

## The LMDZORINCA configurations

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The LMDZORINCA configurations (LMDZORINCA and LMDZORINCA\_v5) allow you to couple the LMDz atmospheric circulation model, the ORCHIDEE land model, and the INCA atmospheric chemistry model close to the CMIP6 coupled model.

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## 1. Description of the configuration

### 1.1. LMDZORINCA\_v6.1.10

LMDZORINCA\_v6.1.10 is the **default configuration** for Inca forced model. It is compatible with the IPSLCM6.1.10\_LR, LMDZOR\_v6.1.10 models. It is constructed with the following models:

- LMDZ branches/IPSLCM6.0.15 rev 3483 for the gcm and the create\_etat0\_limit
- ORCHIDEE tag tags/ORCHIDEE\_2\_0/ORCHIDEE rev 5661
- INCA trunk/INCA6 rev 871

This configuration allows you to work with the INCA version tuned for 39 levels and old LMDZ physics scheme for NMHC, NMHC\_AER, NMHC\_AER\_S, AER, GES and DUSS, and on 79 levels and new LMDZ physics scheme for AER.

The same version of INCA is used in IPSLCM5A2CHT.1 configuration.

#### 1.1.1. LMDZORINCA\_v6

LMDZORINCA\_v6 is the same configuration than LMDZORINCA\_v6.1.10 except for INCA version. We use the previous version of the model, (trunk/INCA5 rev 792). Results will be the same between these two versions.

### 1.2. LMDZORINCA\_v6.2\_work

LMDZORINCA\_v6.2\_work is a configuration close to LMDZORINCA\_v6.1.10 with updated versions of components: LMDZ, ORCHIDEE, XIOS

- LMDZ6 trunk close to HEAD) for the gcm and the create\_etat0\_limit
- ORCHIDEE branches/ORCHIDEE\_2\_2/ORCHIDEE rev 6189
- INCA trunk/INCA6 rev 873

This configuration use the new way of compilation (with a script)

## 2. Technical details

### 2.1. How to use it

#### 2.1.1. Compilation of LMDZORINCA\_v6.1.10

To compile LMDZORINCA\_v6.1.10 configuration you need to use the Makefile store in config/LMDZORINCA/ directory. You can choose between several target :

- VLR and Old LMDZ Physics scheme
  - NMHC\_AERxLMD9695-L39 (default one)
  - NMHC\_AER\_SxLMD9695-L39
  - NMHCxLMD9695-L39
  - AERxLMD9695-L39
  - DUSSxLMD9695-L39
  - GESxLMD9695-L39
- LR and New LMDZ Physics scheme
  - AERxLMD144142-L79

- no maintained anymore - ask to Anne COZIC if you want to use it
  - DUSXLMD144142-L39

You can add the compilation of another resolution by copying the syntax of an existing resolution. If you do so, you will need to regrid all input files for the chosen chemistry model. [documentation To regrid the inca files](#)

### 2.1.2. Compilation LMDZORINCA\_v6.2\_work

To compile LMDZORINCA\_v6.2\_work configuration you need to use the script compile\_lmdzorinca.sh. Options to use this script are :

- **-regular\_latlon** : default is 96x95x39
- **-chimie** : default is NMHC\_AER\_S
- **-clean\_inca** : active it if you want to recompile full inca model. This option will make a remove of mdoles/INCA/build/ directory.
- **-full** : active it you want to recompile full configuration.
- **-debug, -dev, -prod**(default) : choose in which mode you want to compile your configuration.

```
./compile_lmdzorinca.sh -regular_latlon 144x142x79
./compile_lmdzorinca.sh -chimie DUSX
./compile_lmdzorinca.sh -clean_inca
./compile_lmdzorinca.sh -full
./compile_lmdzorinca.sh -debug
./compile_lmdzorinca.sh -regular_latlon 144x142x79 -chimie AER -full
```

If you compile in debug or in dev mode you need to modify the parameter OptMode in config.card. If you change the resolution at the compilation you need to modify the parameter ResolAtm in config.card

Even if the script allow you to compile any resolution for any chemistry, support ones are the same than for LMDZORINCA\_v6.1.10 (see above)

## 2.2. Computing performances

- for VLR resolution (96x95x39) we advice to work with 48MPI and 12OMP for the gcm executable (config.card)
- for LR resolution (144x142x79) we advice to work with 71MPI and 8 OMP for the gcm executable (config.card)

```
ATM= ( gcm_${ResolAtm}_${OptMode}_${ConfChem}.e, lmdz.x, 48MPI, 12OMP )
```

## 2.3. Restart files

For LMDZ and ORCHIDEE you can use restart files from any simulation of v6.1.10 family (even coupled model). For Inca you can start without any restart, or use one from a simulation using a version with a revision number bigger than 838

You can also use default restart files (initial states files) :

With the LMDZ model you can create initial files (start.nc, startphy.nc and limit.nc) for each simulation (for this, use the experiments : EXPERIMENTS/LMDZORINCA/CREATE\_erai/). However, start.nc file only contain zero-values for tracers when the model is coupled to INCA. You must therefore work on those values or use output files from existing simulations. By default, we provide one initial state per configuration.

- $\${R\_INIT}/CHM/LMDZORINCA/INCA\${RESOL\_CHM}/start\_o2a\_noTer.nc$  --> start.nc
- $\${R\_INIT}/CHM/LMDZORINCA/INCA\${RESOL\_CHM}/startphy\_o2a\_noTer.nc$  --> startphy.nc

With

- $\${R\_INIT}$  = igcmg shared space (TGCC and IDRIS - you can find the path in the main Job)  $\$\$shared\_path/IGCM/INIT$
- $\${RESOL\_CHM}$  = 9695-L39 / 9695-L19 / 144142-L19 / 144142-L39

They are defined in the [InitialStateFiles] section of lmdz.card

```
[InitialStateFiles]
List= ( ${R_INIT}/CHM/LMDZORINCA/INCA${RESOL_CHM}/start_o2a_noTer.nc, start.nc ) \
      ( ${R_INIT}/CHM/LMDZORINCA/INCA${RESOL_CHM}/startphy_o2a_noTer.nc, startphy.nc )
```

## 2.4. Output level

for Inca output frequencies, you can choose by default between 1 day and / or 1 month. For this you need to fill in your choice in section [WriteFrequency?](#) for chemistry part

```
#D-- CHM -
[CHM]
#D-- choose inca ...
#D-- you can also ...
WriteFrequency="1D"
```

or

```
[CHM]
#D-- choose inca ...
#D-- you can also ...
WriteFrequency="1D 1M"
```

or

```
[CHM]
#D-- choose inca ...
#D-- you can also ...
WriteFrequency="1M"
```

If you want another output frequency you need to modify the file\_def\_inca\_.xml file in modeles/INCA/src/INCA\_XML/ directory. You will find two files for each chemistry configurations (ex: file\_def\_inca\_NMHC\_daily.xml and file\_def\_inca\_NMHC\_monthly.xml).

## 2.5. Flags to manage LMDZORINCA configuration

In inca.card, lmdz.card and orchidee.card you can modify several parameters in sections [UsersChoices]

### INCA

<b>LMDZ_10m_winds</b>	<b>y</b> (use LMDZ 10 meters winds)	<b>n</b> (use offline winds)		
<b>wind_parameter</b>	<b>0.85</b> (default parameter value for threshold scheme to adjust 10 meters winds calculated by LMDZ)			
<b>feedb</b>	<b>0</b> (no feedback from aerosol on climate with Old Physics scheme)	<b>1</b> (aerosol effects selected by ok_ade and ok_aie in lmdz.card)		
<b>CoupOrchInca</b>	<b>y</b> (coupled model with ORCHIDEE for VOC)	<b>n</b>		
<b>calcul_flux</b>	<b>y</b> (calcul and write in output the chemistry flux of reactions)	<b>n</b>		
<b>flag_plane</b>	<b>0</b> (no aircraft)	<b>1</b> (old inca aircraft scheme)	<b>2</b> (new subsonic inca aircraft scheme)	<b>3</b> (subsonic + hypersonic inca aircraft scheme)
<b>emi_interp_time</b>	<b>0</b> (no time interpolation when using emission files)	<b>1</b> (point to point time interpolation when using emissions files - default)		

### 2.5.10. meters winds

If you choose to use offline winds, you need to define their path in the BoundaryFiles part of inca.card  
For Example :

```
[BoundaryFiles]
List=      (/ccc/work/cont003/subips1/subips1/ECMWF320x160/AN${year}/165_${year}${month}.nc      , u10mec.nc)\
          (/ccc/work/cont003/subips1/subips1/ECMWF320x160/AN${year}/166_${year}${month}.nc      , v10mec.nc)\
          (${R_BC}/ATM/LMDZORINCA/${RESOL_ATM}/NUDGE_FILES/ERA1/AN${year}/u10m_ecmwf_${year}${month}.nc , u10m.nc )\
          (${R_BC}/ATM/LMDZORINCA/${RESOL_ATM}/NUDGE_FILES/ERA1/AN${year}/v10m_ecmwf_${year}${month}.nc , v10m.nc )
```

### 2.5.11. The BVOC and Surface coupling

If you choose to activate the bvoc calcul in Orchidee (CHEMISTRY\_BVOC=y in Orchidee.def) you can copy the new flux value in Inca. For this you need to modify the parameter **CoupOrchInca** in inca.card. By default it will copy all bvoc flux : iso - mono - ORVOC - MBO - methanol - acetone - acetal - formal - acetic - formic - no\_soil - nox - fertil\_no - apinen - bpinen - limonen - myrcen - sabinen - camphen - 3caren - tbocimen - othermono - sesquiter.

And iso and mono are use in inca instead of the value read in sflx.nc.

**WARNING** it can only work with NMHC\_AER configuration.

snow, lai, veget, vegetfrac are also copy from Orchidee to Inca. You can choose to copy only these variables, for this you need to add in PARAM/inca.def the line :

```
nbFlux_FromOrch=0
```

If you want copy some flux, but not all the list, you need to modify your inca.def

```
nbFlux_FromOrch=3
emi_FromOrch=ORVOC acetone bpinen
```

## 2.6. Lengths, frequencies

We advice you to use a PeriodLength of 1 month or 1 year, and a Pack Frequency of 1 year.

## 2.7. Computing centers

LMDZORINCA is only available on TGCC computers