

## **Wikiprint Book**

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## The INCA model

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### 1. Introduction

INCA (INteraction with Chemistry and Aerosols) is a chemistry and aerosol model coupled to the Laboratoire de Meteorologie Dynamique (LMD) General Circulation Model, LMDz. INCA is developed at the Laboratoire des Sciences du Climat et de l'Environnement (LSCE) in collaboration with other laboratories within IPSL.

LMDzINCA accounts for emissions, transport (resolved and sub-grid scale), photochemical transformations, and scavenging (dry deposition and washout) of chemical species and aerosols interactively in the GCM. Several versions of the INCA model are currently used depending on the envisaged applications with the chemistry-climate model. The standard model resolution is 96x95 (3.75° longitude x 1.9° latitude) and 144x142 (2.5° longitude x 1.3° latitude). There are two standard vertical resolutions includes 39 and 79 sigma-p hybrid levels. The model can be run in a nudged mode, relaxing to ECMWF winds and temperature.

LMDz-INCA constitutes the atmospheric component of the IPSL coupled atmosphere-ocean-biosphere model and is coupled to the ORCHIDEE biosphere model in order to determine interactively the exchange of chemical species (emissions, deposition) between the atmosphere and the surface.

### 2. INCA

Inca model is always use coupled with LMDZ and ORCHIDEE models. To have more informations on how compile and launch a simulation you can read [this documentation](#)

### 3. Pass word

Send an email to Anne Cozic to obtain the pass word of Inca model

### 4. Chemistry configurations

The INCA model offers different chemistry configurations:

- NMHC : methane chemistry and non methane chemistry
- AER : aerosols only using a prescribed chemistry
- NMHC\_AER : methane chemistry and non methane chemistry + aerosols
- NMHC\_AER\_S : version NMHC\_AER + stratospheric chemistry
- GES : greenhouse gases
- DUSS : dust and seasalt version

### 5. Manage output using XIOS

XIOS is used by default in v6 configurations.

All files need by INCA model for manage outputs are in the directory INCA/src/INCA\_XML/. In this directory you will find several types of files

- iodef.xml: Main input file for XIOS
- context\_inca.xml: Axis and domain information, include field and file def
- field\_def\_inca.xml: Definition for each variable send from INCA
- file\_def\_inca.xml: Definition of all output files and there variables

#### 5.1. definition in file\_def\_inca

In fact there are two files of type `file_def_inca.xml` for each inca configuration (NMHC, NMHC\_AER, etc.) (except for NMHC\_AER\_S that are using same files than NMHC\_AER).

- `file_def_inca_${chem}_daily.xml` --> output files will have a daily frequency
- `file_def_inca_${chem}_monthly.xml` --> output files will have a monthly frequency

with chem={NMHC, NMHC\_AER, AER, GES, DUSS}

The choice between daily or monthly output frequency is managed by the card `config.card` of your simulation

```
#=====
#D-- CHM -
[CHM]
#D-- choose inca writefrequency between 1D or 1M. it is not possible to cumulate both of them
#D-- you can also manage the writefrequency in INCA/src/INCA_XML/file_*.xml files
WriteFrequency="1D 1M"
```

In files `file_def_inca.xml` you will find keywords **AUTO**

```
<file id="forcagel" name="inca1d_forcage" output_freq="1d" enabled="_AUTO_">
```

They are replaced automatically by the driver `inca.driver` of your simulation. Be careful if you define new outputs files, you need to put the correct value for the parameter **enabled**, and not **AUTO**. (TRUE if you want to write this file in output, FALSE if not)

## 5.2. groups in field\_def\_inca

Each configuration of Inca model (NMHC, AER, etc.) has different tracers from the other ones. For each tracer we want to write on output several diagnostics or values linked with it (ex: concentration, emission, deposit velocity, etc.). To avoid listing all these possible outputs and forgetting one of them, we work with XIOS groups. For each family of output we create a group, and the code will interactively construct it with all tracers used by it.

```
<field_group id="emi_species" /> <!-- species emissions -->
<field_group id="photo_rate" axis_ref="presnivs" /> <!-- rate of photolysis reaction -->
```

Then in the `file_def_inca` file we can ask to write a sublist (by listing variable one by one) or all the group

```
<file id="emissions1" name="inca1d_emi" output_freq="1d" enabled=".TRUE.">
  <field field_ref="Emi_O3" />
  <field field_ref="Emi_O" />
  <field field_ref="Emi_O1D" />
  <field field_ref="Emi_H" />
  <field field_ref="Emi_OH" />
  <field field_ref="Emi_HO2" />
  <field field_ref="Emi_H2O2" />
  <field field_ref="Emi_N2O" />
</file>
```

or

```
<file id="emissions1" name="inca1d_emi" output_freq="1d" enabled=".TRUE.">
  <field_group group_ref="emi_species" />
</file>
```

To help the user to know all variables created by groups function, you create an output file `inca_IDxml.out` where are stored all groups variables names.

## 5.3. Output in CMIP6

For CMIP6 we cannot use groups, we need to have the explicit list in field and file xml. For this you can use the file `inca_IDxml.out` described previously, or use examples stored in `src/INCA_XML/CMIP6` directory.

## 5.4. Add a variable in output inca

for these you can read [this documentation](#)