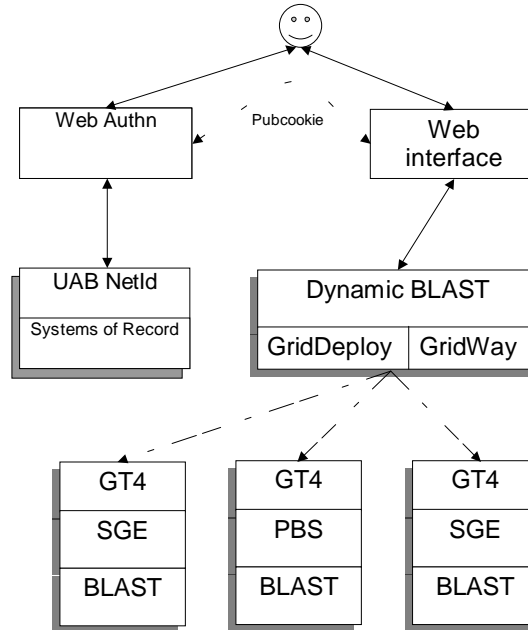


# UABgrid Dynamic BLAST

## Abstract

This application is used for matching protein and nucleotide sequences. Maximizing the throughput of searches is key to improving research results. This distributed implementation of BLAST uses the DynamicBLAST Meta-scheduler to select appropriate grid resources for select query strings. Globus is used for job staging, submission and retrieval. ncbiBLAST performs the computations. Jobs are submitted using a web-based interface that leverages campus identity credentials via Pubcookie and manages grid authentication on behalf of the user via MyProxy, providing a simplified user authentication experience.

## Searching Nucleotide and Protein Databases using SURAGrid Grid-enabling



## Application Project Team

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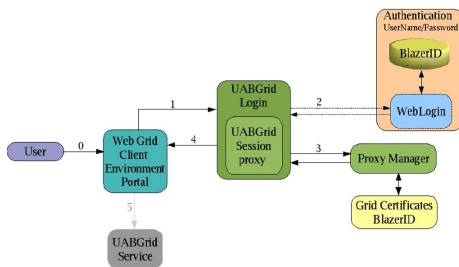
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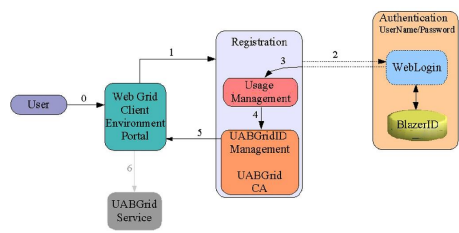
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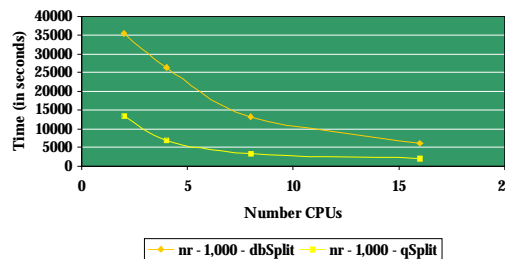
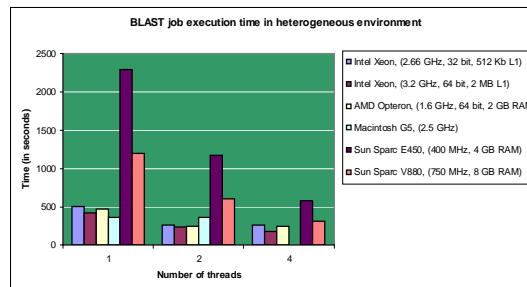
## UABgrid Login



## UABgrid Registration

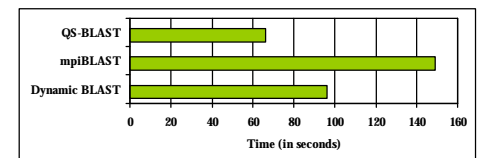


## BLAST execution times in heterogeneous environment



## Run-time Application Performance

Comparison of execution time between query splitting BLAST, Dynamic BLAST and mpiBLAST for searching 1,000 queries against yeast.nt database



Comparison of execution time of Dynamic BLAST on variable number of nodes for 1,000 queries against yeast.nt database

