



Enabling Grids for
E-science in Europe

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Application development Hands-on



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- BLAST (basic local alignment and search tool) is a biological program that compares the alignment between a sequence and a database, with a set of parameters.
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- The output of the blast is a flat file of the different sequences that match.
- BLAST commands: examples
 - format a database: `formatdb -i <file> -p F -o T`
 - launch the blast: `blastall -p blastn -i <sequence_file> -d <database_file> -o <output_file> -b 1 -v 1 -e 0.001`

- goal: see how you can deploy an application, depending on the available grid services
- You have to think about how to launch a blast on the grid
- You need: a sequence file, a database, a software
- You are given 3 different scenarii:
 - 1- use only the UI and the CE to deploy it
 - 2- use the SE
 - 3- use high level services (AMGA)
- For each one, present a solution, and the advantages and misadvantages.
- You don't need to implement anything for the moment, just present a workflow describing how your application will run