

1.

# *Complx API*

## **Known bugs**

## **Known issues**

### **BDD**

- BDDs are very inefficient to describes systems with high degree sites or a huge number of internal states.

The BDU extension should solve this problem.

### **Quantitative compression**

- The quantitative compression could be deeply optimize to avoid an exponential dependences with respect to the size of left hand sides.

## **Current Version**

This API matches version 3.36 (July 9th 2008).

## **Requirement**

Complx can be compiled into any platform.  
Therefore, the Makefile is only provided for Unix like OS.

Furthermore, the installation requires:

- OCaml 3.09.2
- TK/lablTK (for the graphical interface)
- graphviz (to handle .dot documents)
- an X terminal
- Simplx (Version 3.272c).

## **Compilation**

To install **complx** (and also **simplx**) go into the directory plectix/plx-engine:  
**cd plectix/plx-engine**

Then, you can either compile the light version (i.e. without the graphical interface (LabelTK is not required)):

`make`

Or the full version

`make full.`

Binaries are in the directory `bin/`.

To copy them in `/usr/bin` :

`make install.`

In case, you do not have root privilege, please use the following instead:

`make LOCAL_DIR="/home/bin" install_in_local .`

## Usage

In the light version, options are passed in the command line:

`complex file [options]`

In the full version, one can either use command line options:

`complex file [options]`

or launch the graphical interface.

`complex`

In both case, the (updated) list of options can be obtained with the following command:

`complex --help`

## Graphical interface

The graphical interface is just a user-friendly way to set command line options.

- 1) Each command line option may be filled in the graphical interface;  
Some options are meta options that triggers a list of options;
- 2) Command line options are organized by Sections;
- 3) Some buttons allow:
  - to toggle between a normal and an expert mode (in normal mode some options are hidden);
  - to select another section;
  - to browse your file system to upload a file (from now the behavior is only defined whether only one file is downloaded);
  - to quit;
  - to reset options;
  - to load a config file;
  - to save a config file;
  - to launch the complex app.
- 4) When launched:
  - the current setting is stored,
  - the command line is computed,

- the command line is output on the standard output,
- the app is launched.

## Command-line options

We describe here end-users options.

Some options that are restricted to the usage of developpers and experts are not described here.

### General options

**--help**

Verbose help

**-h**

Short help

**--gui**

GUI to select

**--(no-)expert**

Expert mode (more options (not described in this API))

### Actions

The following options set what is computed by complx.

Some computations require others, as a consequence unrequested computation may be performed.

### meta-options

**--do-all**

set all following booleans to **true**

**--reset-all**

set all following booleans to **false**

### regular options

**--(no-)compute-local-views** (default: **enabled**)

compute reachability analysis

**--(no-)enumerate-complexes** (default: **enabled**)

enumerate complexes

--(no-)build-influence-map (default: **enabled**)  
construct influence maps

--(no-)compute-qualitative-compression (default: **enabled**)  
simplify the rules

--(no-)compute-quantitative-compression (default: **enabled**)  
simplify the rules

--(no-)do-low-res-contact-map (default: **enabled**)  
compute the low resolution (aka syntactic) contact map

--(no-)do-high-res-contact-map (default: **enabled**)  
compute the high resolution contact map

--(no-)do-ODE (default: **disabled**)  
compute the ODE system

--(no-)do-refine-to-force-cycles (default: **disabled**)  
refine the system to avoid the formation of polymers.

--(no-)do-compute-dag-refinement-relation (default: **enabled**)  
compute the DAG of refinement relation in order to navigate between refinements of a same rule.

--(no-)do-compute-maximal-refinement-relation (default: **enabled**)  
compute the relation between each rule  $r$  and the most abstract rule  $r'$  such that  $r$  is a refinement of  $r'$ .

--(no-)do-marshalling (default: **enabled**)  
dump marshallization

--(no-)do-HTML (default: **enabled**)  
launch HTML desktop

--(no-)do-XML (default: **enabled**)  
dump XML session

## Input file

--input-marshalling <name> (default: **disabled**)  
Start computation from this marshallized state

--focus-on <name> (default: **disabled**)  
This option takes a ASCII files that contains some Kappa rules.  
The low resolution (syntactic) contact map will only provides information around the agents that are mentioned in these rules.  
If the option is not used, the full contact map is computed.

--refine-only-these-rules <name> (default: **disabled**)  
This option takes a ASCII files that contains some Kappa rules.  
We only compute the refinement for these rules.

## Output

Output options are used to redirect the result of computations. They do not launch computation by themselves (i.e. they are useless if they require a computation that has not been done).

### meta-options

#### `--output-scheme <value>`

This meta options generate all following options using the argument as common prefix. More precisely:

`complx egfr.ka --output-scheme egfr`

is a short cut for:

`complx egfr.ka`

- `--output-ODE-contact egfr_plx_ODE_contact.dot`
- `--output-ODE-mathematica egfr_plx_ODE_system.nb`
- `--output-ODE-matlab egfr_plx_ODE_system.m`
- `--output-ODE-alphabet egfr_plx_ODE_alphabet`
- `--output-ODE-obs egfr_plx_ODE_obs`
- `--output-marshalling egfr_plx.marshalling`
- `--output-influence-map-txt egfr_plx_influence_map.txt`
- `--output-influence-map-dot egfr_plx_influence_map.txt`
- `--output-quantitative-compression egfr_plx_compressed_quantitative.ka`
- `--output-qualitative-compression egfr_plx_compressed_qualitative.ka`
- `--output-low-res-contact-map-dot egfr_plx_low_res_contact.dot`
- `--output-low-res-contact-map-ps egfr_plx_low_res_contact.ps`
- `--output-low-res-contact-map-jpg egfr_plx_low_res_contact.jpg`
- `--output-low-res-contact-map-txt egfr_plx_low_res_contact.txt`
- `--output-high-res-contact-map-dot egfr_plx_high_res_contact.dot`
- `--output-high-res-contact-map-ps egfr_plx_high_res_contact.ps`
- `--output-high-res-contact-map-jpg egfr_plx_high_res_contact.jpg`
- `--output-high-res-contact-map-txt egfr_plx_high_res_contact.txt`
- `--output-intermediate-encoding egfr_plx_ckappa.txt";`
- `--output-gathered-intermediate-encoding egfr_plx_ckappa_gathered.txt";`
- `--output-pretty-qualitative-compression egfr_plx_compressed_qualitative.txt`
- `--output-pretty-quantitative-compression egfr_plx_compressed_quantitative.txt`
- `--output-boolean-encoding egfr_plx_boolean_encoding.txt`
- `--output-gathered-boolean-encoding egfr_plx_boolean_encoding_gathered.txt`
- `--output-pack-constraints egfr_plx_site_constraints.txt`
- `--output-reachable-complexes egfr_plx_reachables.txt`
- `--output-specie-map egfr_plx_specie_map.txt`
- `--output-dag-ref-dot egfr_plx_dag_refinement_relation.dot`
- `--output-dag-ref-jpg egfr_plx_dag_refinement_relation.jpg`
- `--output-maximal-ref-dot egfr_plx_maximal_refinement_relation.dot`
- `--output-maximal-ref-jpg egfr_plx_maximal_refinement_relation.jpg`
- `--output-xml egfr_plx.xml`
- `--output-html egfr_plx.html`
- `--output-refined-system egfr_plx_refinement.ka`

### regular options

`--output-quantitative-compression <name>` (default: `disabled`)  
write the compressed quantitative compression in a .ka format

`--output-qualitative-compression <name>` (default: `disabled`)  
write the compressed qualitative compression in a .ka format

`--output-pretty-qualitative-compression <name>` (default: `disabled`)  
write the pretty compressed qualitative compression

`--output-pretty-quantitative-compression <name>` (default: `disabled`)  
write the pretty compressed quantitative compression

`--output-refined-system <name>` (default: `disabled`)  
write the result of rule refinement

`--output-influence-map-txt <name>` (default: `disabled`)  
write the causality map with .txt format

`--output-influence-map-dot <name>` (default: `disabled`)  
write the causality map with .dot format

`--output-low-res-contact-map-dot <name>` (default: `disabled`)  
write the low resolution (aka syntactic) contact map with a .dot format

`--output-low-res-contact-map-ps <name>` (default: `disabled`)  
write the low resolution (aka syntactic) contact map with a .ps format

`--output-low-res-contact-map-jpg <name>` (default: `disabled`)  
write the low resolution (aka syntactic) contact map with a .jpg format

`--output-high-res-contact-map-txt <name>` (default: `disabled`)  
write the high resolution contact map with a .txt format

`--output-high-res-contact-map-dot <name>` (default: `disabled`)  
write the high resolution contact map with a .dot format

`--output-high-res-contact-map-ps <name>` (default: `disabled`)  
write the high resolution contact map with a .ps format

`--output-high-res-contact-map-jpg <name>` (default: `disabled`)  
write the high resolution contact map with a .jpg format

`--output-high-res-contact-map-txt <name>` (default: `disabled`)  
write the high resolution contact map with a .txt format

`--output-ODE-mathematica <name>` (default: `disabled`)  
write the ODE in mathematica format

`--output-ODE-matlab <name>` (default: `disabled`)  
write the ODE in matlab format  
also create subsidiary files of the form `r<int>v<int>.m`

`--output-ODE-alphabet <name>` (default: `disabled`)  
write the meaning of the ODE variables as a list of equation between numbered variable

and kappa observables

- output-ODE-obs <name>** (default: disabled)  
write the meaning of the ODE variables as a list of observables  
this file can be appended to the kappa file in order to perform simulations
- output-pack-constraints <name>** (default: disabled)  
output the constraints used to define packs for the reachability analysis
- output-reachable-complexes <name>** (default: disabled)  
write the reachable species (or just their number) in a file
- output-specie-map <name>** (default: disabled)  
write the specie map in a file
- output-dag-ref-dot** (default: disabled)  
contains the DAG that relates rules and their refinement in a dot file
- output-dag-ref-jpg** (default: disabled)  
contains the DAG that relates rules and their refinement in a jpg file
- output-maximal-ref-dot** (default: disabled)  
contains the relation between rules and their most abstract instances in a dot file
- output-maximal-ref-jpg** (default: disabled)  
contains the relation between rules and their most abstract instances in a jpg file
- output-xml <name>** (default: disabled)  
write any computed (in this session or in previous sessions) into an xml file
- output-html <name>** (default: disabled)  
write any output results in a html file
- output-marshalling <name>** (default: disabled)  
marshallize the computation state

## Debug

- (no-)trace\_iteration\_number** (default: enabled)  
Dump rule Id before interpreting it
- (no-)version** (default: disabled)  
to dump version number

## Compression

`--(no-)compute-qualitative-compression` (default: `enabled`)  
simplify the rules

`--(no-)compute-quantitative-compression` (default: `enabled`)  
simplify the rules

`--output-quantitative-compression <name>` (default: `disabled`)  
write the compressed quantitative compression in a .ka format

`--output-qualitative-compression <name>` (default: `disabled`)  
write the compressed qualitative compression in a .ka format

`--output-pretty-qualitative-compression <name>` (default: `disabled`)  
write the pretty compressed qualitative compression

`--max-lens-size <int>` (default: `5`)  
not compress rules with more connected components in their left hand side

`--(no-)comment-in-compression` (default: `enabled`)  
put(or remove) the initial kappa file in comments in the .ka output

`--(no-)dump-concrete-rules` (default: `enabled`)  
dump rules before compression in the pretty printed output

`--(no-)dump-abstract-rules` (default: `enabled`)  
dump rules after compression in the pretty printed output

## Concretization

`--(no-)enumerate-complexes` (default: `disabled`)  
enumerate complexes even if there are too numerous

`--(no-)dump-all-complexes` (default: `enabled`)  
display complexes, otherwise just show their number

`--output-reachable-complexes <name>` (default: `disabled`)  
write reachable species (or just their number) in a file

`--(no-)sort-complexes` (default: `enabled`)  
to sort complexes before dumping them

`--complex-limit <int>` (default: `1000000`)  
only enumerate complexes when there are less complexes or the option `--enumerate-complexes` is triggered

## Contact map

`--(no-)do-low-res-contact-map` (default: `enabled`)



compute the low resolution (aka syntactic) contact map

**--(no-)do-high-res-contact-map** (default: **enabled**)  
compute the high resolution contact map

**--focus-on** (default: **disabled**)  
narrow the syntactic contact map around the rules in these file

**--output-low-res-contact-map-dot <name>** (default: **disabled**)  
write the low resolution contact map with a .dot format

**--output-low-res-contact-map-ps <name>** (default: **disabled**)  
write the low resolution contact map with a .ps format

**--output-low-res-contact-map-jpg <name>** (default: **disabled**)  
write the low resolution contact map with a .jpg format

**--output-low-res-contact-map-txt <name>** (default: **disabled**)  
write the low resolution contact map with a .txt format

**--output-high-res-contact-map-dot <name>** (default: **disabled**)  
write the high resolution contact map with a .dot format

**--output-high-res-contact-map-ps <name>** (default: **disabled**)  
write the high resolution contact map with a .ps format

**--output-high-res-contact-map-jpg <name>** (default: **disabled**)  
write the high resolution contact map with a .jpg format

**--output-high-res-contact-map-txt <name>** (default: **disabled**)  
write the high resolution contact map with a .txt format

**--(no-)find-cycles** (default: **disabled**)  
computes the cycles in the contact map

**--(no-)find-connected-components** (default: **disabled**)  
computes the connected components in the contact map

**--boolean-site-color <name>** (default: **yellow**)  
color of sites that cannot be bound

**--boundable-site-color <name>** (default: **cyan**)  
color of sites that cannot be marked

**--both-site-color <name>** (default: **green**)  
color of sites that can be both marked and bound

**--agent0 <name>** (default: **floralwhite**)  
color of agent that have no site

**--agent1 <name>** (default: **skyblue1**)  
color of agent that have one site

`--agent2 <name>` (default: `deeppink`)  
color of agent that have two sites

`--agent3 <name>` (default: `darkorchid`)  
color of agent that have three sites

`--agentn <name>` (default: `red`)  
color of agent that have many sites

## External applications

`--html-browser <name>` (default: `firefox`)  
comand line for launching an html browser

## HTML

`--(no-)do-HTML` (default: `enabled`)  
Launch HTML desktop

`--output-html <name>` (default: `disabled`)  
write an html file

`--html-browser <name>` (default: `firefox`)  
comand line for launching an html browser

## Influence map

`--(no-)build-influence-map` (default: `enabled`)  
construct influence maps

`--output-influence-map-txt <name>` (default: `disabled`)  
write the causality map with .txt format

`--output-influence-map-dot <name>` (default: `disabled`)  
write the causality map with .dot format

`--(no-)wake-up-map` (default: `enabled`)  
build wake up relations

`--(no-)inhibition-map` (default: `enabled`)  
build inhibition map

## Marshalling

`--(no-)do-marshalling` (default: `enabled`)  
Dump mashallization

**--input-marshalling <name>** (default: disabled)

Start computation from this marshallized state

**--output-marshalling <name>** (default: disabled)

marshallize the computation state

## Memory usage

**--memory-limit <int>** (default: 0)

Limit the memory usage in Mb, if 0 then there is no limitation

Any value greater than 4Gb will be considered as 4Gb

## ODE

**--(no-)do-ODE** (default: disabled)

compute the ODE system

**--output-ODE-mathematica <name>** (default: disabled)

write the ODE in mathematica format

**--output-ODE-matlab <name>** (default: disabled)

write the ODE in matlab format

also create subsidiary files of the form `r<int>v<int>.m`

**--output-ODE-alphabet <name>** (default: disabled)

write the meaning of the ODE variables as a list of equation between numbered variable and kappa observables

**--output-ODE-obs <name>** (default: disabled)

write the meaning of the ODE variables as a list of observables

this file can be appended to the kappa file in order to perform simulations

**--initial-time <float>** (default: 0.000000)

initial time for ODE integration

**--final-time <float>** (default: 1.000000)

final time for ODE integration

**--epsilon-value <float>** (default: 0.000010)

smallest float greater than 0.

**--(no-)flat-mode** (default: disabled)

compute the flat ODE system instead of the compressed one

## Polymers prevention

`--(no-)do-refine-to-force-cycles` (default: `disabled`)  
refine the system to avoid the formation of polymers.

`--output-refined-system <name>` (default: `disabled`)  
write the refined system in the given file

`--cycles-depth <int>` (default: `10`)  
only prevents polymeres for cycles bigger than the argument

`--(no-)cycle-detection-mode` (default: `disabled`)  
show warning, but not refine rule

`--(no-)use-constraints-to-refine` (default: `disabled`)  
use constraints to avoid combinatorial blow up

`--refine-only-these-rules` (default: `disabled`)  
refine only these rules

`--kynetic-amplifier <float>` (default: `1.000000`)  
multiplifying factor for the kynetics of rules that close cycles

## Reachability analysis

`--(no-)compute-local-views` (default: `enabled`)  
compute reachability analysis

`--output-pack-constraints <name>` (default: `disabled`)  
dump constraints among sites in a file

`--output-reachable-complexes <name>` (default: `disabled`)  
write the reachable states in a file

`--output-specie-map <name>` (default: `disabled`)  
write the specie map in a file

`--(no-)auto-packs` (default: `enabled`)  
use automatic packing

`--(no-)abstract-away-relations-between-sites` (default: `disabled`)  
Abstract away any relation between sites

`--(no-)abstract-away-relations-between-phosphorilation-and-binding` (default: `disabled`)  
to abstract away any relation between phosphorilation and binding

`--(no-)abstract-away-information-about-phosphorilation` (default: `disabled`)  
to abstract away information about binding

`--(no-)abstract-away-information-about-binding` (default: `disabled`)

to abstract away information about phosphorylation

## Semantics

`--(no-)forward` (default: `disabled`)  
ignore reciprocal reactions

## Standard output

`--(no-)dump-rule-iteration` (default: `enabled`)  
to dump the number of rules when iterating

`--(no-)dump-iteration-number` (default: `enabled`)  
to dump whole iteration number

## XML

`--(no-)do-XML` (default: `enabled`)  
dump XML session

`--output-xml <name>` (default: `disabled`)  
write an xml file

## Input formats

Complx can accept a kappa file:  
`complx models/egfr/egfr.ka`  
The grammar of kappa file is given in the Simplx API.

When the option `--input-marshalling` is used, complx restore the state of a previous session, and perform further computation according to command line options.

The options `--focus-on <name>` and `--refine-only-these-rules <name>` input some ASCII files containing Kappa rules.  
These rules are used to narrow the contact map or the refinement algorithm to a subset of rules

## Output formats

The following line:

```
complx models/egfr/egfr.ka --output-scheme models/egfr/egfr
```

produces many output files:

`models/egfr/egfr_plx_boolean_encoding_gathered.txt`

this file is a boolean representation of the transition system

in this file, rules are gathered when they perform the same sequence of actions

`models/egfr/egfr_plx_boolean_encoding.txt`

this file is a boolean representation of the transition system.

- `models/egfr/egfr_plx_ckappa_gathered.txt`

this file is a description of the transition system in a precompiled form

in this file, rules are gathered when they perform the same sequence of actions

- `models/egfr/egfr_plx_ckappa.txt`

this file is a description of the transition system in a precompiled form.

- `models/egfr/egfr_plx_compressed_qualitative.ka`

this file is a kappa file;

some rules have been commented and replaced with simple ones;

some rules have been commented because they are covered by other;

some rules are commented because they have been detected to be unapplicable;

the new transition system is equivalent with respect to qualitative properties

(it may break kinetics).

- `models/egfr/egfr_plx_compressed_qualitative.txt`

dump the compression in a pretty way.

the new transition system is equivalent with respect to qualitative properties

(it may break kinetics).

- `models/egfr/egfr_plx_compressed_quantitative.ka`

this file is a kappa file;

some rules have been commented and replaced with simple ones;

some rules have been commented because they are covered by other;

some rules are commented because they have been detected to be unapplicable;

the new transition system is equivalent whatever the kinetic parameters are.

- `models/egfr/egfr_plx_compressed_quantitative.txt`

dump the compression in a pretty way.

the new transition system is equivalent whatever the kinetic parameters are.

- `models/egfr/egfr_plx_high_res_contact.dot`

this file contains a description of the high resolution contact map in a dot file;  
the following instruction:  
`dot -Tps models/egfr/egfr_plx_high_res_contact.dot -o models/egfr/  
egfr_plx_high_res_contact.ps`  
generates a postscript file.

- [models/egfr/egfr\\_plx\\_high\\_res\\_contact.jpg](#)  
this file is a jpg image of the high resolution contact map.

- [models/egfr/egfr\\_plx\\_high\\_res\\_contact.ps](#)  
this file is a ps image of the high resolution contact map.

- [models/egfr/egfr\\_plx\\_high\\_res\\_contact.txt](#)  
this file contains a text description of the low resolution contact map.

- [models/egfr/egfr\\_plx.html](#)  
this file contains a html desktop.

- [models/egfr/egfr\\_plx\\_influence\\_map.txt](#)  
this file is a text description of the influence map;  
it may be an overapproximation (i.e. some edges are false positive).

- [models/egfr/egfr\\_plx\\_low\\_res\\_contact.dot](#)  
this file contains a description of the low resolution contact map in a dot file;  
the following instruction:  
`dot -Tps models/egfr/egfr_plx_low_res_contact.dot -o models/egfr/  
egfr_plx_low_res_contact.ps`  
generates a postscript file.

- [models/egfr/egfr\\_plx\\_low\\_res\\_contact.jpg](#)  
this file is a jpg image of the low resolution contact map.

- [models/egfr/egfr\\_plx\\_low\\_res\\_contact.ps](#)  
this file is a ps image of the low resolution contact map.

- [models/egfr/egfr\\_plx\\_low\\_res\\_contact.txt](#)  
this file contains a text description of the low resolution contact map.

- [models/egfr/egfr\\_plx.marshalling](#)  
this file contains the marshallization of the current session.

- [models/egfr/egfr\\_plx\\_ODE\\_alphabet](#)  
this file contains the meaning of the ODE variables.

- [models/egfr/egfr\\_plx\\_ODE\\_contact.dot](#)

this file contains the contact map with dotted edges  
dotted edges are link that are ignored when computing the ODE

- [models/egfr/egfr\\_plx\\_ODE\\_obs](#)

this file contains the meaning of the ODE variables as kappa observable,  
it can be appended to a kappa file for further simulation

- [models/egfr/egfr\\_plx\\_ODE\\_system.m](#)

this file contains the ODE in matlab format  
it uses subsidiary files of the form [models/egfr/<int>v<int.mr](#)

- [models/egfr/egfr\\_plx\\_ODE\\_system.nb](#)

this file contains the ODE in mathematica format

- [models/egfr/egfr\\_plx\\_reachables.txt](#)

this file contains a description of all reachable complexes;  
first some acyclic complexes are given;  
then some partial complexes to generate others are given;  
they all satisfy Kappa-syntax, but semi-links may contain more information:  
 $A(x!B.y)$  means that the site  $x$  is bound to the site  $y$  of an agent  $B$

An upper bound to the number of complexes is given when it is possible.

- [models/egfr/egfr\\_plx\\_refinement.ka](#)

this file contains a refinement of rules that are given in arguments, so that the transformed  
system cannot build polymers  
rules are given in a kappa-friendly grammar

- [models/egfr/egfr\\_plx\\_site\\_constraints.txt](#)

this file contains a description of constraints among sites.  
they all satisfy Kappa-syntax, but semi-links may contain more information:  
 $A(x!B.y)$  means that the site  $x$  is bound to the site  $y$  of an agent  $B$

- [models/egfr/egfr\\_plx\\_specie\\_map.txt](#)

this file contains a description of all local views;  
they all satisfy Kappa-syntax, but semi-links may contain more information:  
 $A(x!B.y)$  means that the site  $x$  is bound to the site  $y$  of an agent  $B$

- [models/egfr/egfr\\_plx.xml](#)

this file contains a XML description of the session.



- `models/egfr/egfr_plx_dag_refinement_relation.dot`  
this file contains a dot description of the refinement relation between rules
- `models/egfr/egfr_plx_dag_refinement_relation.jpg`  
this file contains a jpg description of the refinement relation between rules
- `models/egfr/egfr_plx_maximal_refinement_relation.dot`  
this file contains a dot description of the refinement relation between each rule and their most abstract instance
- `models/egfr/egfr_plx_maximal_refinement_relation.jpg`  
this file contains a jpg description of the refinement relation between each rule and their most abstract instance

## Internal representation

The internal representation signature is described in the file [frontend/pb\\_sig.ml](#). Some external applications may use this data-structures and update it by using the pipeline methods.

Here the signature of the data-structures (subsidiary types are declared in [frontend/pb\\_sig.ml](#)).

```
type 'a pb =
{
  options: options option;
  this field describes analysis options
  quarks: bool;
  this field contains quark information to compute the influence map
  txt_lines: Comment_sig.commented_line list option;
  this field contains the structure of the kappa file (with comments)
  simplx_encoding: (Rule.t list * Solution.t) option;
  this field contains the output of simplx parser
  first_encoding: 'a cpb option;
  intermediate_encoding: 'a cpb option;
  ckappa encoding (rules are isolated)
  it also contains the low resolution contact map
  gathered_intermediate_encoding: 'a cpb option;
  ckappa encoding (rules are gathered)
  boolean_encoding: 'a boolean_encoding option;
  boolean encoding (rules are isolated)
  gathered_boolean_encoding: 'a boolean_encoding option;
  boolean encoding (rules are gathered)
  packs: string list list StringMap.t option;
  packing definition
  reachability_analysis: ((string*'a) list StringMap.t) option;
```

sub local views (abstract representation)  
 contact\_map:contact\_map option ;  
 high resolution contact map  
 bdd\_sub\_view: 'a internalsubviews option ;  
 sub local views (bdd abstract representation)  
 bdd\_false:'a internalsubviews option ;  
 internal representation for missing agents (bdd abstract representation)  
 concretization:(string \* (bool \* pretty StringMap.t) \* pretty\_fun) list list option ;  
 list of reachable complexes (abstract encoding)  
 reachable\_complexes: (string intinf \* (string list list \* int) list \* (string list list \* int) list)  
 option ;  
 list of reachable complexes (numbers and pretty printed complexes)  
 wake\_up\_map:influence\_map option ;  
 low resolution influence map (positive)  
 inhibition\_map:influence\_map option ;  
 low resolution influence map (negative)  
 pretty\_map: pretty StringMap.t StringMap.t ;  
 data to pretty print local views and complexes  
 qualitative\_compression: compression option ;  
 compression result  
 quantitative\_compression: compression option ;  
 compression result  
 unreachable\_rules: RuleIdSet.t option ;  
 dead rules  
 rule\_warning: string list RuleIdMap.t ;  
 a list of warning associated to rules  
 specie\_map:(string \* string list list) list option ;  
 local views  
 pack\_value:(string \* (string list \* string list list) list) list option ;  
 sub local views (pretty printed)  
 n\_complex:string intinf option ;  
 number of complexes  
 n\_rules:int option ;  
 number of rules  
 n\_classes:int option ;  
 number of classes of rules (gathered by sequence of actions)  
 potential\_cycles:(string\*string) list list option ;  
 list of any potential cycle in the contact map  
 connected\_components:string list list option ;  
 list of any connected component in the contact map  
 refined\_system:'a boolean\_encoding IntMap.t ;  
 maps each rule to the internal (boolean) representation of its refinement  
 drawers:drawers option ;  
 contains the relations between contact map items and rules  
 refinement\_relation\_closure:IntSet.t IntMap.t list option ;  
 contains the closure of the relation between rules and their refinements  
 first partitionned into a list of action sequences, and for each action sequence the relation  
 refinement\_relation\_dag:IntSet.t IntMap.t list option ;  
 contains the relation between rules and their most concrete refinements  
 first partitionned into a list of action sequences, and for each action sequence the relation  
 refinement\_relation\_maximale:IntSet.t IntMap.t list option ;  
 contains the relation between rules and their most abstract refinements  
 first partitionned into a list of action sequences, and for each action sequence the relation

```
}
```

## Pipeline methods

The pipeline provides some methods to progress in the computation.  
Each method fill fields in the data structure.  
Built-in dependences help methods in computing required fields before making its own computation.

```
type prefix = (string*(string list)) (the first component should be printed before progress  
line status in the standard output, the second one is a calling stack for handling exceptions)  
type file_name = string  
type simplx_encoding = (Rule.t list * Solution.t) option  
type 'a intermediate_encoding = 'a Pb_sig.cpb option  
type 'a boolean_encoding = 'a Pb_sig.boolean_encoding option  
type 'a internal_encoding = 'a Pb_sig.pb option  
type log = (string*float) list  
type message = string list  
type output_channel = log*message  
type influence_map = IntSet.t IntMap.t * IntSet.t IntMap.t
```

```
type 'a step = 'a internal_encoding -> output_channel -> 'a internal_encoding *  
output_channel
```

A standard method takes two arguments:

- the current step of computation
- a message channel

and returns two values:

- the updated step of computation
- the updtated channel.

```
type ('a,'b) step_with_output = 'a internal_encoding -> output_channel -> 'b * 'a  
internal_encoding * output_channel
```

A standard method takes two arguments:

- the current step of computation
- a message channel

and returns three values:

- a result
- the updated step of computation
- the updtated channel.

```
type 'a pipeline =  
{
```

```
  reset:'a step;
```

to remove any obsolete information (due to analysis option modification)

## message handlers

`dump_version: prefix -> output_channel -> output_channel;`  
to add the version number in the output channel

`print_footpage: prefix -> output_channel -> output_channel;`  
to dump the footpage

`print_headpage: prefix -> output_channel -> output_channel;`  
to dump the headpage

`empty_channel: output_channel;`  
to build an empty channel

`log_time: prefix -> string -> output_channel -> output_channel;`  
to log a computation step in a channel

`add_message: prefix -> string -> output_channel -> output_channel;`  
to add a message in a channel

`print_channel: prefix -> output_channel -> unit;`  
to dump the content of a channel

## other methods

`parse_file: file_name -> prefix -> output_channel -> 'a  
internal_encoding*output_channel;`  
to use parse a file thanks to simplx

`parse_line_by_line: file_name -> 'a step ;`  
to parse a file for complx backend

`unmarshallize: file_name -> output_channel -> 'a internal_encoding*output_channel;`  
to restore a marshallized computation step

`marshallize: file_name -> 'a step;`  
to save a computation step

`build_pb: simplx_encoding -> 'a internal_encoding;`  
to translate simplx compilation output in an internal representation

`translate: 'a step;`  
to translate simplx computation encoding into ckappa encoding

`dump_ckappa: file_name -> compile -> 'a step;`  
to dump the ckappa encoding; when the second argument is "Smashed", rules are gathered in equivalence classes

`compile: compile -> 'a step;`  
to convert ckappa encoding into boolean encoding; when the second argument is "Smashed", rules are gathered in equivalence classes

`dump_boolean_encoding: file_name -> compile -> 'a step;`  
to dump the boolean encoding; when the second argument is "Smashed", rules are gathered in equivalence classes

`build_contact: precision -> 'a step;`  
to build the contact map

`find_potential_cycles: precision -> 'a step;`  
detect the set of cycles in the contact map,  
the first argument can be either `Low`, or `High`  
in low precision, we smash all sites

`find_connected_components: precision -> 'a step;`  
detect the set of connected components in the contact map  
the first argument can be either `Low`, or `High`  
in low precision, we smash all sites

`reachability_analysis: 'a step;`  
to compute local views

`refine_subviews: 'a step;`  
take into account the computation of subviews

`refine_views: 'a step;`  
gather subviews into views

`dump_local_views: file_name -> 'a step;`  
to dump local views

`dump_packs_constraints: file_name -> 'a step;`  
to dump sub-local views

`dump_contact_map_txt: precision -> ile_name -> 'a step;`  
to dump the contact map in txt format

`dump_contact_map_dot: precision -> file_name -> 'a step;`  
to dump the contact map in dot format

`dump_contact_map_ps: precision -> file_name -> 'a step;`  
to dump the contact map in ps format

`dump_contact_map_jpg: precision -> file_name -> 'a step;`  
to dump the contact map in jpg format

`quarkification: 'a step;`  
to compute the quark encoding

`count_complexes: 'a step;`  
to count reachable complexes without enumerating them

`build_influence_map: file_name -> file_name -> 'a step;`  
to build the influence map

`build_compression: compression_mode -> file_name -> file_name -> 'a step;`  
to compute the compression

`build_enumeration: file_name -> 'a step;`  
to enumerate reachable complexes

`dump_session: file_name -> 'a step;`  
to dump the XML output

`dump_html_output: file_name -> 'a step;`  
to compute the HTML desktop

`good_vertice: file_name -> prefix -> output_channel -> StringSet.t option *`  
`output_channel;`  
compute the set of agents that occurs in a list of rules

`template: file_name -> file_name -> file_name -> file_name -> file_name -> file_name`  
`-> file_name -> file_name -> 'a step;`  
compute the ODE

`dump_potential_cycles: precision -> 'a step;`  
dump the potential cycles on the standard output  
if precision = Low, sites are smashed.

`refine_system_to_avoid_polymers: file_name -> simplex_encoding option ->`  
`Avoid_polymere.mode -> int option -> float -> ('a,('a rule_class list)) step_with_output;`  
refine some rules to prevent polymerization

`build_drawers: 'a step;`  
build the relations between items in the contact map and the rules

`compute_refinement_relation_maximal: 'a step;`  
build the relations between rules and their most abstract instance

`export_refinement_relation_maximal: ('a,Rule.t list option) step_with_output;`  
export the result of the relation between rules and their most abstract instance in the list  
of rules of simplex

`compute_refinement_relation_dag: 'a step;`  
build the DAG between rules and their refinements

`compute_refinement_relation_closure: 'a step;`  
build all the relations between rules and their refinements

`dump_maximal_refinement_relation: file_name -> file_name -> 'a step;`  
dump the relations between rules and their most abstract instance, the first file is the dot  
file, the second one is the jpg file

`dump_refinement_relation_dag: file_name -> file_name -> a step;`  
build the DAG between rules and their refinements, the first file is the dot file, the second  
one is the jpg file

`save_options: 'a step`  
to remember which options have been used

}

## Module tree

### **complx\_rep/:**

<code>abstract_expr</code>	abstract domain for expressions description
<code>backend</code>	
<code>compressor</code>	compression modules
<code>config</code>	config files
<code>cyclical_complexes</code>	detection of potential cycles and automatic refinements to avoid them
<code>data_structures</code>	
<code>expr</code>	expression description
<code>frontend</code>	
<code>influence_map</code>	influence map construction
<code>lib</code>	external libraries
<code>main.ml</code>	usual pipeline
<code>Makefile</code>	
<code>ODE</code>	ODE synthesis
<code>pipeline</code>	pipeline modules
<code>reachability</code>	reachability analysis modules
<code>refinements</code>	detection of refinement relation between rules
<code>share</code>	
<code>tools</code>	tools modules
<code>vars</code>	variable description

### **complx\_rep/abstract\_expr:**

<code>abstract_expr_sig.ml</code>	signature for abstract expression modules
<code>bdd.ml</code>	binary decision diagram implementation module
<code>partition.ml</code>	partitioning functor
<code>rough.ml</code>	propositional logic implementation module

### **complx\_rep/backend:**

<code>contact_map</code>	dump the contact map
<code>HTML</code>	
<code>parse_comment</code>	(re)parse the kappa file to insert comments
<code>XML</code>	

### **complx\_rep/backend/contact\_map:**

<code>acyclicity.ml</code>	check whether they might be polymers according to the contact map
----------------------------	-------------------------------------------------------------------

[connected\\_components.ml](#) compute the connected components in the contact map  
[fin\\_cycles.ml](#) enumerate the cycles according to a contact map  
[neighborhood.ml](#) restrict a contact map around some agents  
[output\\_contact\\_map.ml](#) output the contact map in various format

## **complx\_rep/backend/HTML:**

[html.ml](#) generate the HTML desktop

## **complx\_rep/backend/parse\_comment:**

[comment\\_sig.ml](#) result signature  
[lexeur.mll](#) alphabet  
[yacc.mli2](#) grammar signature  
[yacc.mly](#) grammar

## **complx\_rep/backend/XML:**

[xml.ml](#) generate the XML data-structure

## **complx\_rep/compressor:**

[compressor.ml](#) library to compress rule system

## **complx\_rep/config:**

[config\\_complx.ml](#) default values, option list and parsing command line option

## **complx\_rep/data\_structures:**

[big\\_array.ml](#) to use array with size < max\_int  
[data\\_structures.ml](#) data structures (maps, sets)  
[hash.ml](#) hashtables implementations

## **complx\_rep/expr:**

[expr.ml](#) module for boolean expressions  
[kleenean\\_expr.ml](#) module for three value-logic expressions



### **complx\_rep/frontend:**

<a href="#">cbng.ml</a>	translation from ckappa to boolean encoding
<a href="#">cbng_sig.ml</a>	ckappa signatures
<a href="#">pb_sig.ml</a>	boolean encoding signature
<a href="#">translate.ml</a>	translation from simplx encoding to ckappa.

### **complx\_rep/influence\_map:**

<a href="#">influence_map.ml</a>	functions to build the flow map
<a href="#">quarkification.ml</a>	build the quark encoding

### **complx\_rep/lib:**

<a href="#">full</a>	version for Labltk
<a href="#">light</a>	version without Labltk
<a href="#">with_key</a>	version with key-protection
<a href="#">without_key</a>	version without key-protection
<a href="#">ml_wordexp.c</a>	Antoine's library
<a href="#">superarg.ml</a>	Antoine's library (for command line options)
<a href="#">wordexp.ml</a>	Antoine's library

### **complx\_rep/lib/full:**

<a href="#">superargTk.ml</a>	Antoine's library
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### **complx\_rep/lib/light:**

<a href="#">superargTk.ml</a>	Antoine's library (patched to compile without LablTk)
-------------------------------	-------------------------------------------------------

### **complx\_rep/lib/with\_key:**

<a href="#">key.ml</a>	Deal with key protection
------------------------	--------------------------

### **complx\_rep/lib/without\_key:**

<a href="#">key.ml</a>	Avoid key protection
------------------------	----------------------

## **complx\_rep/ODE:**

<a href="#">annotated_contact_map.ml</a>	Primitives to compute the annotated contact map
<a href="#">fragments.ml</a>	Primitives to handle with fragments
<a href="#">ode_computation.ml</a>	Compute the projection of ODE over frgements
<a href="#">ode_print.ml</a>	Pretty-printing primitives
<a href="#">ode_print_sig.ml</a>	Type definition for pretty printing primitives
<a href="#">views.ml</a>	Primitives to handle with views

## **complx\_rep/pipeline:**

<a href="#">pipeline.ml</a>	pipeline definition
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## **complx\_rep/reachability:**

<a href="#">concretization.ml</a>	complex enumeration
<a href="#">contact_map.ml</a>	contact map signature
<a href="#">count_complexes.ml</a>	count complexes without enumerating them
<a href="#">packing.ml</a>	automatic packing algorithm
<a href="#">reachability.ml</a>	reachability analysis iterator

## **complx\_rep/refinements:**

<a href="#">refinements.ml</a>	primitives to deal with refinement relation between rules
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## **complx\_rep/share:**

<a href="#">share.ml</a>
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## **complx\_rep/tools:**

<a href="#">array_ext.ml</a>	potentially infinite array (for simplx)
<a href="#">error_handler.ml</a>	primitives to catch exceptions and dump XML output
<a href="#">exceptions.ml</a>	exception declaration
<a href="#">map2.ml</a>	patched map module (for binary operators)
<a href="#">map_random.ml</a>	patched map module (for random choice)
<a href="#">map_random.ml</a>	patched map module (with optimized sharing)
<a href="#">memory_usage.ml</a>	track memory usage and launch exception
<a href="#">tools2.ml</a>	various functions
<a href="#">tools.ml</a>	various functions

[unbounded\\_array.ml](#) potentially infinite array (for complx)

## complx\_rep/vars:

[var.ml](#) variable description

## Bug report

The errors are stacked LOG file of the XML output.

For instance:

```
<Log>
<Entry Type="ERROR" Application="Complx" Method="reachability_analysis"
Exception="Exit" Stack="reachability_analysis,convert_contact,get_intermediate_encoding"
Message="MEMORY OVERFLOW"/>
</Log>
```

Please warn me by sending me both the input files and the XML output.