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Sea air land modelling operational network

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ABSTRACT: The SALMON project's purpose is to develop an integrated model to describe the water quality in a whole regional system including marine, river and ground-waters forced by atmospheric inputs. It is based on the General Domain Decomposition Method. The first domain decomposition relies on the different physics in the sea, the river and the ground-water. It is also used in a specific domain to allow parallelisation. Three models simulate the evolution of the water taking into account processes and state variables adequate to the domain. Fluxes of water, nutrients, pollutants... are computed in submodels and transferred continuously from one to the other at the boundaries. The connections of the models are done through interfaces (junctions), designed to allow the data exchange between models based on different numerical methods. The SALMON application is made of models, junctions, servers and manager, each running on IBM SP2 nodes and running the PVM library.

1 INTRODUCTION

The purpose of the SALMON project is to develop an integrated model for the description of the water quality in a whole system of regional scale including marine, river and ground-waters forced by atmospheric inputs. The project is based on the General Domain Decomposition Method including the concept of Junctions. The first domain decomposition relies on the different physics in the sea, the river and the ground-water. Thus, three models are used to simulate the evolution of the water taking into account processes and state variables adequate to the domain. In this complete three-fold model, fluxes of water, nutrients, pollutants... are computed in each submodel and transferred continuously from one sub-model to the other at the common boundaries. The connections of the different models are done through specific interfaces (junctions), designed to allow the data exchange between models based on different numerical methods. The decomposition is also used in a specific domain to allow parallelisation or other kinds of refinement. This is applied to the marine domain.

The SALMON application is made of models, junctions, servers and manager, each running

on IBM SP2 nodes. Some are sequential and other are parallel depending on the requirements in CPU time and/or memory. The exchange of information relies on the PVM library.

This meta-model is applied to the Belgian coast meaning that the marine domain is made of the whole North-western European continental shelf, the surface water domain is made of the Sheldt watershed basin and the groundwater domain is made of the Antwerp area.

This document will first present the three models, then we will describe the architecture of the SALMON model before considering the junctions and the graphical server. The last section will gather some results of different simulations and the conclusion.

2 THE SUB-MODELS

2.1 *The Ocean model*

The marine domain is described by means of a serie of three coupled hydrodynamic and biochemical models. The large-scale features are modelled with a general circulation model (GCM) covering the whole Northwestern European Continental Shelf with a horizontal resolution of 10' in longitude

and latitude. This model provides open boundary conditions for a small scale 500m horizontal resolution local model of the Belgian Coastal Waters where the influence of the Scheldt outflow is studied. Both the GCM and the local hydrodynamic model are three-dimensional (σ -coordinate), baroclinic, fully non-linear and include a refined and robust turbulent closure (Delhez 1998). To modulate the inflow of Scheldt water into the coastal region, a 1D model of the tidal stream in the Scheldt River is added and coupled to the previous models. The three models include also a description of the biological interactions adapted to the characteristics of each particular sub-domain; the shelf model computes the nitrogen and carbon cycles through the marine food-web, the local model includes the nitrogen, phosphate and silicate cycles to account for the finer biological dynamics, and the 1D Scheldt model embodies a sub-model of the complex bio-chemistry of the estuary (Regnier 1997).

The series of marine models form a replica of the whole SALMON project: the three models (each comprising a hydrodynamic and a biological sub-model) are run at the same time and exchange continuously information at their boundaries. This is greatly simplified by the parallel environment in which they run as the synchronisation and information exchanges are supported by PVM. Where external information or simplifications are usually needed to evaluate the boundary conditions in stand-alone runs, the necessary information can now be obtained directly from the other models. The only thing that has to be done is therefore to write an appropriate interface, i.e. a junction, between the models.

Complex 3D hydrodynamic and biological models are very demanding in computer resources, especially CPU time. It is therefore necessary to parallelize the code of the shelf and coastal models. The strategy adopted is that of the domain decomposition in as many bands as the number of processors allocated to the sub-model. Each processor solves then the equations in its own band using the same code as in a sequential run. The choice of the band decomposition is based on the particular characteristics of both the original sequential models and of the machine on which the parallel runs are carried out. The models are explicit in the horizontal but implicit (or partly implicit) in the vertical. Therefore, no particular difficulty arises when one divides the domain into sub-domains extending from top to bottom pro-

vided that the state variables at the outer boundaries of each sub-domain are made available by the other sub-domains when they are updated. Then, as the different nodes do not share their central memory, the volume of data exchanged between the different nodes has to be minimised. Therefore, the whole domain is divided into parallel bands the widths of which are adapted by an automatic procedure to balance the load among the different nodes.

2.2 The River model

The river model is a unidimensional (computation of cross-section averaged values), non-stationary model which calculates deterministically the aquatic ecosystem and water quality variables (about 25 variables). It is an integrated river/basin model capable of simulating annual cycles for a net of hundred of rivers on a watershed of thousands of square kilometres.

The integrated approach means that the relation between any point load and any distributed load located in the watershed and the rivers is described. This is particularly interesting for dispersed and diffused pollution sources, and avoids a detailed description of the sewer networks.

The transport equation is solved by means of a characteristic method. The time step used for calculation is of the order of magnitude of an hour, which enables simulation of daily cycles (like oxygen for example), and description of very important non-stationary phenomena.

The model is structured as a series of three consecutive sub-models with the following functions :

- the hydrodynamic sub-model calculates discharge and the other hydrodynamic parameters (water velocity, depth, ...) in different reaches, on the basis of the morphometric characteristics of the river (slope, width, presence of dams, ...) as well as the daily values of discharge measured on any point;
- the thermic sub-model calculates water temperature in the different reaches on the basis of the temperature measured at any point, and of the various warm water inputs;
- the biological sub-model computes
 - the development of planktonic biomass (phyto-, zoo- and bacterioplankton) on the basis of light (surface irradiance) as the main supplementary entry data;

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- the degradation of organic matter, as well as the production of autochthonous organic matter (primary production of phytoplankton), the heterotrophic activity being also fed by domestic, industrial and agricultural organic waste inputs, nutrient input and transformation in the ecosystem are taken into account so that concentrations of various forms of N and P are also calculated;
- the oxygen budget of the water column on the basis of the metabolic activities of planktonic biomasses (primary production, degradation of organic matter, respirations), taking into account surface reaeration.

The kinetics of the major processes involved in the ecological functioning and the corresponding parameters are mostly derived from experimental data so that no (or only minor) calibration procedure is required.

In the frame of the SALMON project, the river model is to be applied to the Scheldt river basin. The basin considered is of 18.000 km², for more than one hundred explicitly computed rivers. The characteristics of the river Scheldt leads to consider the singularities of the unnatural hydrological flows due to the numerous channels of the northern part of Belgium.

2.3 The Groundwater model

The groundwater model code "Saturated Unsaturated Flow and Transport in 3D" (SUFT3D) can treat full 3D real cases in steady or transient conditions for both confined or unconfined aquifer. This is a finite element code solving the groundwater flow (which can be density dependent) and the transport of a dissolved contaminant through the saturated and unsaturated porous media (Dassauques 1994). The transport processes, which can be represented, are convection, diffusion, dispersion linear degradation, adsorption (with linear, Langmuir or Freundlich isotherm) and immobile water effect.

For solving the transport equation, an Eulerian Upstream (EUM) or an Hybrid Eulerian-Lagrangian (HELM) finite element method can be used in the cases of high Peclet numbers (<10 with EUM and unlimited with HELM) and high courant numbers (only with HELM). To improve the efficiency of the SUFT3D, the previous solver has

been replaced by a sparse matrix iterative solver package named WATSOLV (Van der Kwaak et al. 1997). The solving method implemented in WATSOLV is an iterative process that is preconditioned using an Incomplete Lower-Upper factorisation. The particularity is that the iterative process is accelerated using one of two algorithms : GMRES (Generalised Minimal RESidual) or Bi-CGSTAB (Biconjugate Gradient STABILised).

A limitation of the groundwater model lies in the fact that the code was designed to treat one solute in the groundwater flow-transport simulations. If the adopted solution consists in the use of parallel multi-transport computations, the different studied components are non-reactive and independent. For the first application of SALMON, the groundwater model is applied to a part of the Scheldt basin (about 680 km² containing the Antwerp area). The studied domain is composed of heterogeneous sandy layers lying on a thick clay layer. It can be considered as the bottom of the modelled domain at a depth varying from 2 to 180 metres. The whole domain is discretized using 136,212 finite elements (95,415 nodes).

3 SALMON ARCHITECTURES

The main idea of the project is to develop a tool allowing the coupling of existing models. To take advantage of the scalable SP2 machine, an additional layer using the PVM software is added to the three models. This layer is composed of

- the meta-junction which is the managerial task; it starts the execution of the other tasks and sends them information necessary to the data exchange with the other elements.

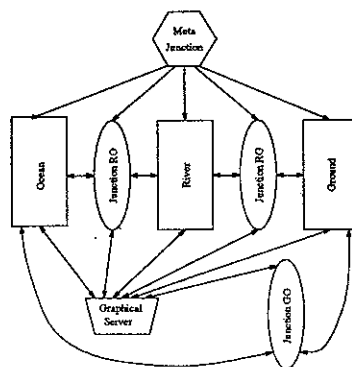


Figure 1: The meta-model architecture

- a graphical server visualising the results as described in section 5.

Since the models compute lots of different state variables and use different time and space scales, some interface tasks (junctions) are introduced to adapt the data exchanged between couples of models. That basic architecture is shown on figure 1. The main disadvantages of that organisation are the difficulty to add a model or to replace an existing one. Indeed, adding a model in a system containing n models requires the development of $n - 1$ new junctions. Secondly, as the send operations of PVM messages are hard coded in the models codes, a special execution sequence must be adopted in order to avoid deadlocks.

A reorganisation of the system into Client/Server architecture would solve the problem (Fig. 2). A single junction centralises all the models requests and treats them as soon as possible.

The integration of a new model into the system is carried out by taking advantage of the communication protocol and the tools provided by the junction. The order of messages exchanged with the junction adapts dynamically to the needs of the system. The junction is considered as a server as shown on figure 3. When a model is added to the meta-model, the message handler has to be updated. A treatment unit and an outgoing message queue have also to be added.

Presently, the SALMON project combines these two architectures.

4 THE JUNCTIONS

The junctions are processes performing specific pre-processing operations as for instance the trans-

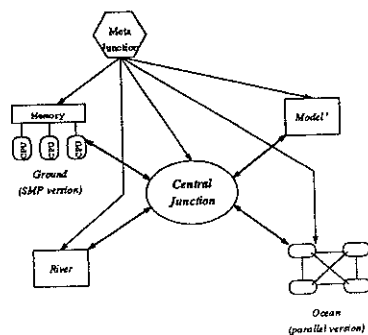


Figure 2: The client/server architecture

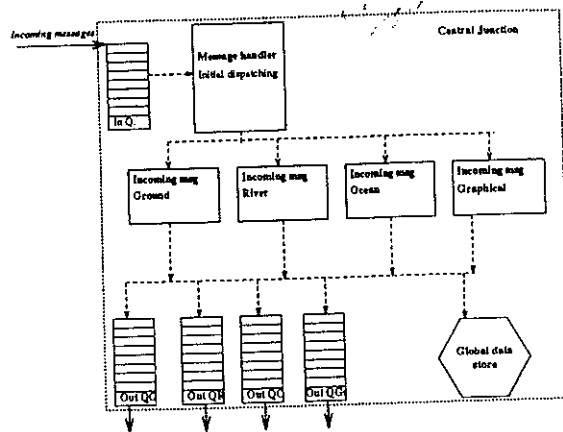


Figure 3: The server architecture

lation of the models digitalisation data into a common coordinate system, the computation of corrections to tune the value that will be used in the coupling processes and an automatic mapping between the nodes of the two models that must communicate. To illustrate the previous explanation, the mapping between the groundwater and river nodes is shown on figure 4, each groundwater node of the set Γ is associated with the two river nodes r_1 and r_2 surrounding it. The coupling operation starts as soon as the initialisation has been completed.

4.1 The Groundwater/River junction

This junction is developed using the basic architecture (Fig. 1). It computes first the water flow at each groundwater node using interpolated water heights of the selected river nodes and the water piezometric head in the aquifer. Depending on the flow direction, the junction computes the mass flow considering the concentrations in the aquifer or in the river (Dassargues et al. 1996). Since the river model treats more substances than the groundwater model, the junction also performs aggregation

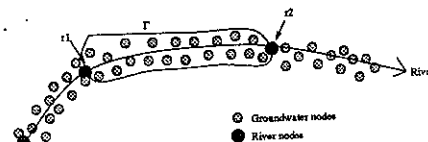


Figure 4: Mapping between groundwater and river nodes

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or splitting operations. The latter depends on a breakdown key taking into account the nature of the variable, the soil type and the soil occupation. The value sent to a river node, i.e. r_2 on figure 4, is the sum of the values associated with the ground-water nodes directly up-stream, i.e. those belonging in the set Γ in figure 4.

4.2 The River/Ocean junction

This process, based on the Client/Server architecture is composed of two modules. The hydrodynamical module transmits the water flow issued by the river model to the 1D model of the tidal stream in the river, a part of the ocean model. The location of that boundary correspond where the upper limit of influence of the tidal wave into the river. The biological module is charged to transmit the mass flow from the endpoint of the river to the 1D model of the tidal stream where the estuary ecosystem begins. As the ocean module treats the same biological variables as the river model, this junction performs neither aggregation nor splitting operations.

5 THE GRAPHICAL SERVER

The graphical server enables interactive visualisation of simulated data and offers the ability to modify data before making the simulations, such that the next simulation iteration, take these modifications into account. As a consequence the graphical server may be considered as a visualisation and managing tool.

5.1 Visualisation

The visualisation module retrieves data of interest from the simulations, performs synchronisation operations in order to guarantee coherent data and communicates with a visualisation tool rendering incoming data.

In order to get coherent data, two levels of synchronisation are introduced. By taking advantage of PVM built in synchronisation requests (`pvm_barrier()`), all variables belonging to a same group of data are constantly synchronised within the graphical server system. For the combination of data of different groups, eventually computed at different frequencies, a softer synchronisation is implemented. As a consequence all data correspond to compatible time steps with a time lag of at most one iteration while all variables in a

same group are completely synchronised. These soft synchronisations are performed on users' requests and are managed by a control process steering the various slave processes, each of which is responsible of a single variable. Taking advantage of the IBM Visualisation Data Explorer (DX), which was extended in order to be able to treat incoming PVM messages as data source, does the rendering. All DX built in rendering operations remain available to DX programs.

5.2 Modification

A graphical user interface was developed in order to do the retrieval and modification of data before returning them to the graphical server. This part of the server sends the modified data to the simulation models, which continue their computation of the next iteration with these new data. The extraction of modified data is based on a client/server architecture where the simulation processes are considered as clients. This architecture based on a rather complex management of messages makes sure that modified data are extracted only once by the simulation processes and that modification operations do not impact onto the smooth execution of the simulations.

6 APPLICATIONS

The validation of the SALMON model system includes the computing/programming aspects and the management of the environment aspect. Indeed, while the models describe the evolution of rather similar properties (velocity, concentrations of nutrients), they represent different processes with different levels of aggregation of the genuine state variables. One of the key aspects of the coupling of these models is therefore to ensure the

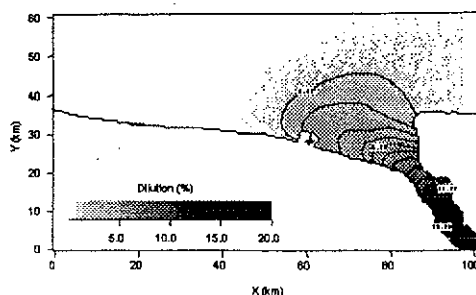


Figure 5: Dilution rate of river water in the coastal region

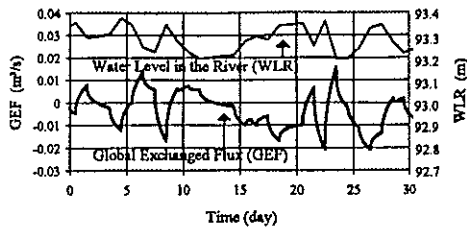


Figure 6: Evolution of the flow between the aquifer and the river

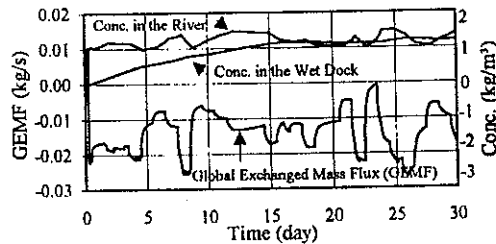


Figure 7: Transfer of a passive substance from the river to the groundwater

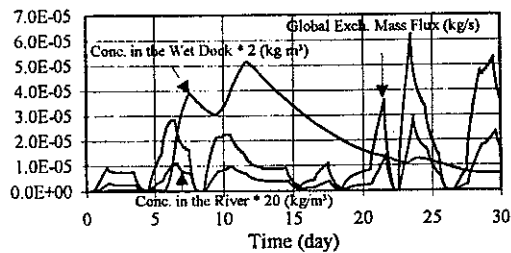


Figure 8: Transfer of a passive substance from the groundwater to the river

suitable interaction of the sub-models by appropriate processing of the information at the different junctions.

The first test passed by the meta-model consists in tracing a passive substance in its way through the different parts of the model system and the different media. Several artificial releases are considered at different locations and in different conditions (flow from river to the ground-water and vice-versa). These runs provide a serious test of the architecture and junction of the meta-model. They allow also a systematic study of the mutual influences of ground, river and ocean waters including the determination of regions of influence

and interactions time scales.

More applied tests are currently going on to test different environmental scenarios corresponding to the application of the European Directive (EC/91/271) according to which the amounts of nutrients rejected into the river must be cut by a factor 2. Results will be reported later.

The influence of the river flow on the coastal environment can be assessed from the distribution of the passive tracer. Figure 5 shows, for instance, the dilution rate of the river water in the coastal region (the distribution shown corresponds to the situation on 1/1/1993 after 3 months of simulation). For this simulation, a continuous release of a passive tracer into the river water was considered. The ratio of the concentration computed in the coastal waters and in the river was then expressed as a percentage and taken as a measure of the dilution of the river water into the sea. The plume of the Scheldt can be clearly seen with its natural extension south-westwards along the Belgian coast. Offshore, the diluted water masses is then entrained northwards by the residual flow.

The figure 6 illustrates the interaction between the groundwater and the river models on a test site. This figure shows the time evolution of the exchanged flux between the models essentially induced by the fluctuation of the water level in the river and the pumping rate in the aquifer. The results of the transfer of a passive substance from the river to the groundwater (release in the river) and vice-versa (release in the aquifer) are shown respectively in the figures 7 and 8. In this site, supplementary equations based on flow and solute mass balance have been added to take into account the role of a buffer zone played by a wet dock in connection with the river. In the case of an initial

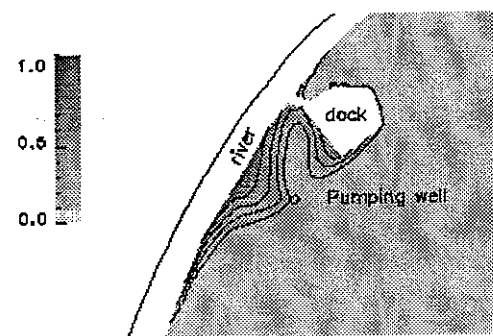


Figure 9: Intrusion of a passive tracer in the aquifer after 30 days of simulation

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input in the aquifer (Fig. 8), the tracer is diluted in the 45 m³/s river flow rate whereas in the wet dock, the tracer is accumulated and then released in the river or the aquifer. The figure 9 shows the intrusion of the passive tracer in the aquifer after 30 days of simulation.

7 CONCLUSIONS

Resulting from years of research and developments, we have now a powerful tool, the SALMON meta-model, that is able to handle description of environmental quality in a whole system of regional scale including marine, river and groundwater inputs. The model has been tested in the North Sea Belgian/Dutch coastal zone taking advantage of existing databases. At the same time, our network of models is now ready to be applicable on any coastal zone where interface fluxes between river, groundwater and ocean are to be taken into account (an application has been made to the Black Sea continental shelf) (Grégoire et al. 1997a) (Grégoire et al. 1997b).

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