

Home

[Jump to bottom](#)

Welcome to the KIMERA wiki!

KIMERA is a scientific tool for the study of mineral dissolution. It implements a reversible [Kinetic Monte Carlo](#) (KMC) method to study the time evolution of a dissolving system, obtaining the dissolution rate and information about the atomic scale dissolution mechanisms. KIMERA is an [on-lattice](#) KMC program that allows to define the dissolution process in multiple ways, uses a wide diversity of event types to mimic the dissolution reactions, and defines the mineral structure in great detail, including topographic defects, dislocations, and point defects. Therefore, KIMERA ensures to perform numerous studies with great versatility. In addition, it offers a good performance thanks to its parallelization and efficient algorithms within the KMC method. In this repository, we present the code features and show some examples of its capabilities. KIMERA is controllable via user commands, it is written in object-oriented C++, and it is distributed as open-source software.

In this wiki you will find instructions guiding you through the installation of KIMERA, and the creation of input files to run your simulations.

Whenever you use KIMERA, please cite "Martin, P., Gaitero, J. J., Dolado, J. S., & Manzano, H. (2020). KIMERA: A Kinetic Montecarlo Code for Mineral Dissolution. Minerals, 10(9), 825" <https://www.mdpi.com/2075-163X/10/9/825/htm>

▼ Pages 12

[Home](#)[1. Installation](#)[2. Input structure](#)[2A. Simulation box](#)[2B. Topography](#)[2C. Particle type modifiers](#)[2D. Events definition](#)[2E. Reactive surface](#)[2F. Output requests](#)[2G. Other parameters](#)[3. KIMERA format](#)

4. Questions and answers

Clone this wiki locally

`https://github.com/hegoimanzano/KIMERA.wiki.git`



1. Installation

[Jump to bottom](#)

KIMERA is written in the standard C++11. Therefore, in order to install it, we will need the proper C++ compiler. Moreover, KIMERA is parallelized by means of the [OPENMP library](#) so such library is also required.

For the moment, I have managed the installation of KIMERA in some Windows and Linux machines:

REQUIREMENTS:

-a **C++ compiler**. I have used TDM-GCC on Windows and GCC on linux. You need 4.9.2 or higher (the current version on 21/12/2020 for TDM-GCC is 9.2.0 and for GCC is 10.2)

-**openmp library**.

WINDOWS:

1. Installation of [TDM-GCC](#)

- Installation of openMP library, **which is available as an optional component in the TDM-GCC compiler installation**

[Image](#)

- After the installation of [TDM-GCC](#) and the openMP library, restart your system.

2. Compilation of KIMERA.

In the command prompt (you can access the windows command prompt by writting `cmd` after preessing Windows key and 'r' key), go to your KIMERA folder by indicating the path to it.

```
cd C:\Path\to\your\KIMERA\folder\
```

for example:

```
cd C:\Programs\Kimera\
```

compile it with the following command, change the compiler paths if necessary. (In this example we have installed the 64 version in the default installation folder):

```
C:\TDM-GCC-64\bin\g++.exe -L\C:\TDM-GCC-64\lib\gcc\x86_64-w64-mingw32\9.2.0\include\ -
Wl,-rpath=C:\TDM-GCC-64\lib\gcc\x86_64-w64-mingw32\9.2.0\include\ -Wall -fexceptions -
fopenmp -std=c++11 -O3 include\Atom.h include\Box.h include\Cell.h include\Control.h
include\Data_printer.h include\Data_reader.h include\Event.h include\Event_definition.h
include\Event_stack.h include\Event_stack_unstuck.h include\Linked_neighbour.h
include\Models.h include\Position.h include\RandomGenerator.h include\Record.h
include\Simulation.h include\Sym_equation.h include\Tracker.h include\Util.h main.cpp
src\Atom.cpp src\Box.cpp src\Cell.cpp src\Control.cpp src\Data_printer.cpp
src\Data_reader.cpp src\Event.cpp src\Event_definition.cpp src\Event_stack.cpp
src\Event_stack_unstuck.cpp src\Linked_neighbour.cpp src\Models.cpp src\Position.cpp
src\RandomGenerator.cpp src\Record.cpp src\Simulation.cpp src\Sym_equation.cpp
src\Tracker.cpp src\Util.cpp -Iinclude -o Kimera.exe
```

TIP: If you get an error of 'Permission denied' ([see Image](#)), You must deselect the 'Read-only' attribute of your KIMERA folder ([see Image](#)) (left click -> Properties in the KIMERA folder).

3. (OPTIONAL, BUT RECOMMENDED) Install zip program. KIMERA will automatically zip your output files. [zip 3.0](#)

For Windows to recognise the 'zip' command, you will need to 'edit the system environment variables'.

1- [image](#)

2- [image](#)

3- [image](#)

4- add new line with the path where zip have been installed, for example by default

C:\Program Files (x86)\GnuWin32\bin

5- Ok to all

4. USAGE TIPS

A. It is better to use KIMERA from the command prompt by specifying the path to the input file

```
Kimera.exe path\to\kimera\inputfile\kimera.input
```

for example

```
Kimera.exe C:\Programs\Kimera\examples\AB_Kossel_crystal_random\kimera.input
```

same, but print the log in a text file:

```
Kimera.exe C:\Programs\Kimera\examples\AB_Kossel_crystal_random\kimera.input >
log.txt
```

B. Nevertheless, you can also move your input files to the same folder as Kimera.exe, and double-click it.

LINUX:

1. Installation of [GCC](#). Write the following commands in the terminal:

```
sudo apt update
```

```
sudo apt install build-essential
```

```
sudo apt-get install manpages-dev
```

- Installation of openMP library

```
sudo apt-get install libomp-dev
```

2. Compilation of KIMERA. In the terminal, go to KIMERA folder

for example

```
cd /home/user/Kimera
```

execute the makefile with `make`

If it doesn't work, try to specify the path to your compiler (see and edit the makefile in the KIMERA folder)

make sure that the program has execution rights:

```
sudo chmod 777 Kimera.exe
```

3. (OPTIONAL, BUT RECOMMENDED) Install zip program. KIMERA will automatically zip your output files.

```
sudo apt-get install zip
```

4. USAGE TIPS

- A. It is better to use KIMERA from the terminal by specifying the path to the input file

```
./Kimera.exe path/to/kimera/inputfile/kimera.input
```

for example

```
./Kimera.exe /home/user/Kimera/examples/AB_Kossel_crystal_random/kimera.input
```

same, but print the log in a text file:

```
./Kimera.exe /home/user/Kimera/examples/AB_Kossel_crystal_random/kimera.input > log.txt
```

- B. Nevertheless, you can also move your input files to the same folder as Kimera.exe, and execute it.

2. Input structure

[Jump to bottom](#)

KIMERA is a command base program in which the user define the system and the simulation parameters by means of commands on an input file. The commands are read by KIMERA subsequently so the effect of a command may be changed or neglected by the effect of a later one. The list with all the commands can be found in this repository in 'intructions/command_list.txt'. In the next step we will classify them in several categories for clearence purposes:

- **Creation of the simulation box.** Unit cell parameters, system dimensions, or Periodic Boundary Conditions (PBC) are essential to start building up your system. These commands are listed in section [2A. Simulation box](#).
- **Simulation box modifications.** The actual topography and shape of the dissolving system can be specified by commands acting as system modifiers. The initial system box in [2A. Simulation box](#) can be sculpted and changed to procude the desired one. The user can use an external script to help them to create their system. For example, In order to introduce in your system hundrends of adatoms (lonely atoms on the surface) at random postions, an external script to print the commands that will be later used in the KIMERA input file is very handy. The topography and shape commands are listed in section [2B. Topography](#). Moreover, the constituent atoms or particles of your system can be also modified after the system creation. Commands intended fo this porpuse are listed in section [2C. Particle type modifiers](#).
- **Events definition.** In the KMC algorithm, in order to study the time evolution of the dissolving system, it is necessary to know beforehand the possible transitions, or events, that may happen in it. KIMERA recognises several commands to do the event definition as detailed as possible. The event definition commands are listed in section [2D. Events definition](#).
- **Reactive surface.** KIMERA creates from the whole system a list with the initially reactive atoms for performance porpuses. Since it may not be to our liking, [2E. Reactive surface](#) contains the commands that modify it.
- **Output requests.** The output of KIMERA consists of several files inteded for visualization and data analysis. The commands that handle the output files are listed in section [2F. Output requests](#).
- **Other parameters.** The finishing condition, the random generator seed, the desired number of cores to run the simulation, the distance threshold, or the searching algorithm (lineal or binary) are some of the side parameters that can be set. The commands that modify them are listed in [2G. Other parameters](#).

Comments

Any word different from a command is not considered by the program and can be treated as a comment. Nevertheless, each command is a close statement and it is not possible to make any comments in between. Since all commands in KIMERA are in capital letters, in our examples we comment using lowercase letters starting with two hyphens '--' to make a clearer differentiation.

System exportation

Through this wiki and the command list, you will find commands with comments like `--(*)`, `--(**)` or `--(***)`. These marks are only important when using the system exportation feature. KIMERA can use the system from a previous simulation to save computational time, but it creates restrictions in the change of the simulation parameters. Specifically, commands from [2A. Simulation box](#) have to be identical to the previous simulation, [2B. Topography](#), [2C. Particle type modifiers](#) and [2E. Reactive surface](#) commands have no longer effect, the structure of [2D. Events definition](#) has to be the same though the values of the parameters can change, and all the commands related to [2E. Output requests](#) and most of the [2G. Other parameters](#) commands can be freely modified.

To recapitulate, marks indicate:

```
--(*)   The change of these parameters is possible.
--(**)  This command is compulsory as was in the original definition. Only the change
of the ED and EP, FFD, DG* values is possible.
--(***) They are not possible to be used or have no effect.
```

The command that export a previous system is:

```
READ_SYSTEM_FROM_KIMERA_FILE      (text)path_kimera_file
```

where 'path_kimera_file' indicates the path of the kimera file in your computer.

Finally, three important points are highlighted:

- 1- It is necessary to request the program to print the KIMERA file in the previous simulation. You can find the details to do it in the [E. Output requests](#) section.
- 2- The [format](#) of this file is specific to KIMERA and can be found in this wiki, or in the 'instructions/KIMERA_format.txt' in this repository.
- 3- It would be possible for the users to use other programs to create their system to later study its dissolution in KIMERA if the proper file transformation is done.

Parameters type

Along this wiki and in the command list file, it can be observed that the command input parameters can be of this three types:

- (text): Only one word, or several words without spacing.
- (int): A natural number. 0,1,2,3,...
- (double): A decimal number.

You can set a double parameter with an int (for example 1 would be threat as 1.0). Nevertheless the opposite is not posible (2.6 would be threat as 2).

Parameter units

The units of the input parameters are the following:

- Energy barriers: $k_B T$ units. k_B is the Boltzman constant (1.380×10^{-23} J K⁻¹) and T the temperature (K).

Tip: $k_B T / N_A = 2.494$ kJ mol⁻¹ at 300 K. N_A [Avogadro constant](#).

- Time: seconds (s).
- Fundamental frequencies: (s⁻¹).
- Distance: [Angstrom](#) (Å).
- Mass: [Atomic mass unit](#) (Dalton or u).

2A. Simulation box

[Jump to bottom](#)

--(**) These command is compulsory as was in the original definition.

--(***) They have no effect.

The first step to create your system is to define the parameters of the unit cell. The unit cell can correspond to a real mineral, like quartz, or to a theoretical one, like a [Kossel crystal](#). Three considerations can be highlighted.

1. You can define as a unit cell, a supercell consisting of several unit cells, or even the hole system. As we will see in section [Events definition](#), this will give more versatility to your simulation, but the program performance is reduced.
2. The particles of your unit cell can represent actual atoms, or [coarse grains](#).
3. You can define 'phantom positions' inside your unit cell without physical meaning but helping define the [events](#) of your system.

The commands for defining the unit cell are the following:

CELL_A	(double)	--(**)
CELL_B	(double)	--(**)
CELL_C	(double)	--(**)
CELL_ALPHA	(double)	--(**)
CELL_BETA	(double)	--(**)
CELL_GAMMA	(double)	--(**)

There are two ways of defining the positions of atoms or particles inside the unit cell.

1- They can be specified directly in the input file:

POSITION	(text)	atom_type	(double)	x	(double)	y	(double)	z
(double)	occupancy	--(***)						

where the `occupancy` (number bettween 0 and 1) represents the likelihood to find that element in that position.

2- Or they can also be read from external files with a simple xyz format, useful to load experimental crystal structures of mineralogist databases ([AMS](#), for example):

```
READ_POSITIONS_FROM_XYZ_FILE          (text)path_xyz_file          --(***)
```

where `path_xyz_file` indicates the path of the xyz file in your computer. These two ways are complementary, so you can define additional positions to the ones in the xyz file.

Tip: There are some crystallographic structures in which one unit cell position can be occupied by different elements with certain likelihood. This likelihood, named occupancy, is not contemplated in a simple xyz file. Therefore, if the occupancy feature needs to be used, the way to proceed is to introduce them with the `POSITION` command by coping them from the xyz file, but taking into account the occupancy value which is available in the [cif](#) file.

Tip: The xyz file is a simplification of the cif file. You can usually download both files from the mineralogist database, or at least the cif one. There are tools, like [VESTA](#) program that allows you to transform your [cif file into a xyz file](#).

Once we have the unit cell with the positions defined, we replicate it in the three space directions

```
DIMENSION_A          (int)          --(**)
DIMENSION_B          (int)          --(**)
DIMENSION_C          (int)          --(**)
```

We can consider the resulting simulation box to have periodicity in any of the three space directions, which is known as [periodic boundary conditions](#) (PBC).

```
PERIODICITY          (optional)A (optional)B (optional)C
```

Usually, dissolution simulations are done in slab models to mimic macroscopic surfaces, i.e. with periodic boundary conditions (PBC) in x and y, making the reactive surface perpendicular to the z axis. In other cases we may want to simulate particles, so PBC are not considered.

Tip: [Studies of different planes](#) are possible by unit cell transformations with external programs such as [VESTA](#).

Once our simulation box is defined, we can modify its shape as described in the next section [2B. Topography](#) or change the constituent particles or atoms, as described in section [2C. Particle type modifiers](#).

2B. Topography

[Jump to bottom](#)

--(***) All the commands listed here are not considered if system exportation from a previous simulation is done

All the possible features you can find in a mineral surface are named as surface topography. The mineral topography has been demonstrated to play an important role in the dissolution rate and mechanisms. Therefore, KIMERA gathers a list of commands as complete as possible to create topographical features. Indeed, there are several ways to obtain the same simulation system.

The resulting simulation box of the [previous step](#) is modified by removing or adding regions of atoms to create the desired morphology and system shape.

There are two ways of performing the changes:

1- By aiming the geometric position.

For example if we want to remove from our system a cube, we introduce the following command:

```
REMOVE_CUBE                (double)x    (double)y    (double)z    (double)side
```

or if we had it previously removed, we introduce next command to recover it

```
ADD_CUBE                   (double)x    (double)y    (double)z    (double)side
```

Additionally, we can set the cube as insoluble

```
DEFINE_INSOLUBLE_CUBE      (double)x    (double)y    (double)z    (double)side
```

For the moment, KIMERA has these commands available for cubes, spheres, ellipsoids, and planes:

```
ADD_SPHERE                 (double)x    (double)y    (double)z
(double)radius
REMOVE_SPHERE              (double)x    (double)y    (double)z
(double)radius
DEFINE_INSOLUBLE_SPHERE    (double)x    (double)y    (double)z
(double)radius
```

```

ADD_ELLIPSOID                (double)x    (double)y    (double)z
(double)radiusx    (double)radiusy    (double)radiusz
REMOVE_ELLIPSOID                (double)x    (double)y    (double)z
(double)radiusx    (double)radiusy    (double)radiusz
DEFINE_INSOLUBLE_ELLIPSOID    (double)x    (double)y    (double)z
(double)radiusx    (double)radiusy    (double)radiusz

```

Note that the ellipsoid and sphere cases can be also described by using the [ellipsoid general equation](#) $Ax^2+By^2+Cz^2+Dxy+Exz+Fyz+Gx+Hy+Jz+K<1$ (Indeed the previous commands does not manage to represent rotated ellipsoids).

```

ADD_GENERAL_ELLIPSOID    (double)A    (double)B    (double)C    (double)D
(double)E    (double)F    (double)G    (double)H    (double)J    (double)K
REMOVE_GENERAL_ELLIPSOID    (double)A    (double)B    (double)C    (double)D
(double)E    (double)F    (double)G    (double)H    (double)J    (double)K
DEFINE_INSOLUBLE_GENERAL_ELLIPSOID    (double)A    (double)B    (double)C    (double)D
(double)E    (double)F    (double)G    (double)H    (double)J    (double)K

```

The planes are defined with the [general equation of a plane](#) $Ax+By+Cz+D=0$.

```

DEFINE_INSOLUBLE_PLANE    (double)A    (double)B    (double)C    (double)D
(double)distance
REMOVE_PLANE    (double)A    (double)B    (double)C    (double)D
(double)distance
ADD_PLANE    (double)A    (double)B    (double)C    (double)D
(double)distance

```

Here the distance parameter set the thickness of the plane (distance is half the tickness).

Tip: Geometric tools like [Geodebra3d](#) can be very helpful to create your system.

2- By aiming the system cells. The changes are produced in the cells of the system. These commands only allow changes in specific cells, or planes of cells:

```

DEFINE_AB_INSOLUBLE_CELLS    (int)pos_cell_a    (int)pos_cell_b    (int)pos_cell_c
(int)length_a    (int)length_b
DEFINE_BC_INSOLUBLE_CELLS    (int)pos_cell_a    (int)pos_cell_b    (int)pos_cell_c
(int)length_b    (int)length_c
DEFINE_AC_INSOLUBLE_CELLS    (int)pos_cell_a    (int)pos_cell_b    (int)pos_cell_c
(int)length_a    (int)length_c

REMOVE_AB_PLANE_BY_CELLS    (int)pos_cell_a    (int)pos_cell_b    (int)pos_cell_c
(int)length_a    (int)length_b
REMOVE_BC_PLANE_BY_CELLS    (int)pos_cell_a    (int)pos_cell_b    (int)pos_cell_c
(int)length_b    (int)length_c
REMOVE_AC_PLANE_BY_CELLS    (int)pos_cell_a    (int)pos_cell_b    (int)pos_cell_c
(int)length_a    (int)length_c

ADD_AB_PLANE_BY_CELLS    (int)pos_cell_a    (int)pos_cell_b    (int)pos_cell_c

```

(int)length_a	(int)length_b			
ADD_BC_PLANE_BY_CELLS		(int)pos_cell_a	(int)pos_cell_b	(int)pos_cell_c
(int)length_b	(int)length_c			
ADD_AC_PLANE_BY_CELLS		(int)pos_cell_a	(int)pos_cell_b	(int)pos_cell_c
(int)length_a	(int)length_c			
ADD_CELL		(int)pos_cell_a	(int)pos_cell_b	(int)pos_cell_c
REMOVE_CELL		(int)pos_cell_a	(int)pos_cell_b	(int)pos_cell_c

Note that in all the cases, the `pos_cell` goes from 0 to `DIMENSION_A - 1`, `DIMENSION_B - 1` and `DIMENSION_C - 1` respectively (see [previous section](#)).

Dislocations

Special mention is given to this topographical feature because it has been experimentally observed that they play a key role in the dissolution rate and dissolution mechanisms. [Dislocations](#) can be screw or edge. Both types of dislocations are usually represented in the bibliography by considering a lineal defect where a line of atoms is removed. This approximation accounts that the energy bond in this spots is so weaken that can be neglectible. A finer approximation can be done in KIMERA, as we will explain in [Question and answers section](#), but this basic approach is also contemplated in KIMERA.

Same as before, we can define a dislocation by aiming the geometric position, or by aiming the system cells:

1- By aiming the geometric position.

It allows a more complete definition since the angle respect to the axes can be defined, and the dislocation radius can be different than a unit cell multiple.

ADD_XY_DISLOCATION	(double)x	(double)y	(double)radius
(optional line) FROM_Z_TO_Z	(double)bot_z	(double)top_z	
(optional line) ANGLE_XZ_ANGLE_YZ	(double)angle_xz	(double)angle_yz	
ADD_XZ_DISLOCATION	(double)x	(double)z	(double)radius
(optional line) FROM_Y_TO_Y	(double)bot_y	(double)top_y	
(optional line) ANGLE_XY_ANGLE_ZY	(double)angle_xz	(double)angle_yz	
ADD_YZ_DISLOCATION	(double)y	(double)z	(double)radius
(optional line) FROM_X_TO_X	(double)bot_x	(double)top_x	
(optional line) ANGLE_YX_ANGLE_ZX	(double)angle_yx	(double)angle_zx	

Two optional lines control the length of the dislocation, where does it start and where does it end, and the angle respect to the axes.

2- By aiming the system cells.

Same commands as before can be used to remove atoms linearly and define a dislocation but the inclination is no longer available. They can be only defined along a, b and c directions.

```
REMOVE_AB_PLANE_BY_CELLS      (int)pos_cell_a  (int)pos_cell_b  (int)pos_cell_c
(int)length_a  (int)length_b
REMOVE_BC_PLANE_BY_CELLS      (int)pos_cell_a  (int)pos_cell_b  (int)pos_cell_c
(int)length_b  (int)length_c
REMOVE_AC_PLANE_BY_CELLS      (int)pos_cell_a  (int)pos_cell_b  (int)pos_cell_c
(int)length_a  (int)length_c
```

Selective topography

All the previous commands can be used selectively by targeting atoms or particles of certain type. They are identical to the previous ones, but they have the `TO_TYPE` surname and an additional input parameter with the target atom type.

1- By aiming the geometric position.

```
ADD_XY_DISLOCATION_TO_TYPE      (text)atom_type  (double)x  (double)y
(double)radius
                                (optional line) FROM_Z_TO_Z
(double)bot_z      (double)top_z
                                (optional line) ANGLE_XZ_ANGLE_YZ
(double)angle_xz    (double)angle_yz

ADD_XZ_DISLOCATION_TO_TYPE      (text)atom_type  (double)x  (double)z
(double)radius
                                (optional line) FROM_Y_TO_Y
(double)bot_y      (double)top_y
                                (optional line)
ANGLE_XY_ANGLE_ZY    (double)angle_xz  (double)angle_yz

ADD_YZ_DISLOCATION_TO_TYPE      (text)atom_type  (double)y  (double)z
(double)radius
                                (optional line) FROM_X_TO_X
(double)bot_x      (double)top_x
                                (optional line)
ANGLE_YX_ANGLE_ZX    (double)angle_yx  (double)angle_zx

ADD_CUBE_TO_TYPE          (text)atom_type  (double)x  (double)y
(double)z      (double)side
REMOVE_CUBE_TO_TYPE      (text)atom_type  (double)x  (double)y
(double)z      (double)side
DEFINE_INSOLUBLE_CUBE_TO_TYPE      (text)atom_type  (double)x  (double)y
(double)z      (double)side

ADD_SPHERE_TO_TYPE        (text)atom_type  (double)x  (double)y
(double)z      (double)radius
REMOVE_SPHERE_TO_TYPE      (text)atom_type  (double)x  (double)y
```

```

(double)z      (double)radius
DEFINE_INSOLUBLE_SPHERE_TO_TYPE      (text)atom_type  (double)x      (double)y
(double)z      (double)radius

ADD_ELLIPSOID_TO_TYPE      (text)atom_type  (double)x      (double)y
(double)z      (double)radiusx      (double)radiusy      (double)radiusz
REMOVE_ELLIPSOID_TO_TYPE      (text)atom_type  (double)x      (double)y
(double)z      (double)radiusx      (double)radiusy      (double)radiusz
DEFINE_INSOLUBLE_ELLIPSOID_TO_TYPE      (text)atom_type  (double)x      (double)y
(double)z      (double)radiusx      (double)radiusy      (double)radiusz

ADD_GENERAL_ELLIPSOID_TO_TYPE      (text)atom_type  (double)A      (double)B
(double)C      (double)D      (double)E      (double)F      (double)G      (double)H      (double)J
(double)K
REMOVE_GENERAL_ELLIPSOID_TO_TYPE      (text)atom_type  (double)A      (double)B
(double)C      (double)D      (double)E      (double)F      (double)G      (double)H      (double)J
(double)K
DEFINE_INSOLUBLE_GENERAL_ELLIPSOID_TO_TYPE      (text)atom_type  (double)A      (double)B
(double)C      (double)D      (double)E      (double)F      (double)G      (double)H      (double)J
(double)K

DEFINE_INSOLUBLE_PLANE_TO_TYPE      (text)atom_type  (double)A      (double)B
(double)C      (double)D      (double)distance
REMOVE_PLANE_TO_TYPE      (text)atom_type  (double)A      (double)B
(double)C      (double)D      (double)distance
ADD_PLANE_TO_TYPE      (text)atom_type  (double)A      (double)B
(double)C      (double)D      (double)distance

```

2- By aiming the system cells.

```

DEFINE_AB_INSOLUBLE_CELLS_TO_TYPE      (text)atom_type  (int)pos_cell_a
(int)pos_cell_b      (int)pos_cell_c      (int)length_a      (int)length_b
DEFINE_BC_INSOLUBLE_CELLS_TO_TYPE      (text)atom_type  (int)pos_cell_a
(int)pos_cell_b      (int)pos_cell_c      (int)length_b      (int)length_c
DEFINE_AC_INSOLUBLE_CELLS_TO_TYPE      (text)atom_type  (int)pos_cell_a
(int)pos_cell_b      (int)pos_cell_c      (int)length_a      (int)length_c

REMOVE_AB_PLANE_BY_CELLS_TO_TYPE      (text)atom_type  (int)pos_cell_a
(int)pos_cell_b      (int)pos_cell_c      (int)length_a      (int)length_b
REMOVE_BC_PLANE_BY_CELLS_TO_TYPE      (text)atom_type  (int)pos_cell_a
(int)pos_cell_b      (int)pos_cell_c      (int)length_b      (int)length_c
REMOVE_AC_PLANE_BY_CELLS_TO_TYPE      (text)atom_type  (int)pos_cell_a
(int)pos_cell_b      (int)pos_cell_c      (int)length_a      (int)length_c

ADD_AB_PLANE_BY_CELLS_TO_TYPE      (text)atom_type  (int)pos_cell_a
(int)pos_cell_b      (int)pos_cell_c      (int)length_a      (int)length_b
ADD_BC_PLANE_BY_CELLS_TO_TYPE      (text)atom_type  (int)pos_cell_a
(int)pos_cell_b      (int)pos_cell_c      (int)length_b      (int)length_c
ADD_AC_PLANE_BY_CELLS_TO_TYPE      (text)atom_type  (int)pos_cell_a
(int)pos_cell_b      (int)pos_cell_c      (int)length_a      (int)length_c

ADD_CELL_TO_TYPE      (text)atom_type  (int)pos_cell_a
(int)pos_cell_b      (int)pos_cell_c

```

```
REMOVE_CELL_TO_TYPE      (text)atom_type  (int)pos_cell_a  
(int)pos_cell_b    (int)pos_cell_c
```

In addition to change the topography and shape of our system, we can perform changes in the type of the atoms, as we will see in the [next section](#).

2C. Particle type modifiers

[Jump to bottom](#)

--(***) All the commands listed here are not considered if system exportation from a previous simulation is done

Once we have our system defined with the desired shape and topography, we can change locally the constituent atoms or particles. Very similar commands to the shown ones in the [previous section](#) do the job. When applying, a region of the system sees its type changed into the desired final atom type:

```
CHANGE_AB_PLANE_TYPE                (int)pos_cell_a  (int)pos_cell_b
(int)pos_cell_c  (int)length_a  (int)length_b  (text)final_atom_type
CHANGE_AC_PLANE_TYPE                (int)pos_cell_a  (int)pos_cell_b
(int)pos_cell_c  (int)length_a  (int)length_c  (text)final_atom_type
CHANGE_BC_PLANE_TYPE                (int)pos_cell_a  (int)pos_cell_b
(int)pos_cell_c  (int)length_b  (int)length_c  (text)final_atom_type

CHANGE_CUBE_TYPE                    (double)x    (double)y    (double)z
(double)side  (text)final_atom_type

CHANGE_XY_DISLOCATION_TYPE            (double)x    (double)y    (double)radius
(text)final_atom_type
                                         (optional line) FROM_Z_TO_Z
(double)bot_z      (double)top_z
                                         (optional line) ANGLE_XZ_ANGLE_YZ
(double)angle_xz    (double)angle_yz

CHANGE_XZ_DISLOCATION_TYPE            (double)x    (double)z    (double)radius
(text)final_atom_type
                                         (optional line) FROM_Y_TO_Y
(double)bot_y      (double)top_y
                                         (optional line) ANGLE_XY_ANGLE_ZY
(double)angle_xz    (double)angle_yz

CHANGE_YZ_DISLOCATION_TYPE            (double)y    (double)z    (double)radius
(text)final_atom_type
                                         (optional line) FROM_X_TO_X
(double)bot_x      (double)top_x
                                         (optional line) ANGLE_YX_ANGLE_ZX
(double)angle_yx    (double)angle_zx

CHANGE_PLANE_TYPE                    (double)A    (double)B    (double)C
(double)D  (double)distance  (text)final_atom_type
CHANGE_SPHERE_TYPE                    (double)x    (double)y    (double)z
(double)radius  (text)final_atom_type
CHANGE_ELLIPSOID_TYPE                (double)x    (double)y    (double)z
```

```
(double)radiusx      (double)radiusy      (double)radiusz      (text)final_atom_type
CHANGE_GENERAL_ELLIPSOID_TYPE                                (double)A      (double)B      (double)C
(double)D      (double)E      (double)F      (double)G      (double)H      (double)J      (double)K
(text)final_atom_type
```

Note that:

- The parameters of this last command `CHANGE_GENERAL_ELLIPSOID_TYPE` indicate the coefficients of the [ellipsoid general equation](#) $Ax^2+By^2+Cz^2+Dxy+Exz+Fyz+Gx+Hy+Jz+K<1$.
- The parameters of the `CHANGE_PLANE_TYPE` command indicate the coefficients of the [plane general equation](#) $Ax+By+Cz+D=0$.
- The `pos_cell` goes from 0 to `DIMENSION_A -1`, `DIMENSION_B -1` and `DIMENSION_C -1` respectively (see [2A. Simulation box section](#)).

Selective particle type modifiers

All the previous commands can be used selectively targeting atoms or particles of certain type. They are identical to the previous ones, but they have the `TO_TYPE` surname and an additional input parameter with the target type:

```
CHANGE_AB_PLANE_TYPE_TO_TYPE                                (text)atom_type (int)pos_cell_a
(int)pos_cell_b      (int)pos_cell_c      (int)length_a      (int)length_b
(text)final_atom_type
CHANGE_AC_PLANE_TYPE_TO_TYPE                                (text)atom_type (int)pos_cell_a
(int)pos_cell_b      (int)pos_cell_c      (int)length_b      (int)length_c
(text)final_atom_type
CHANGE_BC_PLANE_TYPE_TO_TYPE                                (text)atom_type (int)pos_cell_a
(int)pos_cell_b      (int)pos_cell_c      (int)length_a      (int)length_c
(text)final_atom_type

CHANGE_CUBE_TYPE_TO_TYPE                                    (text)atom_type (double)x      (double)y
(double)z      (double)side (text)final_atom_type

CHANGE_XY_DISLOCATION_TYPE_TO_TYPE                            (text)atom_type (double)x      (double)y
(double)radius (text)final_atom_type
                                                                    (optional line) FROM_Z_TO_Z
(double)bot_z      (double)top_z
                                                                    (optional line) ANGLE_XZ_ANGLE_YZ
(double)angle_xz      (double)angle_yz

CHANGE_XZ_DISLOCATION_TYPE_TO_TYPE                            (text)atom_type (double)x      (double)z
(double)radius (text)final_atom_type
                                                                    (optional line) FROM_Y_TO_Y
(double)bot_y      (double)top_y
                                                                    (optional line) ANGLE_XY_ANGLE_ZY
(double)angle_xz      (double)angle_yz
```

```

CHANGE_YZ_DISLOCATION_TYPE_TO_TYPE      (text)atom_type  (double)y    (double)z
(double)radius  (text)final_atom_type

(optional line) FROM_X_TO_X

(double)bot_x      (double)top_x

(optional line) ANGLE_YX_ANGLE_ZX

(double)angle_yx   (double)angle_zx

CHANGE_PLANE_TYPE_TO_TYPE               (text)atom_type  (double)A    (double)B
(double)C    (double)D    (double)distance  (text)final_atom_type
CHANGE_SPHERE_TYPE_TO_TYPE              (text)atom_type  (double)x    (double)y
(double)z    (double)radius  (text)final_atom_type
CHANGE_ELLIPSOID_TYPE_TO_TYPE           (text)atom_type  (double)x    (double)y
(double)z    (double)radiusx  (double)radiusy  (double)radiusz
(text)final_atom_type
CHANGE_GENERAL_ELLIPSOID_TYPE_TO_TYPE   (text)atom_type  (double)A    (double)B
(double)C    (double)D    (double)E  (double)F  (double)G  (double)H  (double)J
(double)K    (text)final_atom_type

```

At this point we have our system perfectly defined. In the next step we are going to [define the dissolution events](#) that may happen in the system.

2D. Events definition

[Jump to bottom](#)

--(**) If system exportation from a previous simulation is done, all the commands listed here are compulsory as they were in the original definition. Only the change of the ED, EP, FFD, FFP, and DG^* values is possible.

The dissolution reactions (or events as commonly known in KMC algorithm) have a rate to happen that follows an [Arrhenius equation](#):

$$r = f_f \cdot \exp\left(-\frac{E_B}{k_B \cdot T}\right)$$

Where the pre-exponential factor f_f is named fundamental frequency (s^{-1}), and E_B (kJ mol^{-1}) is the energy barrier for the transition, k_B the Boltzman constant ($1.380 \times 10^{-23} \text{ J K}^{-1}$) and T the temperature (K).

It is necessary to take also into account the precipitation events to study the dissolution at close to equilibrium conditions, when the dissolution is unlikely to happen and the Gibbs free energy ΔG^* has values closer to 0. Therefore, the previous equation is splitted in the two following ones:

$$\begin{cases} r_D = f_D \cdot \exp\left(-\frac{E_D}{k_B \cdot T}\right) \\ r_P = f_P \cdot \exp\left(-\frac{E_P - \Delta G^*}{k_B \cdot T}\right) \end{cases}$$

Here the fundamental frequency has splitted in f_D and f_P , and the energy barrier in E_D and E_P . The Gibbs free energy ΔG^* is related to the macroscopical ΔG but such relation is dependent with the chosen model. For a deeper explanation, refer to the [article](#). If we make a proper description of the events and know these model parameters, which can be calculated by ab initio simulations or obtained in the bibliography, we can manage an accurate time evolution of a dissolving mineral.

Tip: we can ensure very far from equilibrium conditions by considering a very low value of ΔG^* when the precipitation term is neglected.

The command that starts with the event definition is `DEFINE DISSOLUTION_EVENT`. We will usually use this command once for each type of atom (or particle) in our system.

From the experiments we know that the energy barriers of the reactions changes with the neighbourhood of an atom. We have designed KIMERA in the same way. The definition of the dissolution events is done by indicating the Arrhenius equation parameters, which change with the local neighbourhood. The energy barrier E_B for an atom or particle to be removed from the system changes with the number of 'contributors' or neighbours around it.

$$E_D = \sum_{i=1}^n E_{d_i} \quad E_P = \sum_{i=1}^n E_{p_i}$$

where E_{d_i} and E_{p_i} are the dissolution and precipitation energy barrier contribution to the total E_D and E_P respectively and n is the total number of them.

As KIMERA uses an on-lattice description, we can identify each set of contributors according to their distance to the particle which is dissolving. As we will see in the [2G. Other parameters](#) section, we can set the threshold of this distance to give us more versatility in grouping the contributors. Since there may be two different types of contributors at the same distance to the target dissolving atom, we also need to indicate the contributor atom type.

KIMERA search for the contributors in same cell of the target atom, and in the 26 surrounding cells (up, down, sides, and diagonals). If we need to recognise a contributor out of this range, we will need to redefine the unit cell as a supercell containing a bigger piece of mineral.

The energy barrier of dissolution and precipitation can be determined by more than one different sets of contributors. Every time we use a `NEIGHBOUR` command, like `NEIGHBOUR`, `NEIGHBOUR_LINKED`, `NEIGHBOUR_LINKED DISSOLVED`, `NEIGHBOUR DIRECT LIST`, `NEIGHBOUR_LINKED DIRECT LIST` or `NEIGHBOUR_LINKED DISSOLVED DIRECT LIST`, we are referring to a different set and so we need to specify the distance to them and their type. The `DEFINE DISSOLUTION EVENT` command needs at least one of the previous to indicate the rate of the dissolution. There is no limit in the number of contributors.

Typically in the bibliography, the energy barrier has been considered to change linearly with the contributors. The commands that offer a simpler lineal description are `NEIGHBOUR`, `NEIGHBOUR_LINKED` and `NEIGHBOUR_LINKED DISSOLVED`. Nevertheless, KIMERA also allows to set a specific contribution for each contributor. The commands that allow specific description have the `DIRECT LIST` surname; `NEIGHBOUR DIRECT LIST`, `NEIGHBOUR_LINKED DIRECT LIST` and `NEIGHBOUR_LINKED DISSOLVED DIRECT LIST`.

The `LINKED` feature specify that the contribution is only considered if other atoms are still on the system. To define the 'linked' atoms, two distances are given; one to the contributor atom, and other to the target dissolving atom (or origin atom) in which we are defining the event. There is not limit in the number of 'linked' atoms.

Same as before, but if the contribution is only considered when other atoms are not longer in the system, we have the commands with `LINKED DISSOLVED` surname.

Finally, we can specify one special kind of atoms, named `AFFECTED`, which automatically leave the mineral when the 'father' atoms do. The number of 'affected' atoms has no limit.

To recapitulate, the events definition command list is the following:

```

DEFINE DISSOLUTION_EVENT (text)target_atom_type

    (optional line) NEIGHBOUR (text)target_neighbour_type
(double)distance_to_neighbour (double)ED_in_KT_units (double)EP_in_KT_units
(int)neighbours_to_bulk

    (optional line) NEIGHBOUR_LINKED (text)target_neighbour_type
(double)distance_to_neighbour LINK (text)target_linked_type
(double)distance_from_origin_to_linked (double)distance_from_neighbour_to_linked

LINK (text)target_linked_type (double)distance_from_origin_to_linked
(double)distance_from_neighbour_to_linked

LINK ..... (double)ED_in_KT_units
(double)EP_in_KT_units (int)neighbours_to_bulk

    (optional line) NEIGHBOUR_LINKED DISSOLVED (text)target_neighbour_type
(double)distance_to_neighbour LINK (text)target_linked_type
(double)distance_from_origin_to_linked (double)distance_from_neighbour_to_linked

LINK (text)target_linked_type (double)distance_from_origin_to_linked
(double)distance_from_neighbour_to_linked

LINK ..... (double)ED_in_KT_units
(double)EP_in_KT_units (int)neighbours_to_bulk

    (optional line) NEIGHBOUR_DIRECT_LIST (text)target_neighbour_type
(double)distance_to_neighbour LIST_LENGTH (int)list_length (double)ED1
(double)EP1 (double)ED2 (double)EP2 .....
(int)neighbours_to_bulk

    (optional line) NEIGHBOUR_LINKED_DIRECT_LIST (text)target_neighbour_type
(double)distance_to_neighbour LINK (text)target_linked_type
(double)distance_from_origin_to_linked (double)distance_from_neighbour_to_linked

LINK (text)target_linked_type (double)distance_from_origin_to_linked
(double)distance_from_neighbour_to_linked

LINK .....

LIST_LENGTH (int)list_length (double)ED1 (double)EP1 (double)ED2
(double)EP2 ..... (int)neighbours_to_bulk

    (optional line) NEIGHBOUR_LINKED DISSOLVED DIRECT_LIST
(text)target_neighbour_type (double)distance_to_neighbour LINK

```

```

(text)target_linked_type      (double)distance_from_origin_to_linked
(double)distance_from_neighbour_to_linked

LINK (text)target_linked_type      (double)distance_from_origin_to_linked
(double)distance_from_neighbour_to_linked

LINK .....

LIST_LENGTH (int)list_length      (double)ED1 (double)EP1 (double)ED2
(double)EP2 ..... (int)neighbours_to_bulk
      (optional line) AFFECTED      (text)target_affected_type
(double)distance_to_affected
.....
      (optional line) FFD
(double)dissolution_fundamental_frequency
      (optional line) FFP
(double)precipitation_fundamental_frequency
      (optional line) DG*      (double)event_delta_G

```

where DG^* is ΔG^* , FFD is f_D and FFP is f_P .

Next following points are important to be noted:

- We have to define one event (or more) for each atom type in our system, or consider them as 'affected'. Otherwise they will never dissolve.
- Related with the previous, if we have defined 'B' atoms as neighbours of 'A' atoms, we must also indicate that 'A' atoms are neighbours of 'B' atoms to tell KIMERA they are interconnected.

Tip: We must define events for 'B' atoms respect to the number of 'A' atoms, but if the existence of atoms A has not any influence on the dissolution of the first, we can just consider a very high value of energy barriers E_D and E_P .

- The `DIRECT_LIST` commands needs the specification of n , the number of contributors of that type, in the `list_length` parameter.
- In the `neighbours_to_bulk` parameter we specify if a type of neighbour makes the target atom a bulk atom. A bulk atom does not suffer dissolution until the quantity of that neighbour type is lower than the number we have specified. This represents the accessibility of the atom to react with the solvent after the dissolution of one of its neighbours. If a '0' value is considered, that type of neighbour has not effect in the bulk definition.

At this point we have the system with their possible events perfectly defined. KIMERA automatically creates then a reactive surface in where the dissolution is going to start. As the reactive surface may not be to our liking, the [next section](#) shows the commands that allow to modify it.

2E. Reactive surface

[Jump to bottom](#)

--(***) All the commands listed here are not considered if system exportation from a previous simulation is done

KIMERA automatically creates an initial reactive surface from the whole system which greatly increases the simulation performance. In order to define it, KIMERA considers the [PBC](#), the atoms defined as [insoluble](#), and the atoms defined as [bulk atoms](#). Nevertheless, the initial surface may not be well defined. Impurities, dislocations, or other features that decrease the homogeneity of the atomic structure produce initial reactive sites that should not initially exist since they are not in contact with the solvent (the interior of a dislocation, for example). Therefore, similar commands to previous ones explained in the [Topography](#) and [modifiers](#) sections are available to modify it:

```
REMOVE_AB_PLANE_FROM_SURFACE      (int)pos_cell_a  (int)pos_cell_b
(int)pos_cell_c  (int)length_a  (int)length_b
ADD_AB_PLANE_TO_SURFACE           (int)pos_cell_a  (int)pos_cell_b
(int)pos_cell_c  (int)length_a  (int)length_b

REMOVE_AC_PLANE_FROM_SURFACE      (int)pos_cell_a  (int)pos_cell_b
(int)pos_cell_c  (int)length_a  (int)length_c
ADD_AC_PLANE_TO_SURFACE           (int)pos_cell_a  (int)pos_cell_b
(int)pos_cell_c  (int)length_a  (int)length_c

REMOVE_BC_PLANE_FROM_SURFACE      (int)pos_cell_a  (int)pos_cell_b
(int)pos_cell_c  (int)length_b  (int)length_c
ADD_BC_PLANE_TO_SURFACE           (int)pos_cell_a  (int)pos_cell_b
(int)pos_cell_c  (int)length_b  (int)length_c

REMOVE_CUBE_FROM_SURFACE          (double)x      (double)y      (double)z
(double)side
ADD_CUBE_TO_SURFACE               (double)x      (double)y      (double)z
(double)side

REMOVE_XY_DISLOCATION_FROM_SURFACE (double)x      (double)y      (double)radius
(optional line) FROM_Z_TO_Z
(double)bot_z      (double)top_z
(double)angle_xz    (double)angle_yz
(optional line) ANGLE_XZ_ANGLE_YZ

ADD_XY_DISLOCATION_TO_SURFACE      (double)x      (double)y      (double)radius
(optional line) FROM_Z_TO_Z
(double)bot_z      (double)top_z
(double)angle_xz    (double)angle_yz
(optional line) ANGLE_XZ_ANGLE_YZ
```


REMOVE_XZ_DISLOCATION_FROM_SURFACE	(double)x	(double)z	(double)radius
(double)bot_y	(double)top_y	(optional line) FROM_Y_TO_Y	
(double)angle_xz	(double)angle_yz	(optional line) ANGLE_XY_ANGLE_ZY	
ADD_XZ_DISLOCATION_TO_SURFACE	(double)x	(double)z	(double)radius
(double)bot_y	(double)top_y	(optional line) FROM_Y_TO_Y	
(double)angle_xz	(double)angle_yz	(optional line) ANGLE_XY_ANGLE_ZY	
REMOVE_YZ_DISLOCATION_FROM_SURFACE	(double)y	(double)z	(double)radius
(double)bot_x	(double)top_x	(optional line) FROM_X_TO_X	
(double)angle_yx	(double)angle_zx	(optional line) ANGLE_YX_ANGLE_ZX	
ADD_YZ_DISLOCATION_TO_SURFACE	(double)y	(double)z	(double)radius
(double)bot_x	(double)top_x	(optional line) FROM_X_TO_X	
(double)angle_yx	(double)angle_zx	(optional line) ANGLE_YX_ANGLE_ZX	
REMOVE_PLANE_FROM_SURFACE	(double)A	(double)B	(double)C
(double)D	(double)distance		
ADD_PLANE_TO_SURFACE	(double)A	(double)B	(double)C
(double)D	(double)distance		
REMOVE_SPHERE_FROM_SURFACE	(double)x	(double)y	(double)z
(double)radius			
ADD_SPHERE_TO_SURFACE	(double)x	(double)y	(double)z
(double)radius			
REMOVE_ELLIPSOID_FROM_SURFACE	(double)x	(double)y	(double)z
(double)radiusx	(double)radiusy	(double)radiusz	
ADD_ELLIPSOID_TO_SURFACE	(double)x	(double)y	(double)z
(double)radiusx	(double)radiusy	(double)radiusz	
REMOVE_GENERAL_ELLIPSOID_TO_SURFACE	(double)A	(double)B	(double)C
(double)D	(double)E	(double)F	(double)G
ADD_GENERAL_ELLIPSOID_TO_SURFACE	(double)A	(double)B	(double)C
(double)D	(double)E	(double)F	(double)G
	(double)H	(double)J	(double)K
	(double)H	(double)J	(double)K

Note that:

- The parameters of these last commands `ADD_GENERAL_ELLIPSOID_TO_SURFACE` and `REMOVE_GENERAL_ELLIPSOID_FROM_SURFACE` indicate the coefficients of the [ellipsoid general equation](#) $Ax^2+By^2+Cz^2+Dxy+Exz+Fyz+Gx+Hy+Jz+K<1$.

- The parameters of the `ADD_PLANE_TO_SURFACE` and `REMOVE_PLANE_FROM_SURFACE` commands indicate the coefficients of the [plane general equation](#) $Ax+By+Cz+D=0$.
- The `pos_cell` goes from 0 to `DIMENSION_A -1`, `DIMENSION_B -1` and `DIMENSION_C -1` respectively (see [2A. Simulation box section](#))

Selective modification of the reactive surface

All the previous commands can be used selectively targeting atoms or particles of certain type. They are identical to the previous ones, but they have the `TO_TYPE` surname and an additional input parameter with the target type:

```
REMOVE_AB_PLANE_FROM_SURFACE_TO_TYPE      (text)atom_type (int)pos_cell_a
(int)pos_cell_b (int)pos_cell_c (int)length_a (int)length_b
ADD_AB_PLANE_TO_SURFACE_TO_TYPE            (text)atom_type (int)pos_cell_a
(int)pos_cell_b (int)pos_cell_c (int)length_a (int)length_b
```

```
REMOVE_AC_PLANE_FROM_SURFACE_TO_TYPE      (text)atom_type (int)pos_cell_a
(int)pos_cell_b (int)pos_cell_c (int)length_a (int)length_c
ADD_AC_PLANE_TO_SURFACE_TO_TYPE            (text)atom_type (int)pos_cell_a
(int)pos_cell_b (int)pos_cell_c (int)length_a (int)length_c
```

```
REMOVE_BC_PLANE_FROM_SURFACE_TO_TYPE      (text)atom_type (int)pos_cell_a
(int)pos_cell_b (int)pos_cell_c (int)length_b (int)length_c
ADD_BC_PLANE_TO_SURFACE_TO_TYPE            (text)atom_type (int)pos_cell_a
(int)pos_cell_b (int)pos_cell_c (int)length_b (int)length_c
```

```
REMOVE_CUBE_FROM_SURFACE_TO_TYPE          (text)atom_type (double)x (double)y
(double)z (double)side
ADD_CUBE_TO_SURFACE_TO_TYPE                (text)atom_type (double)x (double)y
(double)z (double)side
```

```
REMOVE_XY_DISLOCATION_FROM_SURFACE_TO_TYPE (text)atom_type (double)x (double)y
(double)radius
                                           (optional line) FROM_Z_TO_Z
(double)bot_z (double)top_z
                                           (optional line) ANGLE_XZ_ANGLE_YZ
(double)angle_xz (double)angle_yz
```

```
ADD_XY_DISLOCATION_TO_SURFACE_TO_TYPE       (text)atom_type (double)x (double)y
(double)radius
                                           (optional line) FROM_Z_TO_Z
(double)bot_z (double)top_z
                                           (optional line) ANGLE_XZ_ANGLE_YZ
(double)angle_xz (double)angle_yz
```

```
REMOVE_XZ_DISLOCATION_FROM_SURFACE_TO_TYPE (text)atom_type (double)x (double)z
(double)radius
                                           (optional line) FROM_Y_TO_Y
(double)bot_y (double)top_y
```

```

(double)angle_xz      (double)angle_yz
                                (optional line) ANGLE_XY_ANGLE_ZY

ADD_XZ_DISLOCATION_TO_SURFACE_TO_TYPE      (text)atom_type      (double)x
(double)z      (double)radius
                                (optional line) FROM_Y_TO_Y
(double)bot_y      (double)top_y
                                (optional line) ANGLE_XY_ANGLE_ZY
(double)angle_xz      (double)angle_yz

REMOVE_YZ_DISLOCATION_FROM_SURFACE_TO_TYPE  (text)atom_type  (double)y      (double)z
(double)radius
                                (optional line) FROM_X_TO_X
(double)bot_x      (double)top_x
                                (optional line) ANGLE_YX_ANGLE_ZX
(double)angle_yx      (double)angle_zx

ADD_YZ_DISLOCATION_TO_SURFACE_TO_TYPE      (text)atom_type  (double)y      (double)z
(double)radius
                                (optional line) FROM_X_TO_X
(double)bot_x      (double)top_x
                                (optional line) ANGLE_YX_ANGLE_ZX
(double)angle_yx      (double)angle_zx

REMOVE_PLANE_FROM_SURFACE_TO_TYPE          (text)atom_type  (double)A      (double)B
(double)C      (double)D      (double)distance
ADD_PLANE_TO_SURFACE_TO_TYPE              (text)atom_type  (double)A      (double)B
(double)C      (double)D      (double)distance

REMOVE_SPHERE_FROM_SURFACE_TO_TYPE         (text)atom_type  (double)x      (double)y
(double)z      (double)radius
ADD_SPHERE_TO_SURFACE_TO_TYPE             (text)atom_type  (double)x      (double)y
(double)z      (double)radius

REMOVE_ELLIPSOID_FROM_SURFACE_TO_TYPE      (text)atom_type  (double)x      (double)y
(double)z      (double)radiusx      (double)radiusy      (double)radiusz
ADD_ELLIPSOID_TO_SURFACE_TO_TYPE          (text)atom_type  (double)x      (double)y
(double)z      (double)radiusx      (double)radiusy      (double)radiusz

REMOVE_GENERAL_ELLIPSOID_TO_SURFACE_TO_TYPE (text)atom_type  (double)A      (double)B
(double)C      (double)D      (double)E      (double)F      (double)G      (double)H      (double)J
(double)K
ADD_GENERAL_ELLIPSOID_TO_SURFACE_TO_TYPE  (text)atom_type  (double)A      (double)B
(double)C      (double)D      (double)E      (double)F      (double)G      (double)H      (double)J
(double)K

```

At this point we can perform our simulation to study the mineral dissolution. In the [next step](#) we will see the necessary commands to indicate KIMERA the output files we need.

2F. Output requests

[Jump to bottom](#)

--(*) All the commands listed here can be freely modified if system exportation from a previous simulation is done

The KMC algorithm within KIMERA makes the dissolution events happen one by one. In each simulation step, the program evaluates to print the information of the simulation in the output files according to what has been specified by the user. Each command enables the printing of a type of output file. The number in the command indicates the steps that are going to be printed uniformly, in time or in steps, depending on the ending clause (see [next section](#)).

The available output files are the following:

DATA_ANALYSIS (int)

It contains information of the quantity and fraction of the dissolved atoms of each type with time, as well as the derivative. Moreover, if we are studying a particle (with no [PBC](#) in any direction), it also reports information about the [gyradius](#), but we need to specify the mass of each type of atom (see [2G. Other parameters section](#)). This file is essential to study the time evolution of the dissolution rate.

MEAN DISSOLVED_ANALYSIS (int)

This file contains information of the average quantity of neighbours an atom has when it dissolves. This file is essential to obtain the ΔG and ΔG^* relation.

LAYER_ANALYSIS (optional)A (optional)B (optional)C (int)

This command prints a maximum of three different files, one for each system direction. They contain information of the time evolution of the quantity of atoms that each system layer has. Each system layer has a thickness of one unit cell.

`BOX_FRAMES``(int)`

This command prints the file with snapshots of the whole system with time, in [LAMMPS](#) format. As this file contains several times all the system positions, the size of the file may be too big. It is readable by visualization tools as [OVITO](#).

`SURFACE_FRAMES``(int)`

This command allows to obtain a similar file to the previous one but it only contains the positions of the reactive surface, thus it is much smaller. Same as before, the output file has [LAMMPS](#) format and can be viewed by [OVITO](#) program.

`INITIAL_KIMERA_STATE``FINAL_KIMERA_STATE`

If these commands are used, the initial and the final states of the system are printed respectively. They have their own KIMERA format, as seen in [3. KIMERA format section](#). These output files can be used in subsequent simulations to save time, although the use of the commands are limited (see [2. Input structure section](#)). In the case that `FINAL_KIMERA_STATE` has been used and KIMERA encounters an error during the simulation, it still prints the final state just before the error.

At this point, the only step remaining is to indicate when we want our simulation to finish. This, and other side commands like the name we give to the simulation or the number of cores we want to use to run it are explained in the next [2G. Other parameters section](#).

2G. Other parameters

[Jump to bottom](#)

--(*) All the commands listed here can be freely modified if system exportation from a previous simulation is done, with the exception of the `SEED_BOX` command, which its change does not have any effect.

One of the most important commands of the simulation is to tell KIMERA when to stop it, the ending clause. The number of the snapshots of the output files are calculated respect to this ending clause. A lower than expected quantity of snapshots may be obtained if the system has expired before the ending clause. On the other hand, if we consider a too short ending clause, we may not appreciate any evolution of the system.

There are two ways to set the ending clause, indicating the `TARGET_TIME` or indicating the `TARGET_STEP`. In KIMERA it is easier to use the `TARGET_STEP` command. As one step removes one particle of the system, we know that the maximum number of steps are the total maximum of atoms (we have to rest the atoms defined as [insoluble](#) and the atoms removed by the [topography](#) commands). The `TARGET_TIME` is more difficult to know beforehand in a KMC algorithm. Nevertheless KIMERA can make an estimation of it using the `ESTIMATE_TIME` command. The following three commands are incompatible with each other:

<code>TARGET_TIME</code>	(double)
<code>ESTIMATE_TIME</code>	
<code>TARGET_STEP</code>	(int)

If we are performing an study of a particle with no [PBC](#) conditions, we can obtain the time evolution of the [gyradius](#) with the `DATA_ANALYSIS` command (see previous [2F. Output requests section](#)). Nevertheless, we need to indicate the mass of the constituent atoms of our system in [atomic mass units](#) (Dalton or u). One command for each atom type.

<code>SET_MASS</code>	(text)element	(double)mass
-----------------------	---------------	--------------

Some of the loops of KIMERA are parallelized. This means that we can reduce our simulation time if we run it using several cores.

<code>PARALLELIZE_SIMULATION</code>	(int)cores
-------------------------------------	------------

One of the most time consuming steps of the [KMC](#) algorithm is the searching of the event that is going to happen in an array of values. There are different ways to do this searching that offer different performances. KIMERA can use the named [binary search](#) or the named [lineal search](#), the first one by default. Although the binary search is more efficient, it is not parallelized, so the lineal search can be considered if we are using several cores.

LINEAL_SEARCH

Tip: If you need your simulation soon, use lineal search with several cores. If you are running several set of simulations (to get the dispersion of the dissolution rate value for example) use 1 core for each one with binary search. More details are given in the [article](#).

As we have explained in the [2A. Simulation box section](#), we can specify the occupancy of the atoms in the unit cell. KIMERA creates randomly the system taking into account that occupancy. But we can give a seed to recreate always the same system.

SEED_BOX (int)

The [KMC](#) algorithm uses random numbers to describe [stochastic processes](#) as is the dissolution of a mineral. Therefore, we will never get two identical simulations unless we indicate it with the simulation seed.

SEED_SIMULATION (int)

Note that the `SEED_SIMULATION` and the `PARALLELIZE_SIMULATION` commands are incompatible if the number of cores > 1.

As explained in the [2D. Events definition section](#), KIMERA recognises an atom as neighbour by indicating the distance to it. It may happen that we want to group several neighbours into a contributor set whose distance is slightly different to the target atom. We can group them all by changing the distance threshold with the following command.

DISTANCE_ACCURACY (double)

Tip: For example, imagine a mineral in where a 'A' atom has 4 neighbouring 'B' atoms, two of them at 1.550 Å and the other two at 1.570 Å. To group them all, we can set a `distance_to_neighbour` of 1.560 Å and then change `DISTANCE_ACCURACY` to 0.011 Å.

When [defining the events](#), we are usually going to indicate the value of ΔG , f_d and f_p for each event. Other option is to indicate its value using the following general commands. The event definition without any of the commands `DG*`, `FFD` and `FFP` will see their values replaced with the values of these ones, respectively:

<code>DELTA_G*</code>	(double)
<code>DISSOLUTION_FUNDAMENTAL_FREQUENCY</code>	(double)
<code>PRECIPITATION_FUNDAMENTAL_FREQUENCY</code>	(double)

We can give to our simulation a name. All the output files will get this name.

<code>WORK_NAME</code>	(text)
------------------------	--------

These were all the commands of KIMERA. in the next [4. Questions and answers section](#) you can find the answer to some question you may have.

3. KIMERA format

[Jump to bottom](#)

The goal of a Kimera file is to enhance the efficiency of successive simulations with the same system. The data in a kimera file is as follows:

1- Cells and their corresponding atoms forming the box of the system. Next code is applied in the format of `type_atom`:

```
1:  NORMAL
-1:  INSOLUBLE
-2:  REVOMED_ATOM (it is already dissolved)
```

2- Neighbours of each atom and the distance to each one.

3- Affected atoms for every atom. An affected atom dissolves as soon as the father does.

4- Linked atoms, related with the neighbour by the order that they follow in this file. The contribution of one neighbour is only considered if the linked atom exist. Next code is applied in the format of `type_link`:

```
0:  NOT LINKED
1:  LINKED
-1: LINKED TO A DISSOLVED ATOM
```

```
CELL 0
0  Si  1  2.505  0  0
1  Si  1  -1.2525  2.16939  3.64667
2  Si  1  1.2525  2.16939  1.82333
CELL 1
9  Si  1  2.505  -9.79754e-013  5.47
10 Si  1  -1.2525  2.16939  9.11667
11 Si  1  1.2525  2.16939  7.29333
12  O  1  1.59543  0.92112  6.38167
CELL (int)cell_id
(int)atom_id  (text)element  (int)type_atom  (double)position_x  (double)position_y
(double)position_z
(int)atom_id  (text)element  (int)type_atom  (double)position_x  (double)position_y
(double)position_z
(int)atom_id  (text)element  (int)type_atom  (double)position_x  (double)position_y
(double)position_z
(int)atom_id  (text)element  (int)type_atom  (double)position_x  (double)position_y
(double)position_z
...  ...  ...  ...  ...  ...
...  ...  ...  ...  ...  ...
CELL (int)cell_id
```

```

(int)atom_id      (text)element  (int)type_atom   (double)position_x (double)position_y
(double)position_z
(int)atom_id      (text)element  (int)type_atom   (double)position_x (double)position_y
(double)position_z
...      ...      ...      ...      ...      ...
...      ...      ...      ...      ...      ...
NEIGHBORS
0  2  3.09832  407  3.09832  405  5.01  45  5.01  1  5.66774  856  5.66774
406  4.42416  451  4.42416
1  2  3.09832  4052  3.09832  54  3.09832  4059  3.09832  4051  5.01  451
5.01  496  5.01  4456  5.01  0  5.66774
2  0  3.09832  1  3.09832  45  3.09832  451  3.09832  407  5.01  47  5.01
4052  5.01  452  5.01  4059  5.66774
(int)atom_id (int)neighbour_id (double)distance_atom_neighbour (int)neighbour_id
(double)distance_atom_neighbour ... ...
(int)atom_id (int)neighbour_id (double)distance_atom_neighbour (int)neighbour_id
(double)distance_atom_neighbour ... ...
(int)atom_id (int)neighbour_id (double)distance_atom_neighbour (int)neighbour_id
(double)distance_atom_neighbour ... ...
...      ...      ...      ...      ...      ...
...      ...      ...      ...      ...      ...
...      ...      ...      ...      ...      ...
AFFECTED
0  3  411
1  7  8  4054  4055
2  3  5  6  8
(int)atom_id (int)affected_id (int)affected_id ... ...
(int)atom_id (int)affected_id (int)affected_id ... ...
...      ...      ...      ...      ...      ...
...      ...      ...      ...      ...      ...
LINKED
0  L  0  L  0  L  1  407  L  1  2  L  1  2  L  1  407  L  1  407  L  1  2
1  L  0  L  0  L  0  L  0  L  1  4052  L  1  2  L  1  54  L  1  4059  L  1  2  L
1  4052  L  1  54
2  L  0  L  0  L  0  L  0  L  1  0  L  1  45  L  1  1  L  1  451  L  1  1  L  1
451  L  1  451  L  1  1
(int)atom_id L (int)type_link (int)linked_id (int)linked_id ... L
(int)type_link (int)linked_id (int)linked_id ...
(int)atom_id L (int)type_link (int)linked_id (int)linked_id ... L
(int)type_link (int)linked_id (int)linked_id ...
...      ...      ...      ...      ...      ...
...      ...      ...      ...      ...      ...

```

4. Questions and answers

[Jump to bottom](#)

1- Is KIMERA useful to study precipitation?

No, it is not. Although KIMERA takes into account the precipitation of the ions back into the mineral, precipitation is not explicitly considered.

2- I want to study the dissolution of an specific plane of the mineral using a slab model, how can I do it?

You have 'simply' to change the orientation of your mineral unit cell. [VESTA](#) program allows to do this transformation. In the next [link](#) you have an example. Note that you may have to change the unit cell parameters in your input file.

3- Is there any way to define a dislocation with higher detail rather that the proposed one in the [Topography section](#)?

Instead of using the dislocations commands of the [Topography section](#), you can change the type of the atoms where you want to define the dislocation, using one of these commands of the [Particle type modifiers section](#):

CHANGE_XY_DISLOCATION_TYPE	(double)x	(double)y	(double)radius
(text)final_atom_type			
		(optional line) FROM_Z_TO_Z	
(double)bot_z	(double)top_z		
		(optional line) ANGLE_XZ_ANGLE_YZ	
(double)angle_xz	(double)angle_yz		
CHANGE_XZ_DISLOCATION_TYPE	(double)x	(double)z	(double)radius
(text)final_atom_type			
		(optional line) FROM_Y_TO_Y	
(double)bot_y	(double)top_y		
		(optional line) ANGLE_XY_ANGLE_ZY	
(double)angle_xz	(double)angle_yz		
CHANGE_YZ_DISLOCATION_TYPE	(double)y	(double)z	(double)radius
(text)final_atom_type			
		(optional line) FROM_X_TO_X	
(double)bot_x	(double)top_x		
		(optional line) ANGLE_YX_ANGLE_ZX	
(double)angle_yx	(double)angle_zx		

And then define the desired contribution to the energy barrier of that type of atom in the [events definition](#).