Contact

jarno.verkaik@deltares.nl

T +31(0)88 335 7775

Parallel Krylov Solver for groundwater at the national and global scales

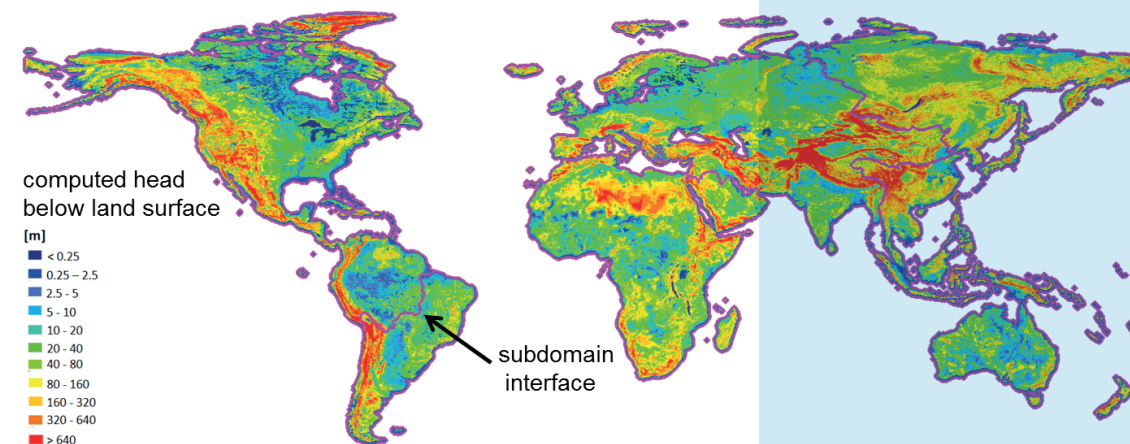### Speedups NHI model
groundwater-only

Measured — — Ideal
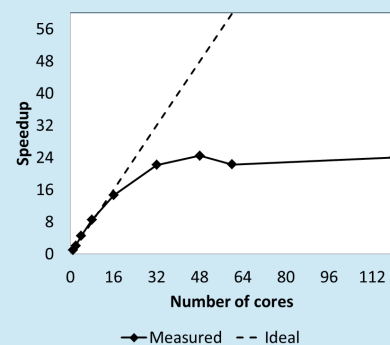
Speedups PCR-GLOBWB model
groundwater-only

Measured, SIO — Measured, no SIO — — Ideal
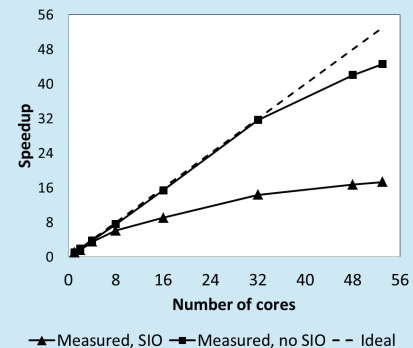
Integrated high-resolution hydrological models are increasingly being used for the evaluation of water management in the field. Unfortunately, they require large amounts of memory and long run times. An efficient way of obtaining realistic run times and memory requirements is parallel computing, where the problem is divided between multiple processor cores. The new Parallel Krylov Solver (PKS) for the groundwater simulation code MODFLOW has been applied to the national Netherlands Hydrological Instrument (NHI) model and the global PCRaster Global Water Balance (PCR-GLOBWB) model. The Parallel Krylov Solver was developed in cooperation with the USGS, Utrecht University, Alterra and Delft University of Technology.

Numerical experiments for both the NHI and PCR-GLOBWB model were carried out on the Cartesius Dutch National supercomputer. The Cartesius has approximately 40,000 computational cores and a fast InfiniBand interconnect. Experiments were conducted on supercomputer nodes consisting of 2 Haswell 12-core CPUs with 64 GB RAM. Experiments for the NHI model were also carried out on a Windows server consisting of 2 Haswell 16-core CPUs with 128 GB RAM. The scaling results show that the new Parallel Krylov Solver results in significantly faster computing.

The NHI is a state-of-the-art coupling of several models: a 7-layer confined groundwater iMODFLOW model (structured grid of 10 million cells), a MetaSWAP groundwater model for the unsaturated zone (0.5 million cells), and the surface water model MOZART-DM. Our tests simulated the transient groundwater flow for the year 2006 with daily time steps. On the Cartesius, a serial run for the groundwater-only NHI model

computed head below land surface

[m]
- < 0.25
- 0.25 – 2.5
- 2.5 - 5
- 5 - 10
- 10 - 20
- 20 - 40
- 40 - 80
- 80 - 160
- 160 - 320
- 320 - 640
- > 640

subdomain interface

takes 2 hours and 45 minutes and requires 7.1 GB RAM. Using 48 cores, wall-clock time can be reduced to 6 minutes and 46 seconds, resulting in a speedup of ~24. On the Windows machine, a serial run for the fully-coupled NHI model takes 9 hours and 29 minutes and requires 44.5 GB RAM. Using 24 cores, wall-clock time can be reduced to 2 hours, resulting in a speed-up of ~5.

The global model PCR-GLOBWB provides a grid-based representation of global terrestrial hydrology. In our test we used the 2-layer confined MODFLOW groundwater model (unstructured grid of 4.5 million cells) and simulated groundwater flow for January 1992 with daily time steps. The first test used a Structured Input/Out (SIO), in which the model input and output is set up in a structured way for 53 global catchments and each partition contains one or more catchments. A speedup of ~17 was obtained using 48 cores, reducing the wall-clock time from 4 minutes and 48 seconds to 17.9 seconds. In the second test (no SIO) METIS was used for the partitioning. In this case, a speedup of ~45 was obtained using 48 cores, reducing the wall-clock time from 4 minutes and 43 seconds to 6.7 seconds.