



Contribution ID: 134

Type: **Oral**

Bringing 3D-EM to the Grid

Tuesday 26 September 2006 14:45 (10 minutes)

Bringing 3D-EM to the Grid.

3D-EM is a well established technique that allows us to visualize biological structures across a wide range of sizes. As such, it provides a bridge between more fine-grained techniques (such as X-ray crystallography or NMR) and coarser methods like traditional light microscopy, making an un-substitutable tool for understanding subcellular structures and macromolecular assemblies. Its main downside being the heavy demands on compute power at some steps of the analytical process.

We have undertaken the project of bringing 3D-EM techniques to the Grid.

Initial tests with 3D reconstruction yielded poor speedup results turning up important lessons for subsequent work. We are now dealing with ML classification of data, proceeding to refactor Xmipp and dealing with the major blockstoppers detected. Still, some relevant issues worth noting still remain that result in major conceptual challenges.

In this presentation we deal with the general problem of 3D-EM in its experimental context, describe our approach, preliminary results and directions for future work.

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Session Classification: Life Sciences (NA4)

