

Program: GRANADA4

Version 1.0

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RANDOM DISTRIBUTION OF MOLECULES AROUND A CENTRAL POLYATOMIC SYSTEM

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granada4 is an executable program that is designed to read Cartesian coordinate files in XYZ format that contain atomic data of molecules in order to generate cells where environmental molecules are randomly surrounding it. The files it produces can be the same kind of Cartesian coordinates in the XYZ. It can also produce Cartesian coordinate input files for Gaussian, internal coordinate MOPAC files and Orca input files. This program *does not* use any potential that can alter the random distribution of molecules.

Originally written by Luis A. Montero, Faculty of Chemistry, University of Havana 10400, Cuba at the Technical University of Dresden, in 1995, and completed at the University of Granada, Molecular Design and Modeling Group, Granada 18071, Spain, in June, 1996. This is a revised version of Granada4, October 2019 at the University of Havana.

THE INPUT:

The main input is given by the command line according the following format:

`<program name> solute.xyz [solvent1.xyz [solvent2.xyz]...]`

Where `<program name>` could be either `granada4.exe` in the case of the Windows version or `granada4.x` in the case of the Linux version. `solute.xyz` is the name of the file with the Cartesian coordinates for the geometry of the central molecule or cluster. `solvent i .xyz` are the corresponding for eventual surrounding or solvent molecules. There could be up to 5 different solvent molecules. Default solvent is water, which coordinates are internally stored by the program. Their XYZ files can be avoided in the command line if being the only solvent.

A file named **input.mmh** must be present in the predefined directory and contains the general parameters for the calculation. Numerical input formats are loose and can be entered as numerical data separated by commas.

First line:

`nlim, dimen, nconf, nfsolv, (fracm(i), i=1, nfsolv)`

nlim is the number of desired environmental or solvent molecules. In all cases, the origin of the Cartesian coordinates of the solute is reallocated to the center (middle) of its absolute coordinates.

dimen is the half-dimension (in Ångstroms) on all the Cartesian axes of a virtual cube wherein the environmental molecules will be randomly placed. The volume of the cube will be $(2*\text{dimen})^3$ and no coordinate of solute molecules will have a greater value than **dimen**.

nconf is the number of random geometries to be generated. It means that the output **solvated.xyz** file will hold **nconf** sequences of cell geometries with different random distributions of environmental molecules. The **default value** of **nconf** is 1. Cartesian coordinate files must follow the standard XYZ format for each cell, with an initial line containing the number of atoms, followed by a line of titles, and then a line for each atom with the symbol or atomic number followed by the coordinates X, Y and Z in angstroms, separated by spaces.

nfso1v is the number of environmental molecules other than water to be taken into account (the maximum is 5, and the implicit 0 for water).

fracm(i) is the molar fraction of the *i* environmental molecule. You can write up to **nfso1v** molar fraction values. They only refer to environmental molecules, NOT TO THE SOLUTE OR CENTRAL MOLECULE.

Second line:

INCLUDE: Environmental molecules will be allowed to occupy the entire random space within the limits of the dimensions of the predetermined box, including cavities within the solute molecule. Superposition of molecules in clusters will be allowed up to 0.5 the van der Waals radii distances of component elements.

EXCLUDE: If positive, the solvent molecules will externally surround an ellipsoid with dimensions proportional to the central cluster molecule that is formed in each step. This is the **default option**. Superposition of molecules in clusters will be allowed up to 0.75 the van der Waals radii distances of component elements.

SOLID1: Environmental molecules are placed at a maximum distance of **dimen** Ångstroms perpendicular to the positive side of the XY plane of the solute molecule.

MOPAC: means that there will be an additional **solvated.mop** output file with random configurations in the form of internal coordinate entries for MOPAC. A text of **MOPAC** options limited to 80 columns must be included as text lines following this one of the main **granada4** input file. It which will be used as the input data for most MOPAC program versions for semi-empirical calculations to corresponding expected outputs.

GAUSSIAnn: means that there will be a **solvated.gjf** output of Cartesian coordinates in the Gaussian input format. In this case, it is assumed that the molecules are neutral and singlet and any modification must be made by editing the output file so that it serves as a correct Gaussian input format. The n=1,6 value means the number of Gaussian command line to be written for each output configuration. This desired Gaussian command lines must be entered as text lines following this one of the main **granada4** input file.

ORCAn: means that there will be a `solvated.inp` output of Cartesian coordinates in the Orca input format. In this case, it is assumed that the molecules are neutral and singlet and any modification must be made by editing the output file so that it serves as a correct Orca input format. The n=1,6 value means the number of Orca command line to be written for each output configuration. This desired Orca command lines must be entered as text lines following this one of the main **granada4** input file.

MOPAC, **ORCA** and **GAUSSIAN** keywords are exclusive to each other.

Ending lines:

Ending lines are those expected if MOPAC, GAUSSIAN or ORCA input files are to be created. See above.

THE OUTPUT:

The output of Granada consists of several text files whose common name is "SOLVATED", with the corresponding extensions. A SOLVATED.LOG file is also produced with details of the calculation.

AN EXAMPLE:

COMMAND LINE: `granada4.exe acrolein.xyz ethanol.xyz acetone.xyz`

INPUT .MMH file:

`8,6.5,50,2,0.25,0.75`

`Include MOPAC`

`pm3 specify geo-ok ef`

In this case:

`nlim = 8, dimen = 6.5, nconf = 50, nfsolv = 2, fracm (1) = 0.25, fracm (2) = 0.75`

means that $0.25 \times 8 = 2$ ethanol molecules together with $0.75 \times 8 = 6$ acetone molecules will be surrounding an acrolein molecule. The run will create 50 different cell geometries where solvents are placed randomly around the central solute molecule.

After the run there will be two fixed output files. The one named `solvent.log` contains a record of the generation of cells including cases where a given random geometry is discarded because some superposition occur. It could be originated when a newly generated molecule occupies the van der Waals room of a previously existing one. The other is a `solvent.xyz` file with all the generated cell configurations.

Because the keyword `INCLUDE` is provided environmental or solvent molecules will be allowed to occupy the entire random space within the limits of the dimensions of the predetermined box, including cavities within the solute molecule.

As the keyword `MOPAC` is used, another `solvated.mop` file will be created with the randomly generated geometries written by the internal coordinate MOPAC file format. The command line of each input molecule in the `solvated.mop` file will be: `pm3 specify geo-ok ef`

.XYZ FILES

The .XYZ files have the following format:

Line 1:

Free format: `N # Number of atoms in the entry.`

Line 2:

`80 cols.: # Comments`

Line 3 to 2 + N:

For each atom `I` :

Free format: `NAT (I) or SYMBOL # atomic number or chemical symbol of the atom`

Free format: `X (I) # X coordinate in Ångströms`

Free format: `Y (I) # Y coordinate in Ångströms`

Free format: `Z (I) # Z coordinate in Ångströms`