

Applying High Performance Computing to High Throughput Image Analysis in Biology

Researches at the Max Planck Institute of Molecular Cell Biology and Genetics in Dresden (MPI-CBG) use high throughput image analysis to identify cell components in images from functional genomics assays. Due to the ever increasing speed of high performance automated microscopes, researchers are currently limited not by the availability of experimental data, but by the computing resources for image analysis. In the diploma thesis, high performance computing systems of the Center for Information Services and High Performance Computing (ZIH) were integrated into the workflow of biologists. For the integration, parts of the image analysis software were ported from MS Windows to Linux. The performance of the MS Windows and Linux version of the software were compared and the scalability of this solution was evaluated.