protocols.io

Do an EXAHD GENE run on hazel hen

Version 1

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PROTOCOL STATUS

In development

We are still developing and optimizing this protocol

Fix parameters, upload and create issue

1   Define a scenario (or more that belong together) and push it as a parameters file into https://simsgs.informatik.uni-stuttgart.de:8444/EXAHD/ParameterFiles
(for the combigrid runs, we'll need ctparam files there, too)

Create an issue to have other people have a look at it and so we can guide it through our project board: https://simsgs.informatik.uni-stuttgart.de:8444/EXAHD/ParameterFiles/boards

Add label 1 to the issue once you have completed this step.

Pull onto hazel hen, adapt submit script

2   https://www.protocols.io/view/using-hlrs-hazel-hen-supercomputer-ud8es9w

To pull, log into hazel hen with

> **COMMAND**
>
> ssh -R 7890:simsgs.informatik.uni-stuttgart.de:22 ipvuser@hazelhen.hww.de
> git pull /lustre/cray/ws8/ws/ipvpolli-EXAHD/ParameterFiles

Execute `./newprob` in `/lustre/cray/ws8/ws/ipvpolli-EXAHD/gene-dev/` to create a new problem directory `prob`+number.
Symlink or copy your desired parameters file there as `parameters`.

A template submit script is located in
https://gitlab.mpcdf.mpg.de/ext-ec8a21db5900/gene-dev/blob/exahd/makefiles/hazel_hen/qsub_hazel_hen.sh
use it to submit the job from the problem directory, after adapting the cores and time etc.

Add label 2 to the issue.

Submit

3

> **COMMAND**
>
> qsub /lustre/cray/ws8/ws/ipvpolli-EXAHD/gene-dev/"prob+number"/qsub_hazel_hen.sh

Add label 3 to the issue
... and wait.

Get simulation results into git annex

4 git annex is a storage space where the metadata will be kept in our https://simsgs.informatik.uni-stuttgart.de:8444/EXAHD/ParameterFiles , but the actual files are stored somewhere else.

for this, copy or move the problem directory into a sensible place in /lustre/cray/ws8/ws/ipvpolli-EXAHD/ParameterFiles

====> (Further instructions follow soon once the instance is set up)

Be sure to include (the commit hashes of)
- the GENE version used
- the combigrid module used (if applicable)
- the parameter file used (if not transparent from the file structure)
in the commit message

Add label 4 to the issue.

Do postprocessing

5 Depends on the scenario, and what we want to find out.

For instance, get the files onto draco and run GENE diagnostics there (Tilman can help with that).
Or pull them onto your machine and do visualizations there. Or, do the heavy number crunching on hazel hen directly.

Add label 5 to the issue.