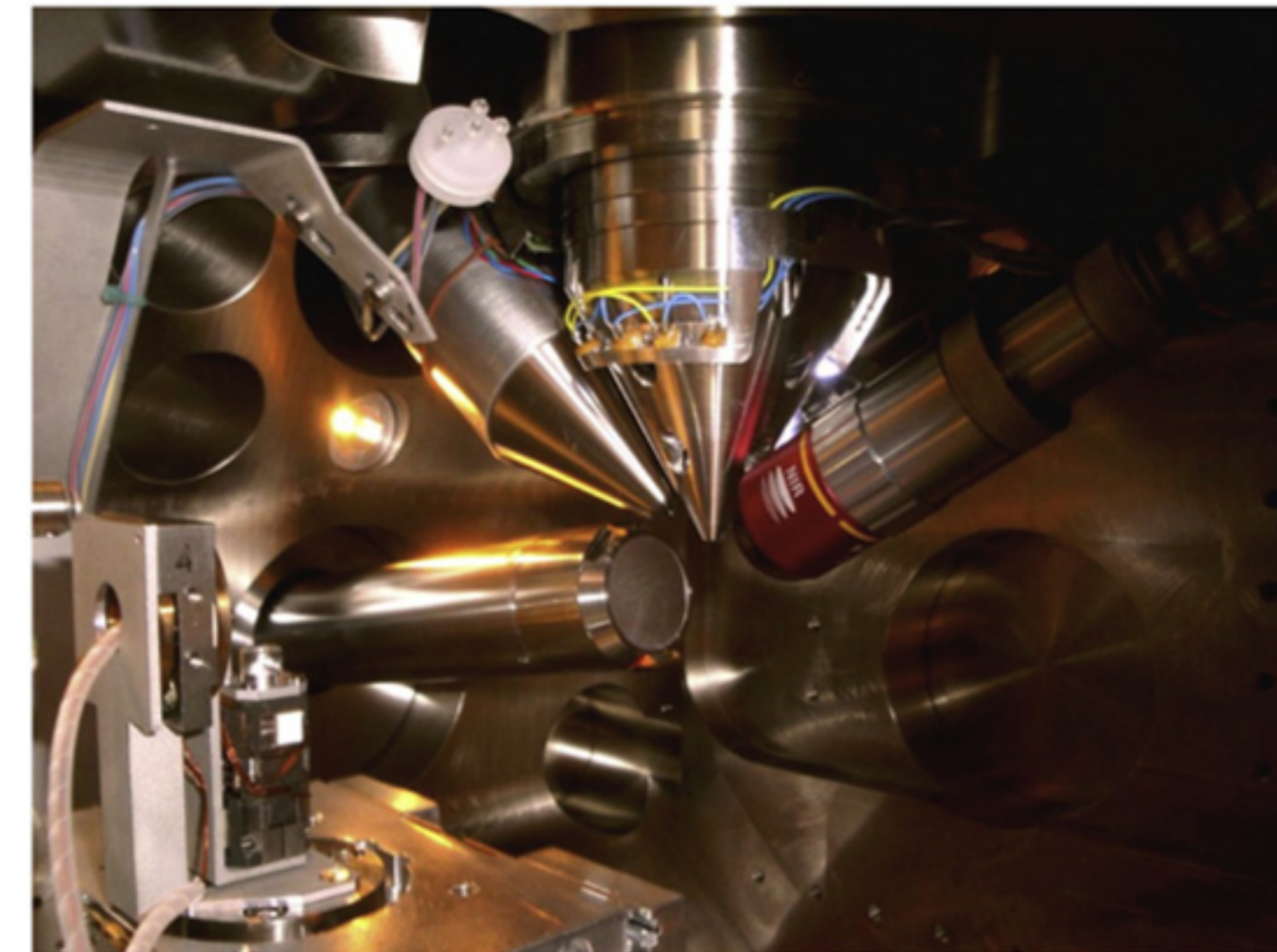


- Integrates a femtosecond laser beam with ion and electron beams to generate 3D multimodal datasets of materials a million times faster than conventional methods [Ech2012]



Nickel Superalloy, NiTiSn, Geological Samples, Strontium Titanate, High Strength Steels, Cu-Polymer Composite, Ti-6-4 Beta Anneal, Laves Phases in Fe-based Alloy, Micro-Tensile Samples, Superconducting Wires, Ti-6-4 Equiaxed Alpha, Beta, $Ti_3AlC$ Ceramic, Carbon Fiber Epoxy Composite, W-Cu Composites

- Resulting large datasets analyzed in stand-alone tools such as Dream.3D [GRO2008]



Data Generation (TriBeam) and Storage — Image Processing and 3D Visualization — Analysis, Property Prediction and Collaboration

- **Urgent need for distributed, collaborative data organization and processing framework**

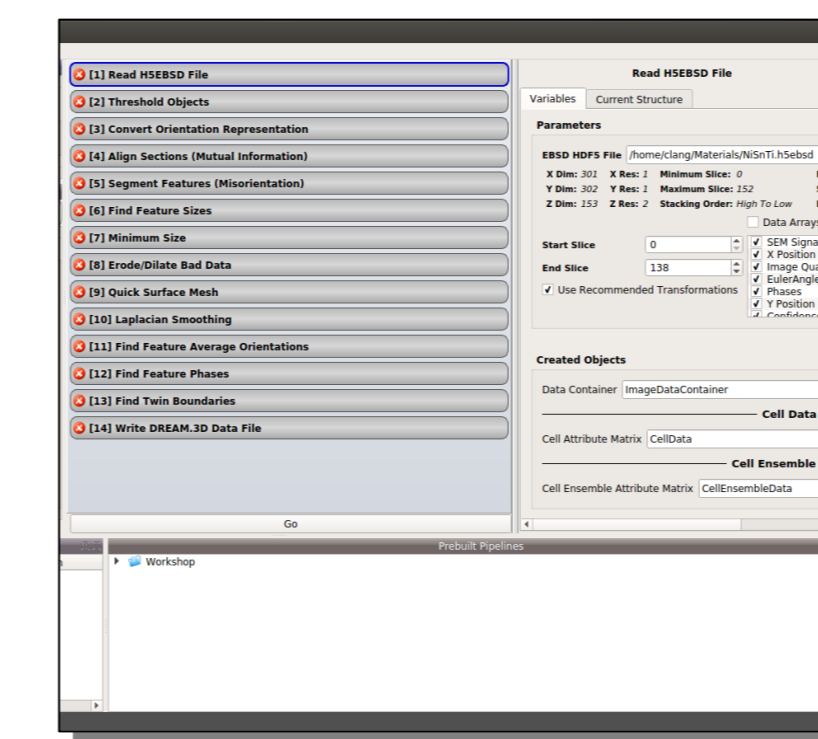## Integrating Materials Science Workflows into BisQue

- Dream.3D pipelines and execution integrated in BisQue

- Input/output datasets and Dream.3D pipelines can be shared with collaborators
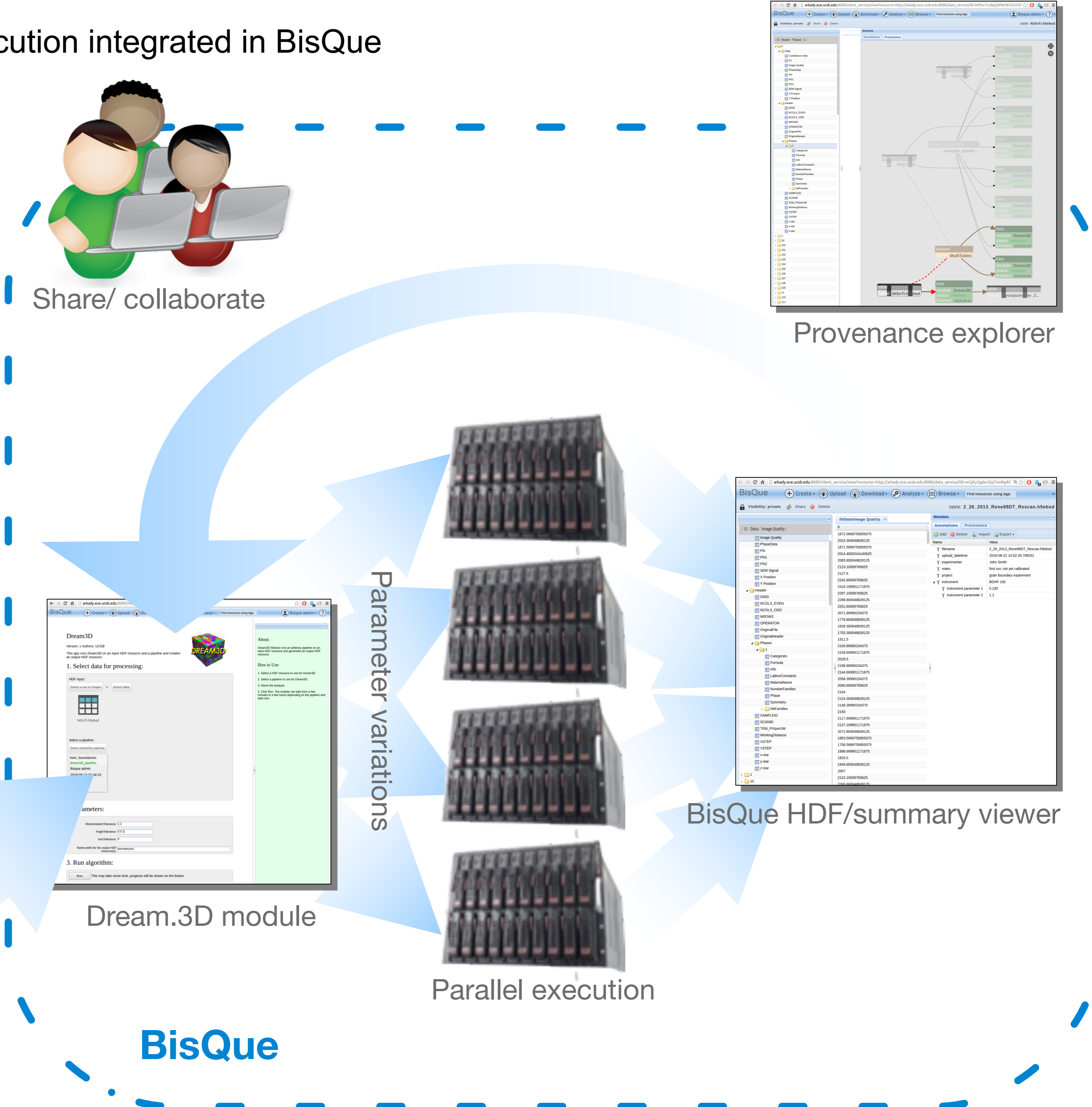
- Parameter variations are automatically parallelized over BisQue's compute grid

- Large datasets can be viewed efficiently in the web browser (data fetch on demand)

- Web-based provenance viewer to explore past analysis runs for improved repeatability



Share/ collaborate — Provenance explorer — BisQue HDF/summary viewer — Parameter variations — Parallel execution — Dream.3D module — BisQue — Dream.3D (local testing)

## Future BisQue Extensions

- **Marine Science:** Methods for automated identification of benthic marine organisms through deep learning. Experiments with state-of-the-art classification of several thousand annotated underwater images demonstrated an overall accuracy >70% for the 15 best performing species and >85% for the top 5 species.
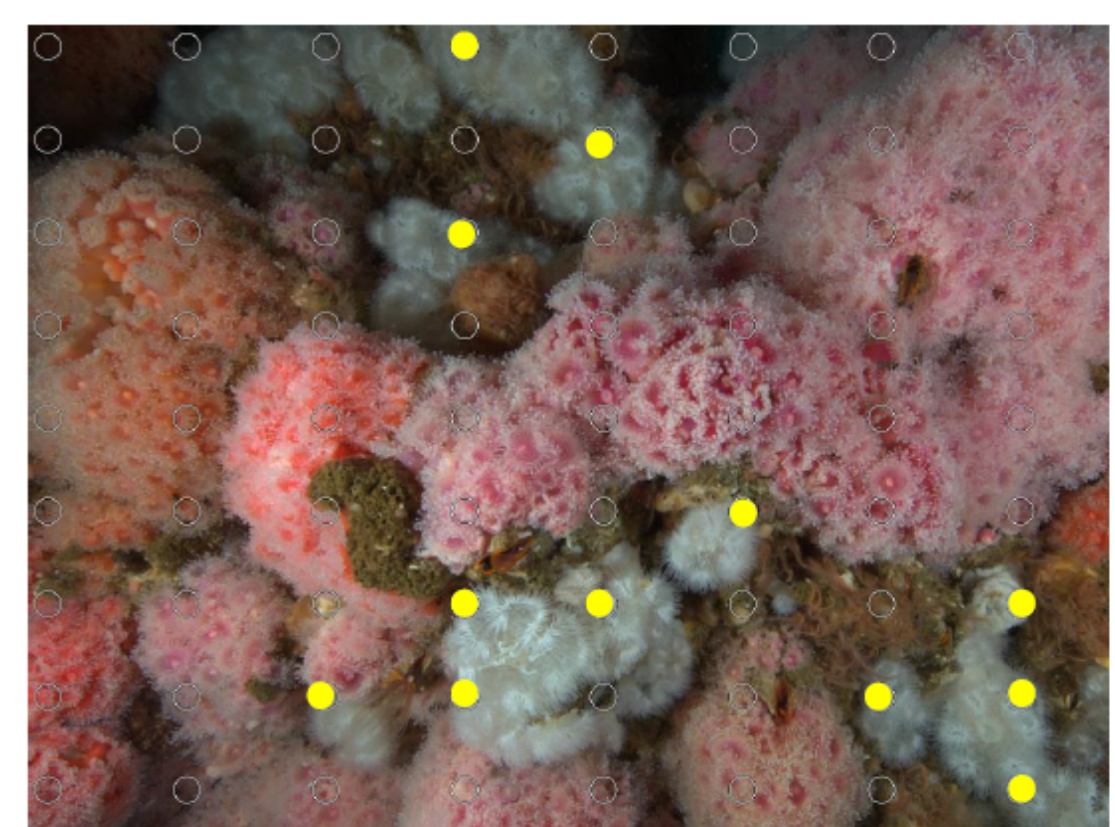


- **Cell Biology:** Integration of CellProfiler package as BisQue module for nuclei detection and cell segmentation in images from confocal laser scanning microscopy. The BisQue system is instrumental in making new cell analysis pipelines immediately useful to a broad audience and applicable to large sets of images (supported by NSF ABI #1356750)
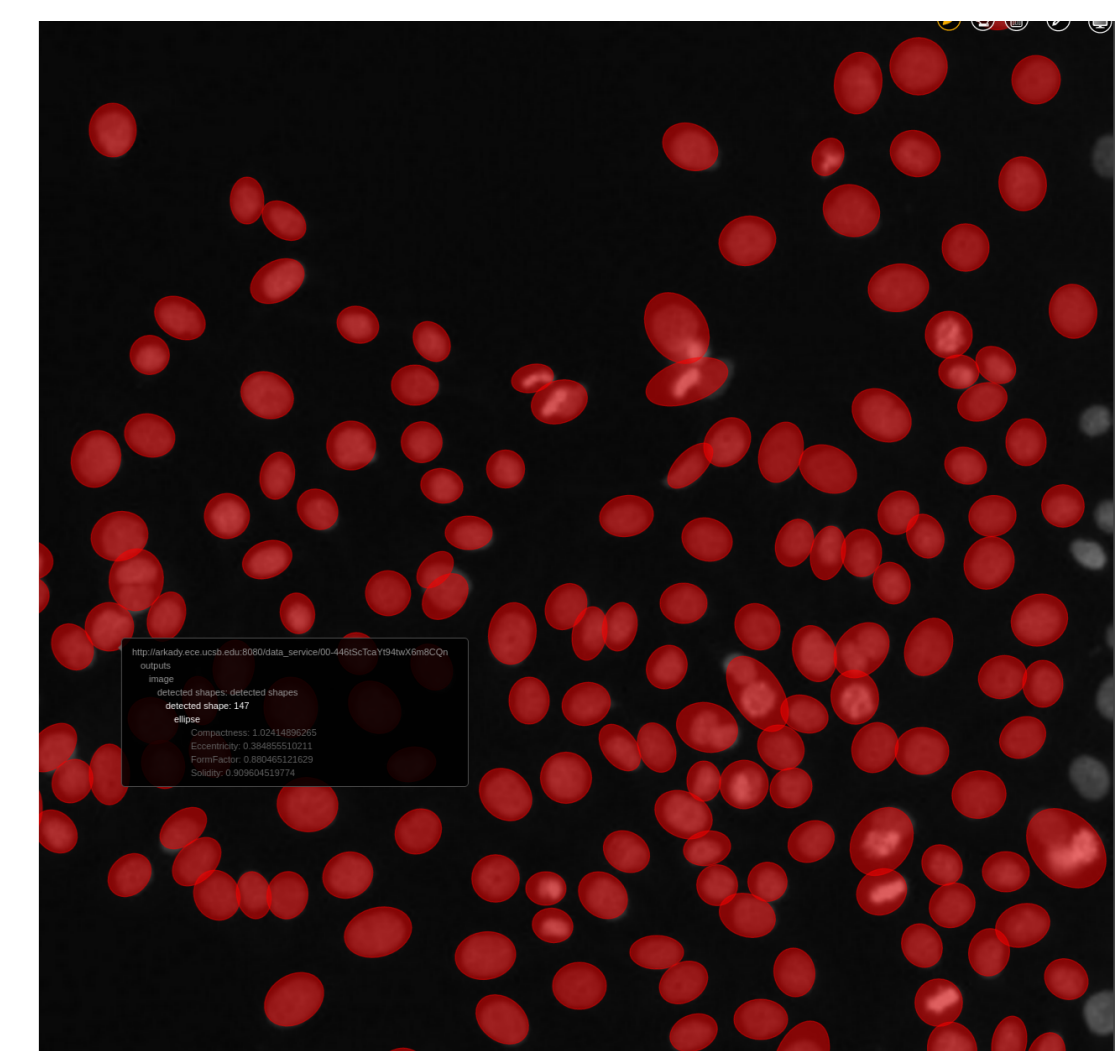


- More information on these projects:
  `https://bigdatahealth.ucsb.edu/`

### References
[Ech2012] M. P. Echlin, A. Mottura, C.J.  Torbet and T. M. Pollock. " A new TriBeam system for three- dimensional multimodal analysis", Review of Scientific Instruments 83.2 (2012), p. 023701
[GRO2008] M. Groeber, S. Ghosh, M.D. Uchic, and D.M. Dimiduk, " A framework for automated analysis and simulation of 3D polycrystalline microstructures.: Part 1: Statistical characterization", Acta Materialia  56.6 (2008), pp. 1257–1273.
[KVI2010] K. Kvilekval, D. Fedorov, B. Obara, A. Singh and B.S. Manjunath. " Bisque: a platform for bioimage analysis and management", Bioinformatics 26.4 (2010), pp. 544–552