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Supercomputing
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Quick start: Basic analysis tool

Presentation slides for PPTM C.Gomez

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Environment

《 Assume we work connected to marenostrum
- ssh -X -l <user> mn3.bsc.es

《 Load the tools modules
- module load INTEL CEPBATOOLS BASICANALYSIS

Basic analysis script

((Assume we have several traces, cut and ready
- Ie: 128.chop1.prv, 256.chop1.prv, 512.chop1.prv

- Traces are part of a strong scaling test

((Execute the script

((
```
model_factors.py -i
/apps/CEPBATOOLS/basicanalysis/0.1/cfgs/indat_modelfactors.cfg -sim
time -sc strong -phase ifs -t 128.chop1.prv 256.chop1.prv
512.chop.prv
```

((Parameters explained:
- -sc strong : indicate to the script we're want to test for strong scaling

- -phase <name> : prefix name to the output files the script will generate

- -t trace1.prv [trace2.prv trace3.prv …] : traces you want to analyze

Comments

❰❰ I have no recommendations for this tool, explore the results by yourself

❰❰ Look at the help info of model_factors.py

❰❰ There's a paper and slides showing results and explaining the tool. Look for them at the raco.

❰❰ Thanks crosas@bsc.es for providing assistance.