

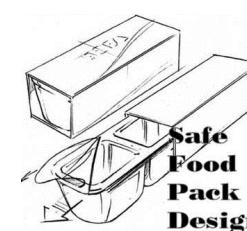
FMECAENGINE

a seamless tool to chain migration simulations and perform related sensitivity analysis

Version 0.45
 (Windows & Linux i386/x64)
 olivier.vitrac@agroparistech.fr

SUPPORTED BY
ANR

August, 2011



GOALS

- **FMECAengine implements FMEA concepts** (<http://en.wikipedia.org/wiki/FMEA>) while being compatible with the underlying physics of mass transfer between food packaging and food.
- **a formalism as an expert system** that enables the simulation of various migration scenarios and the coupling with heterogeneous databases, rulebases and knowledge bases from industry, final users, research laboratory...
- **Possible scopes:** identification of critical steps within a food packaging flow chart (setoff, hot filling, long term storage, household heating...); seeking critical migrants for various designs (e.g. from adhesives, inks); concurrent design of complex food packaging systems (multicomponents, multilayers).

LICENSE

FMECAengine is developed by Olivier Vitrac, PhD (Institut National de la Recherche Agronomique) and distributed under licence CeCILL-B (compatible GPL) as detailed below.

CeCILL-B FREE SOFTWARE LICENSE AGREEMENT
http://www.cecill.info/licences/Licence_CeCILL-B_V1-en.html

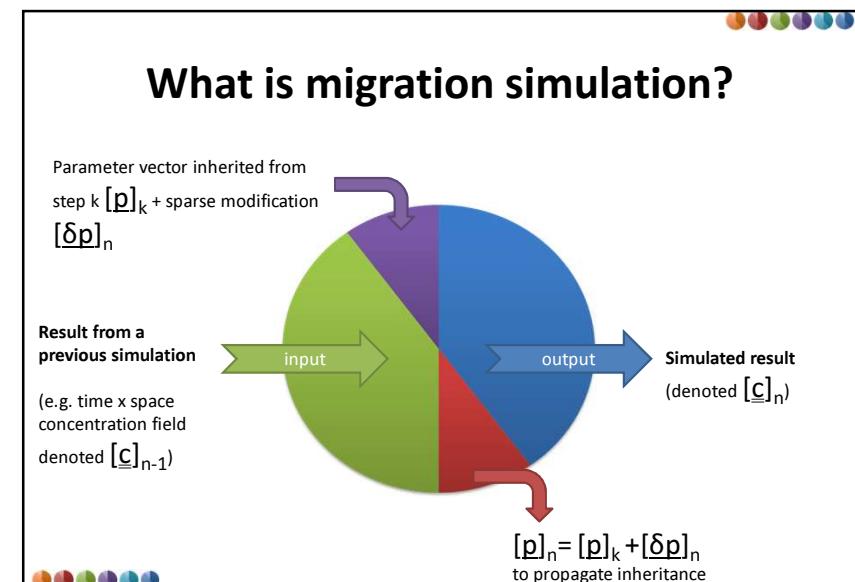
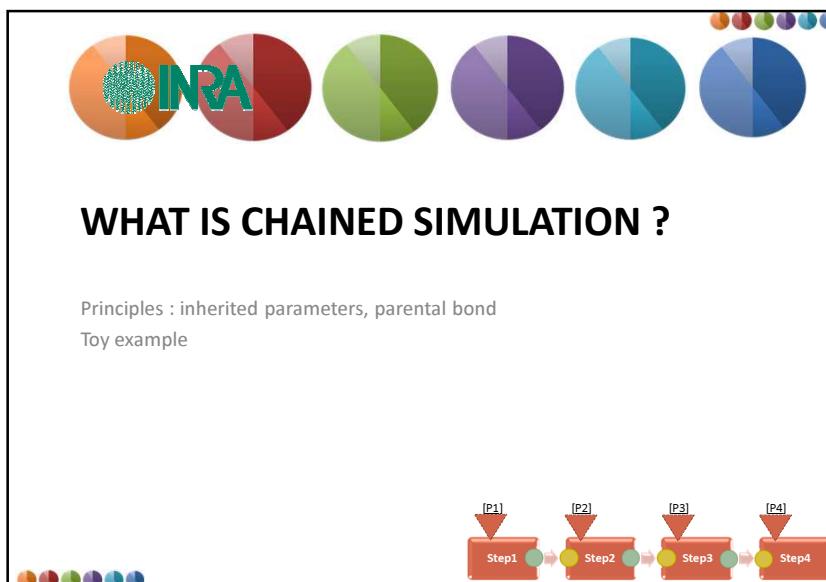
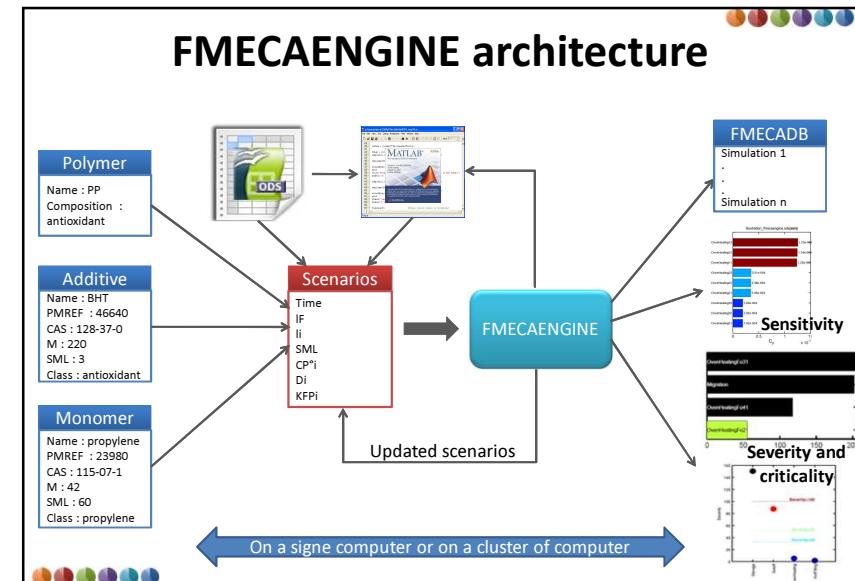
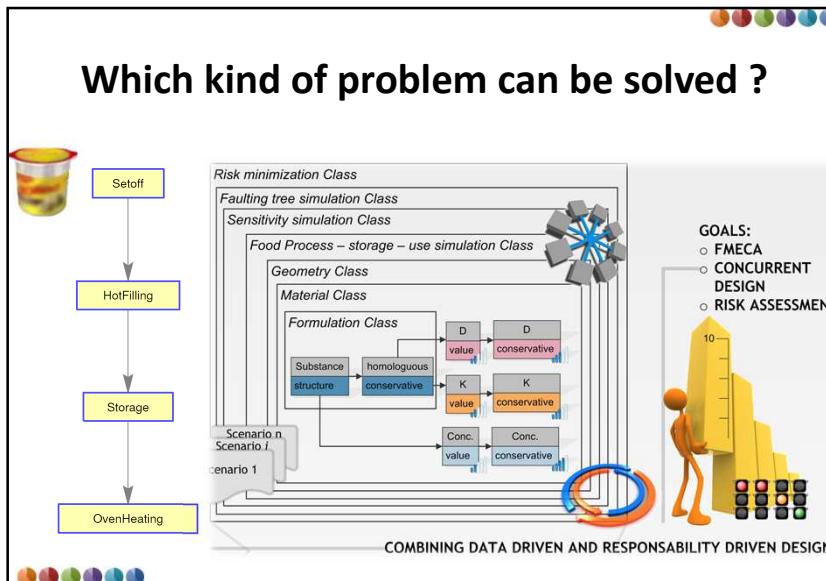
Notice

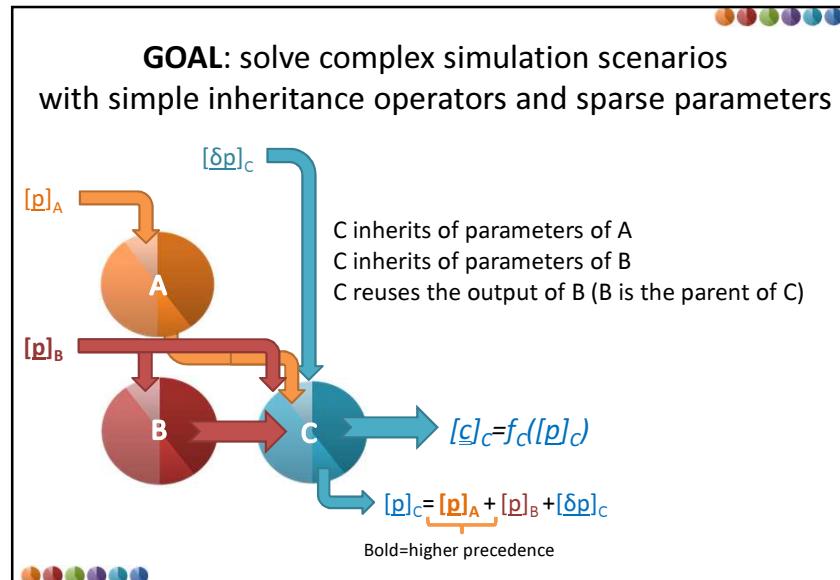
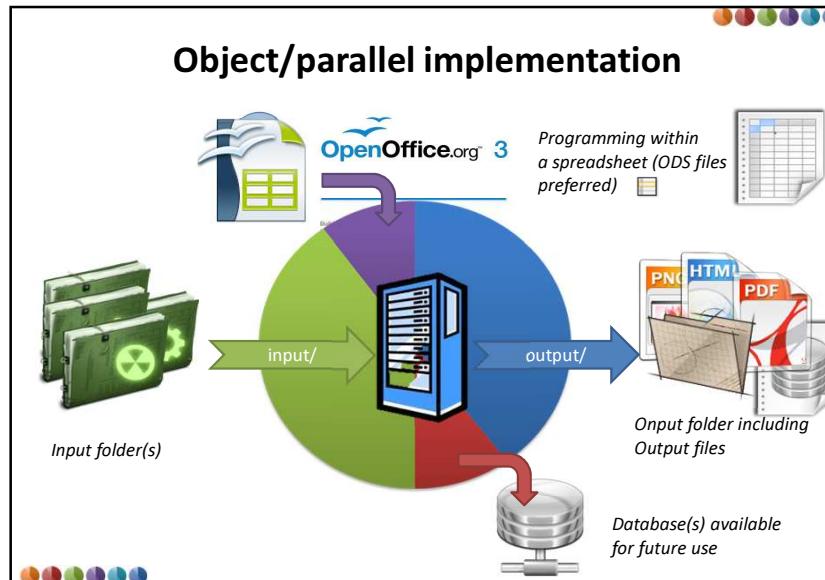
This Agreement is a Free Software license agreement that is the result of discussions between its authors in order to ensure compliance with the two main principles guiding its drafting:

- firstly, compliance with the principles governing the distribution of Free Software: access to source code, broad rights granted to users,
- secondly, the election of a governing law, French law, with which it is conformant, both as regards the law of torts and intellectual property law, and the protection that it offers to both authors and holders of the economic rights over software.

VERSION HISTORY

- Generating migration scenarios (version 0.1)
- Simulating chained scenarios (version 0.2)
- Sensitivity analysis (version 0.3)
- Severity and criticality analysis (version 0.38)
- Connecting with physico-chemical databases (version 0.41)
- Multiple keys enabled in versions 0.43 and later





TOY EXAMPLE: input table

INPUT TABLE =OpenOffice worksheet (ODS v. 3)

Dependence graph plotted by FMECAENGINE

SAFEFoodPack DESIGN

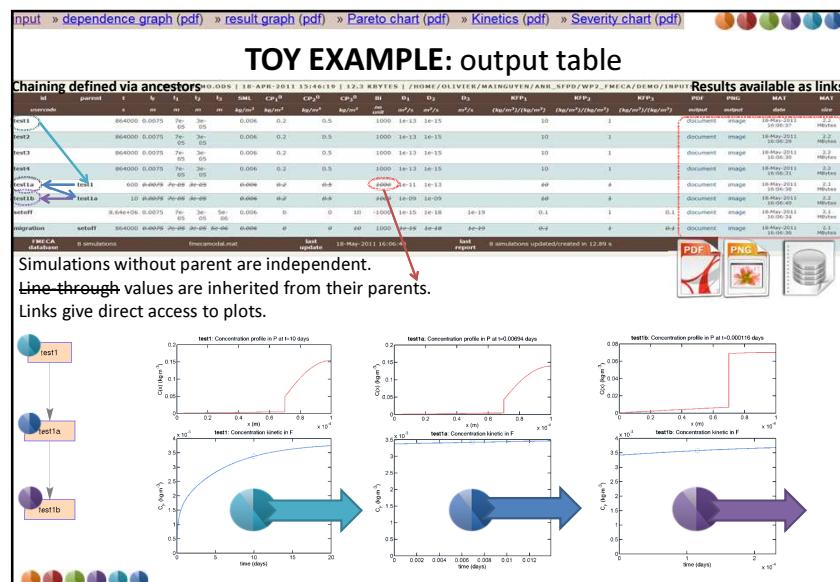
FAILURE MODE, EFFECTS, AND CRITICALITY ANALYSIS (FMECA)

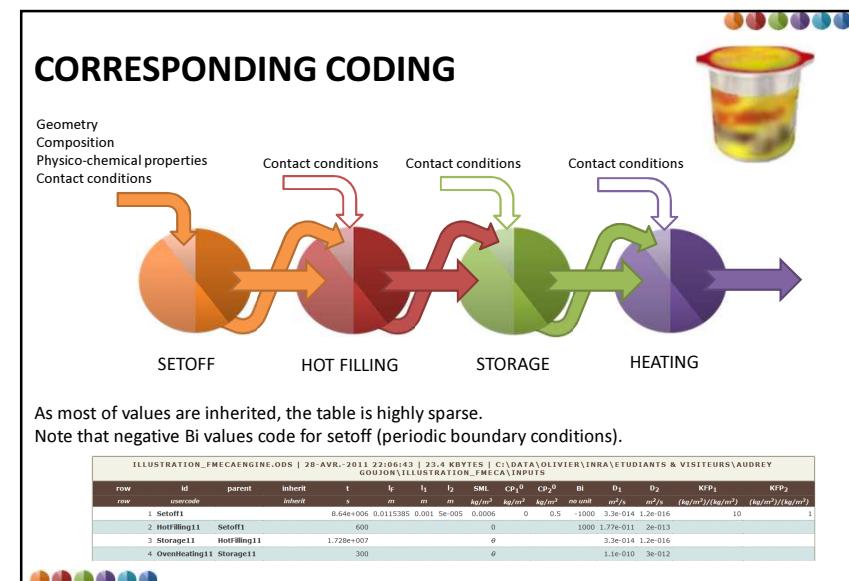
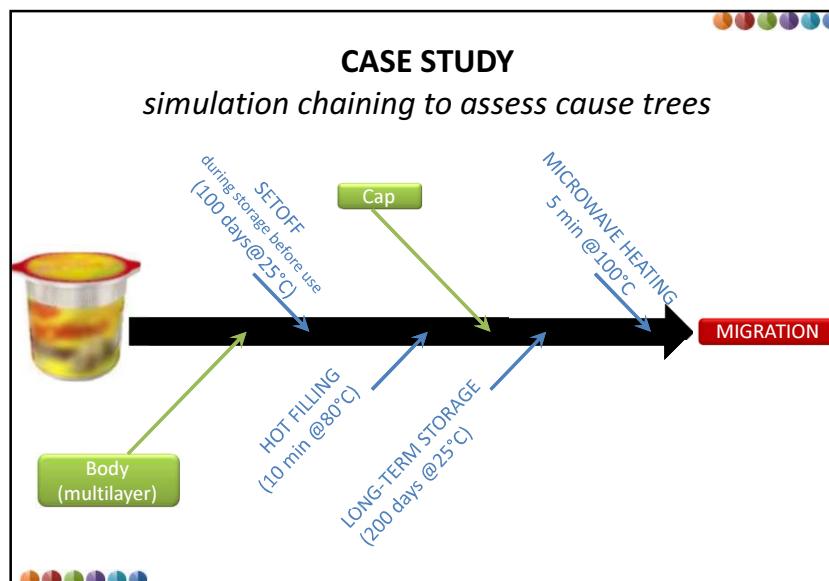
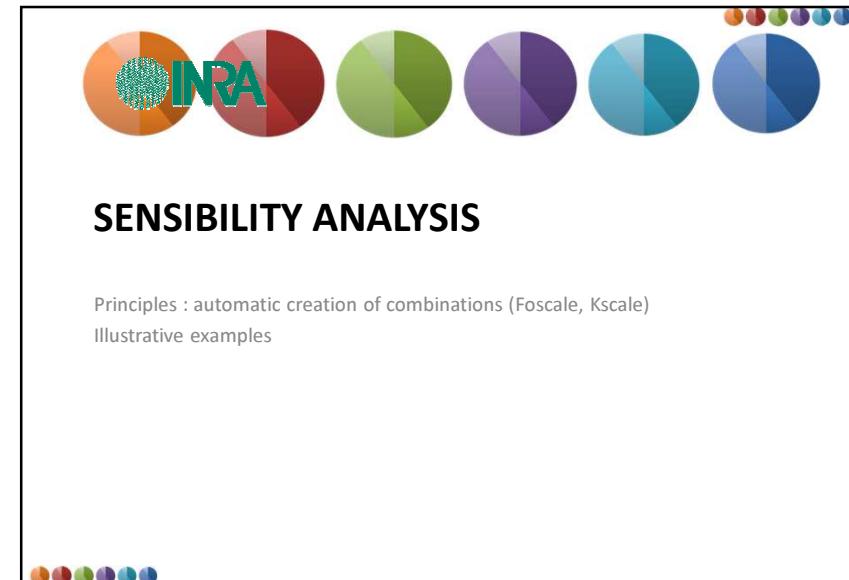
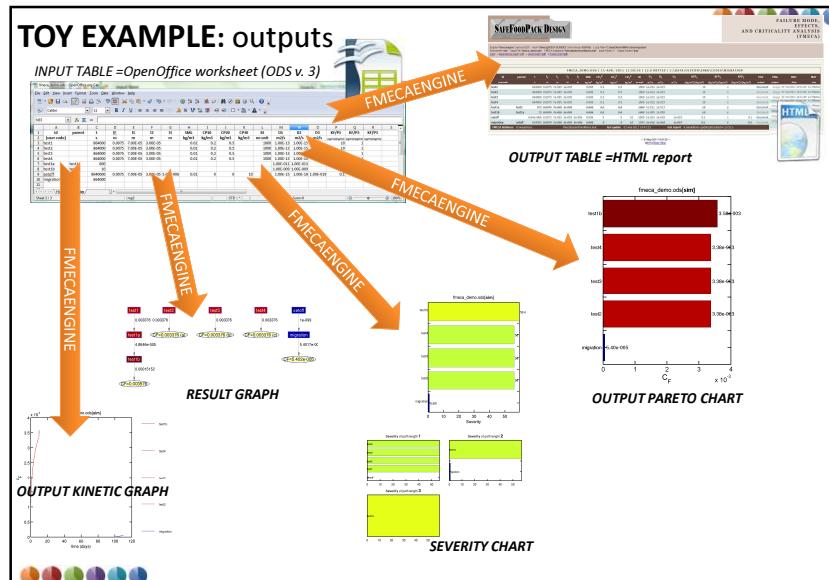
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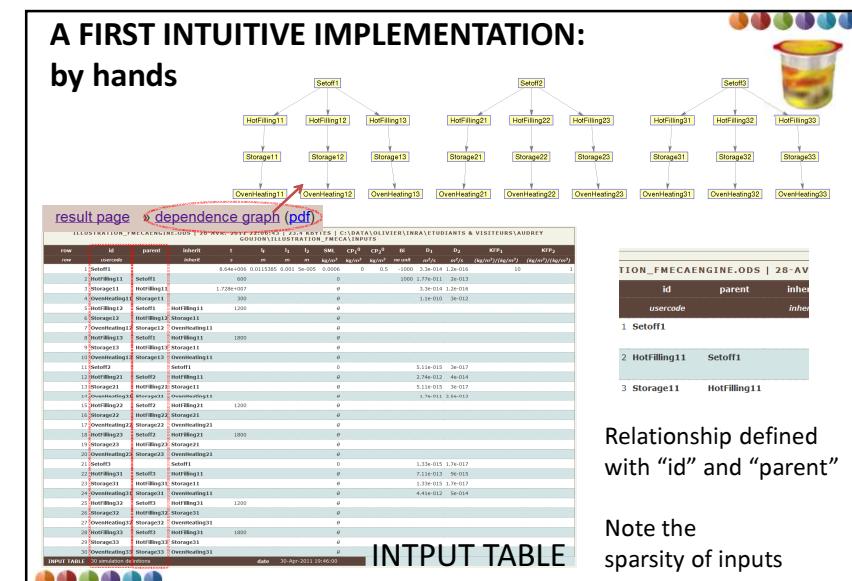
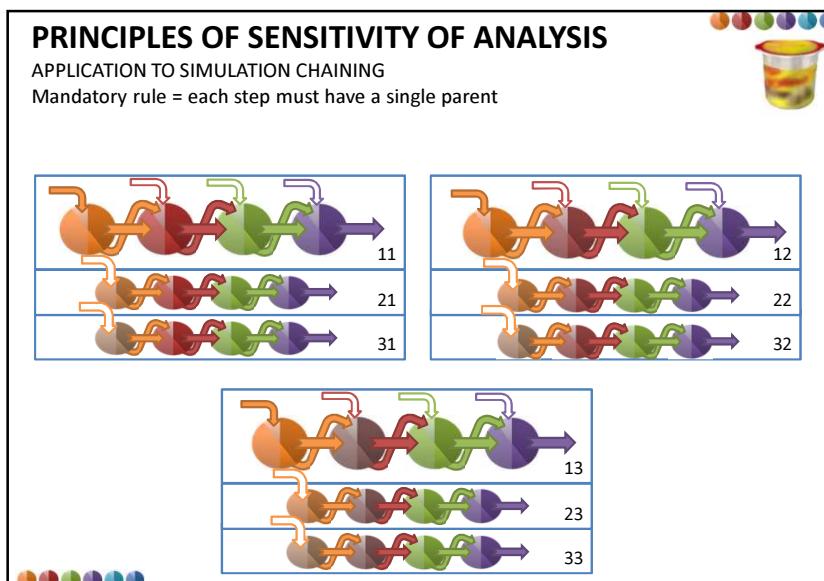
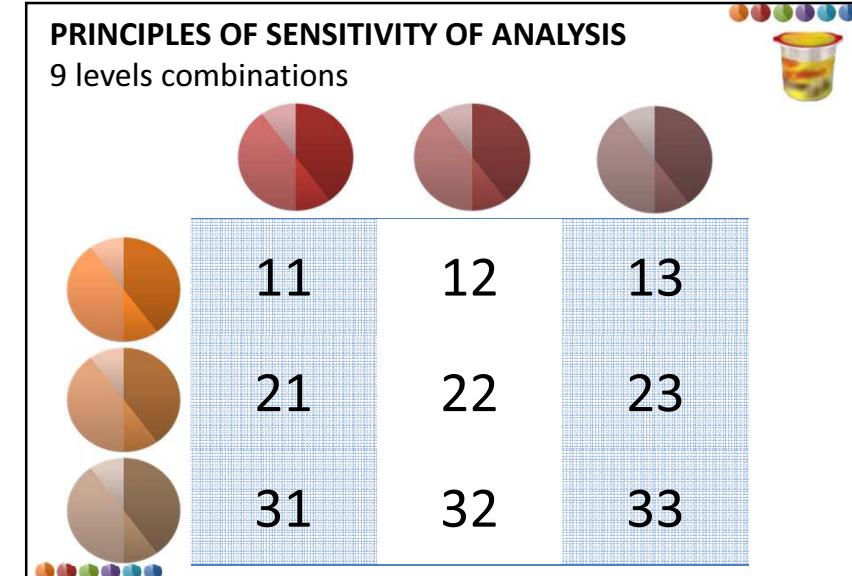
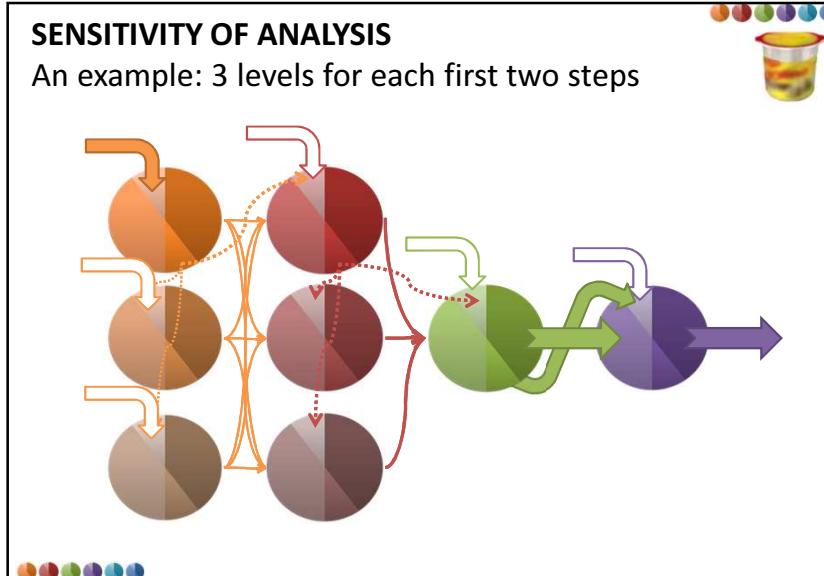
id	parent	t	I _r	I ₁	I ₂	I ₃	SML	CP _{1,0}	CP _{1,0}	CP _{2,0}	B1	D ₁	D ₂	D ₃	KIP ₁	KIP ₂	KIP ₃
usercode	s	m	m	m	m	m	kg/m ³ /s	kg/m ³ /s	kg/m ³ /s	(kg/m ³)/(kg/m ³)	(kg/m ³)/(kg/m ³)	(kg/m ³)/(kg/m ³)					
test1	864000	0.0075	7e-05	3e-05	0.005	0.2	0.5	1000	1e-13	1e-15	10	1					
test2	864000	0.0075	7e-05	3e-05	0.006	0.2	0.5	1000	1e-13	1e-15	10	1					
test3	864000	0.0075	7e-05	3e-05	0.006	0.2	0.5	1000	1e-13	1e-15	10	1					
test4	864000	0.0075	7e-05	3e-05	0.006	0.2	0.5	1000	1e-13	1e-15	10	1					
test1a	test1	600									1e-11						
test1b	test1a	10									1e-09						
setoff		8.64e+06	0.0075	7e-05	5e-06	0.006	0	10	-1000	1e-15	1e-18	1e-19	0.1	1	0.1	0.1	0.1
migration	setoff	864000									1000						

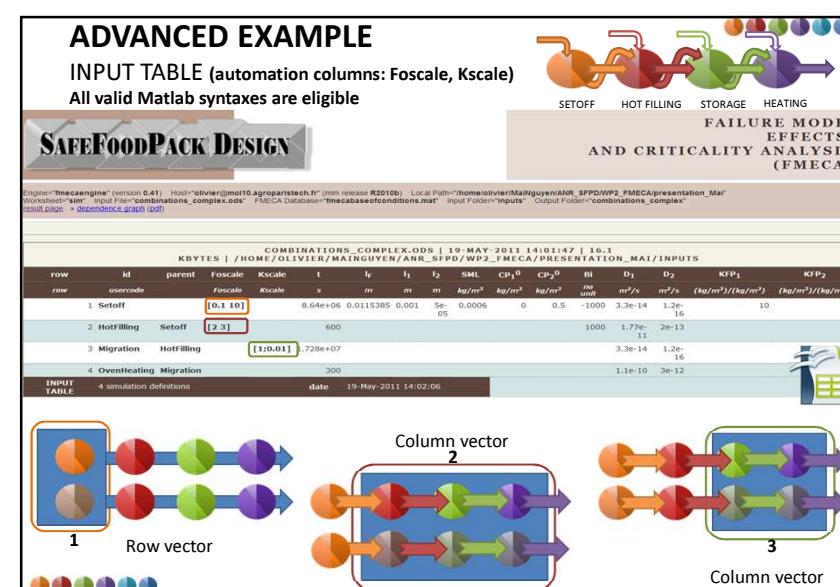
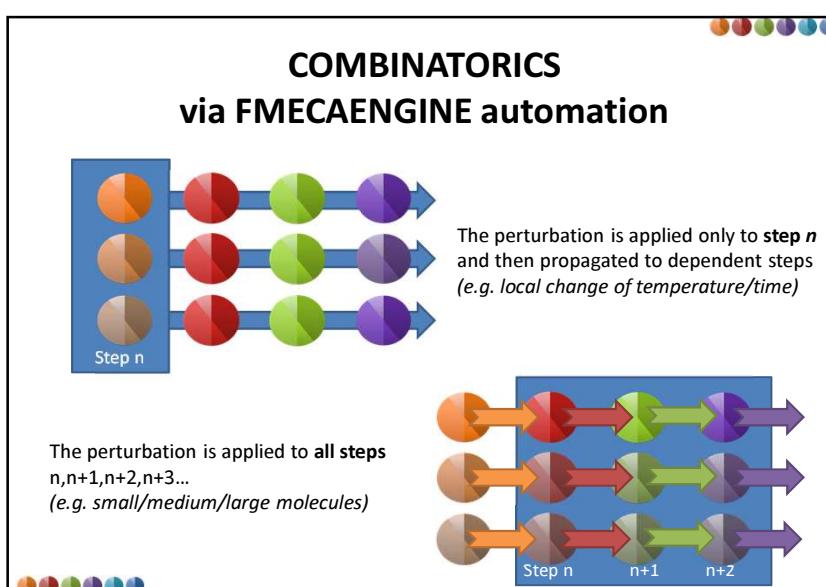
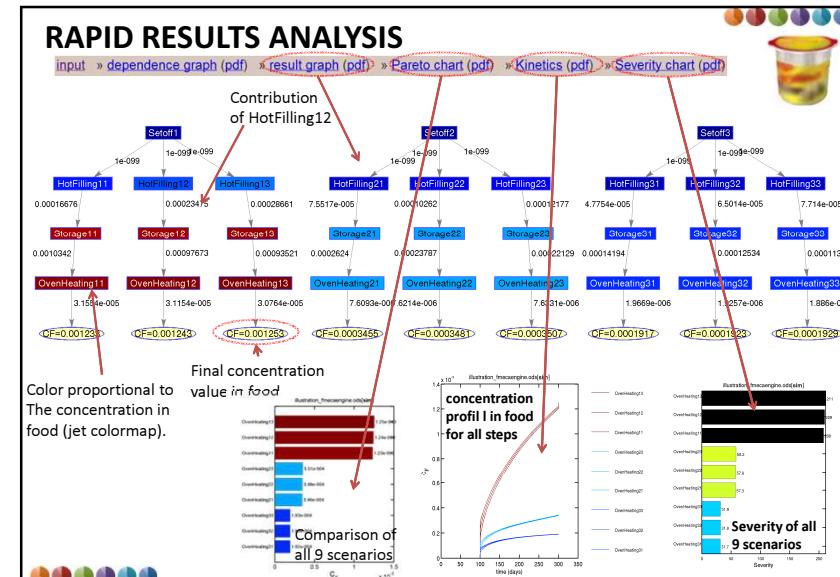
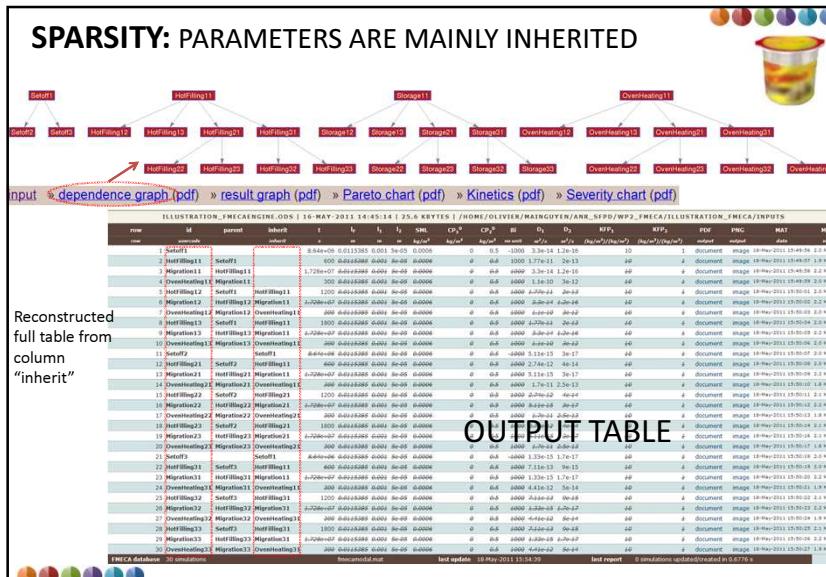
INPUT TABLE 8 simulation definitions date 18-May-2011 16:06:27

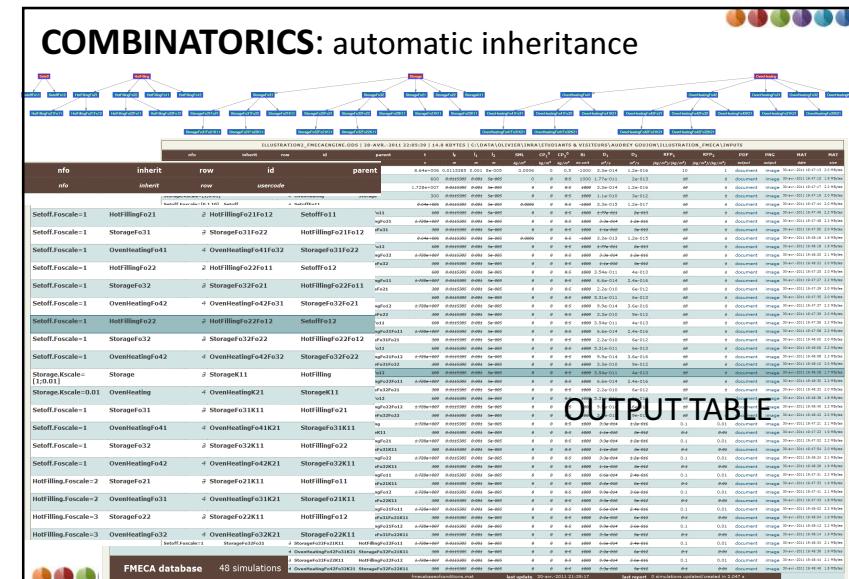
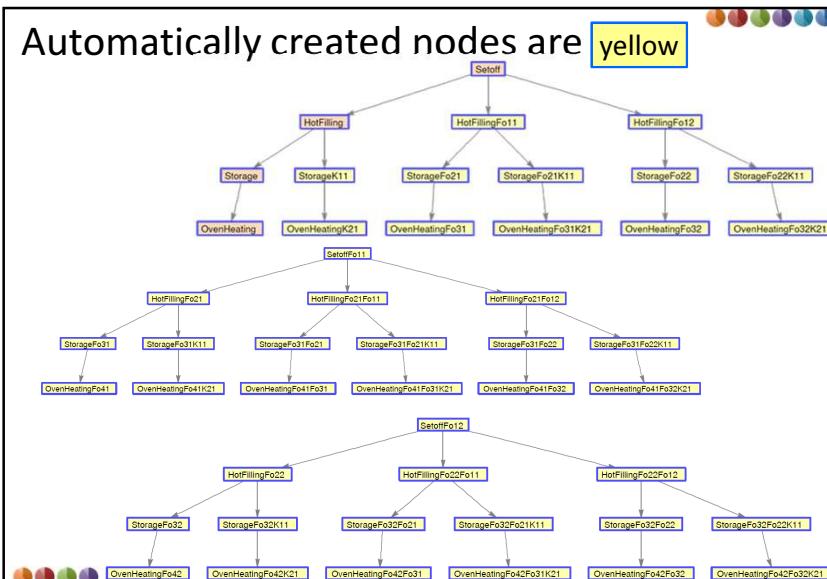
ORIGINAL TABLE repainted by FMECAENGINE



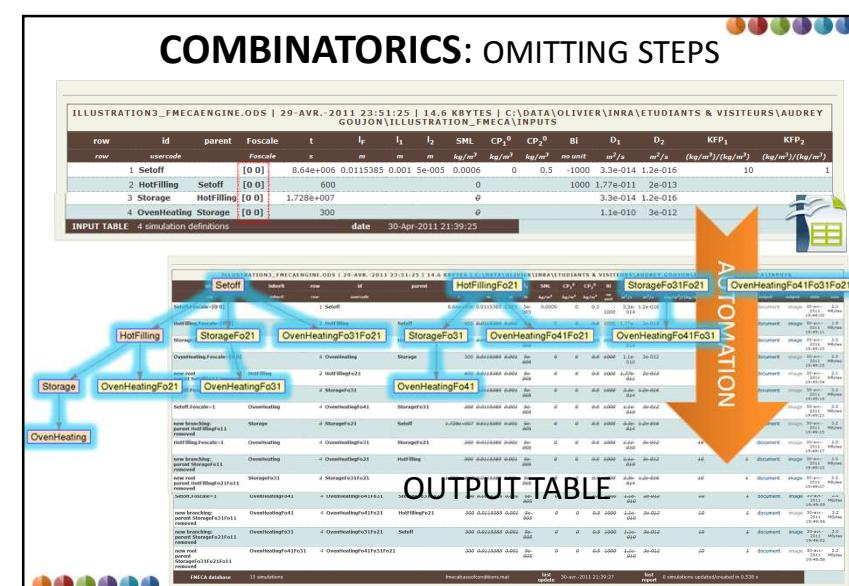
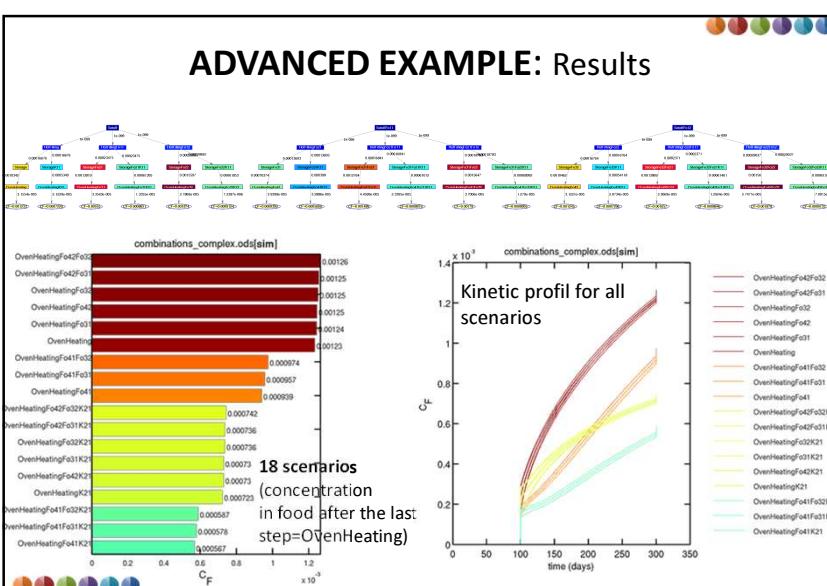






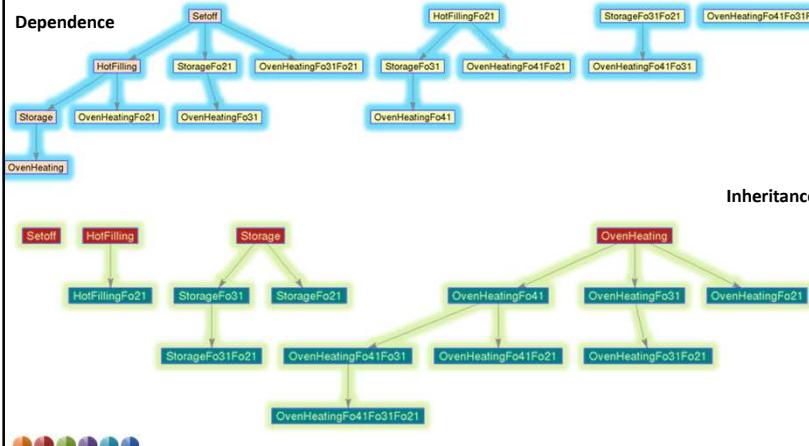


OUTPUT TABLE

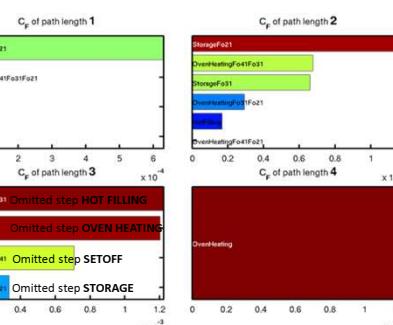


OUTPUT TABLE

OMITTING STEPS: FMECAENGINE builds all trees required to assess the effects of all combinations



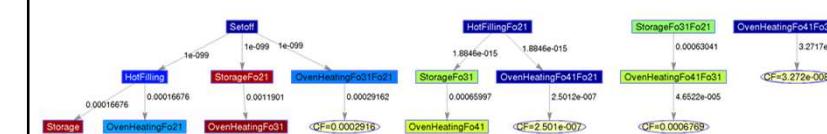
OMITTING STEPS: Results



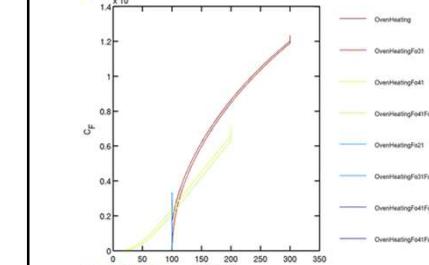
Final concentration in food for each scenario length

8 scenarios (concentration in food after the last step=OvenHeating)

OMITTING STEPS: Results



Result graph: variation of final migration depending on combination

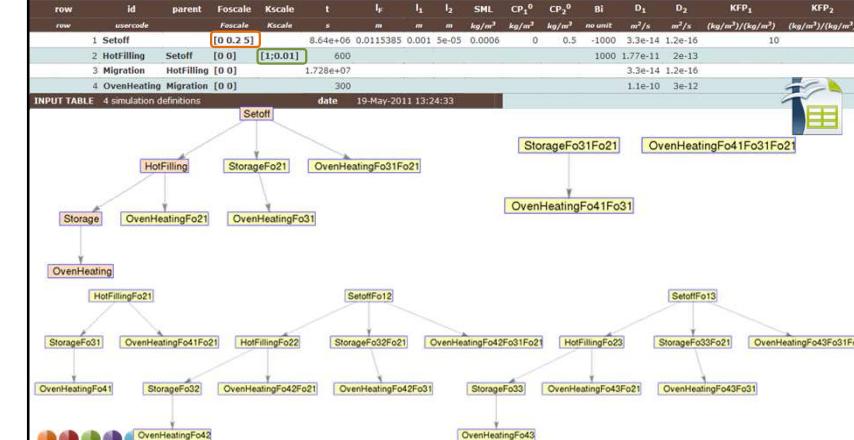


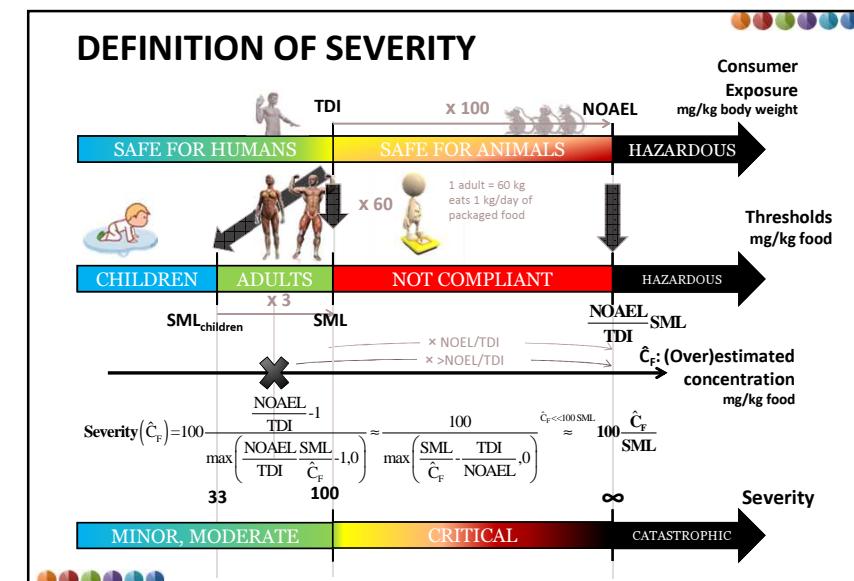
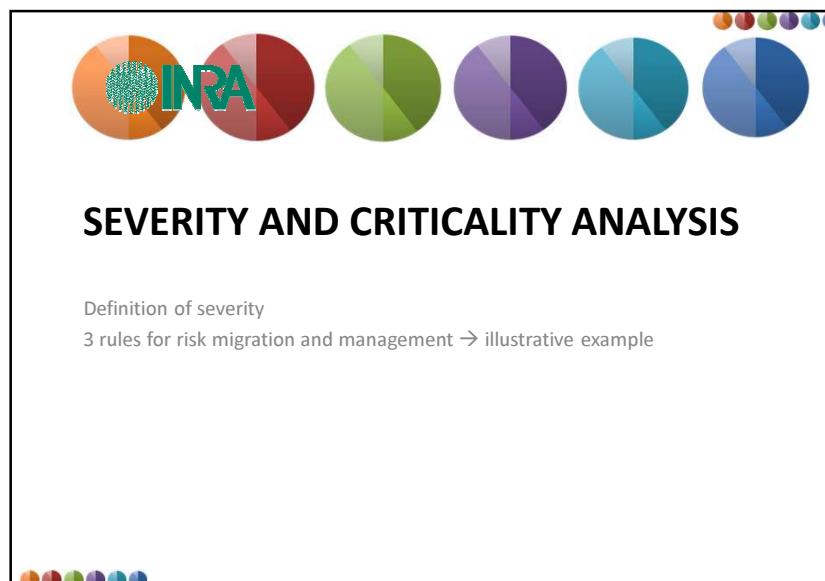
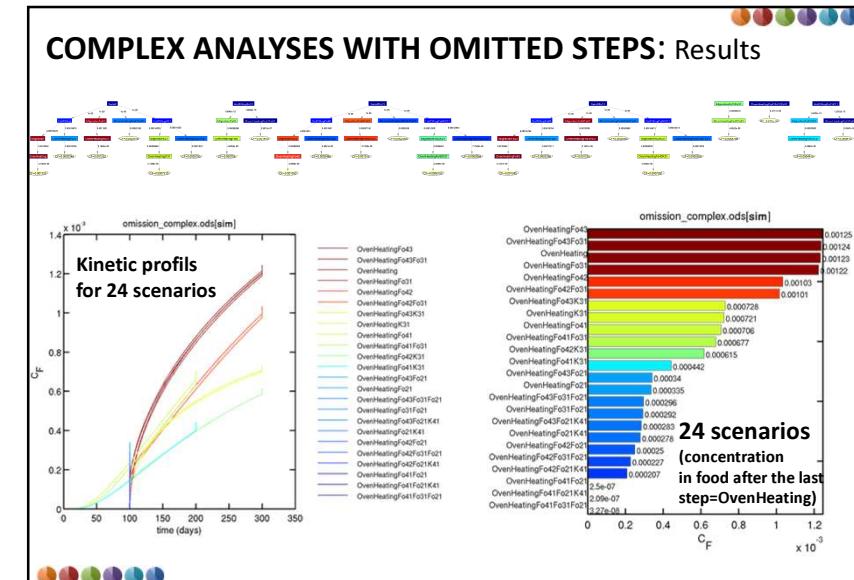
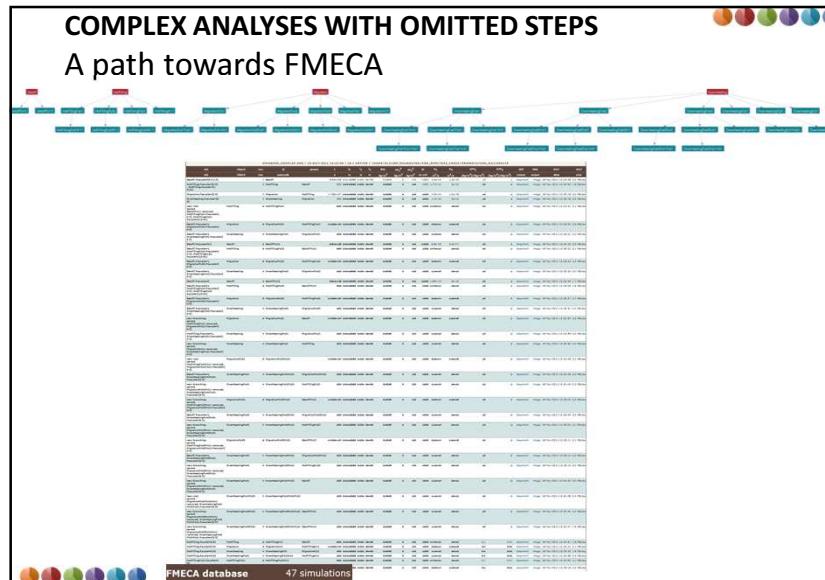
Kinetic graph: concentration profile in food for all steps (color corresponds to severity of final migration)

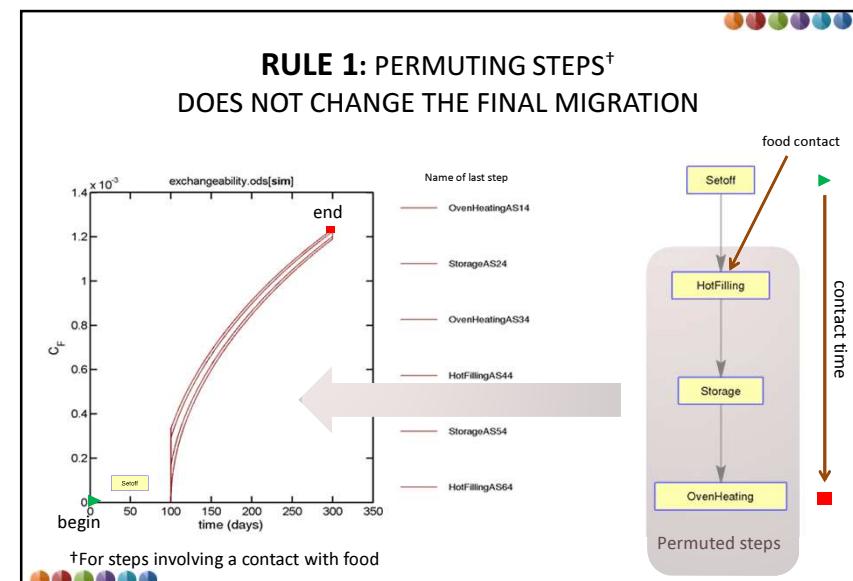
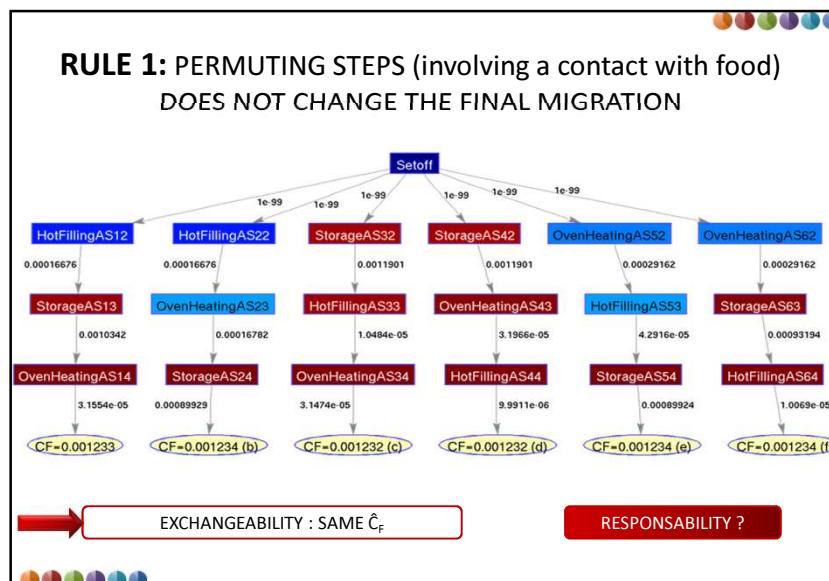
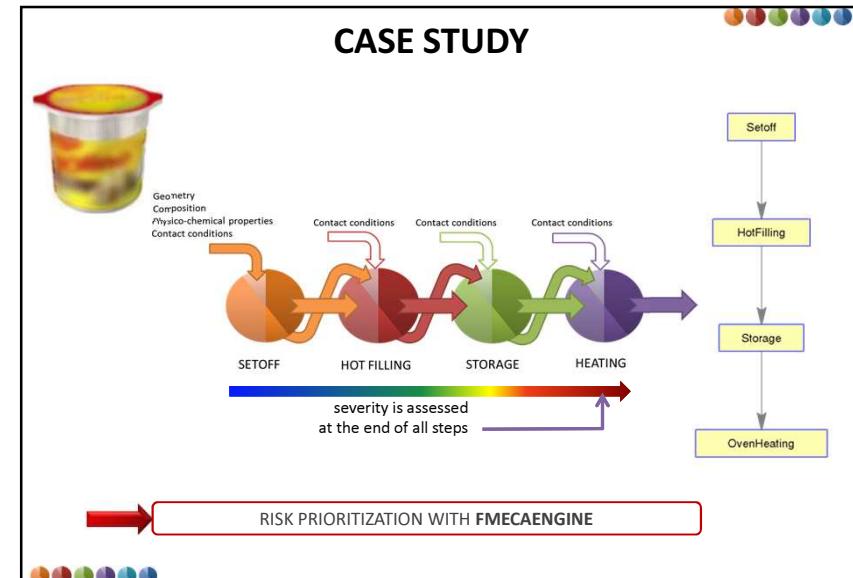
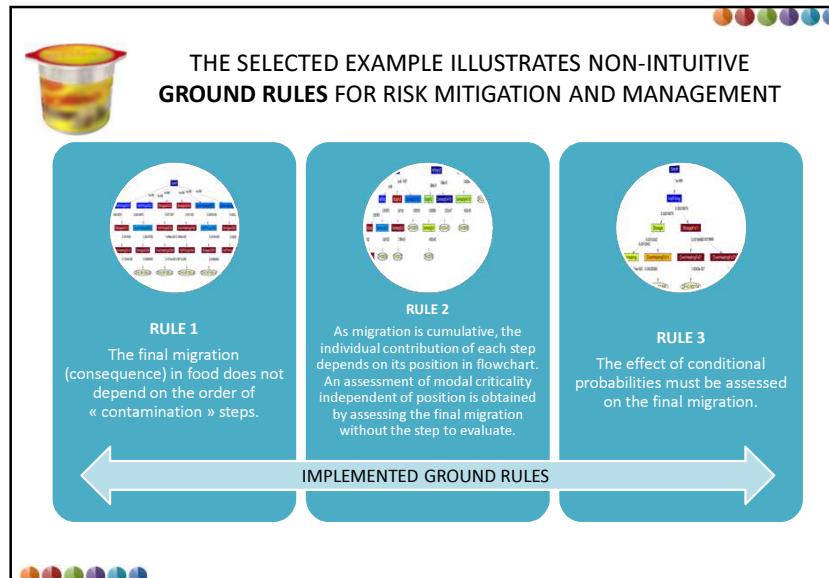
COMPLEX ANALYSES WITH OMITTED STEPS

A path towards FMECA-based risk assessment

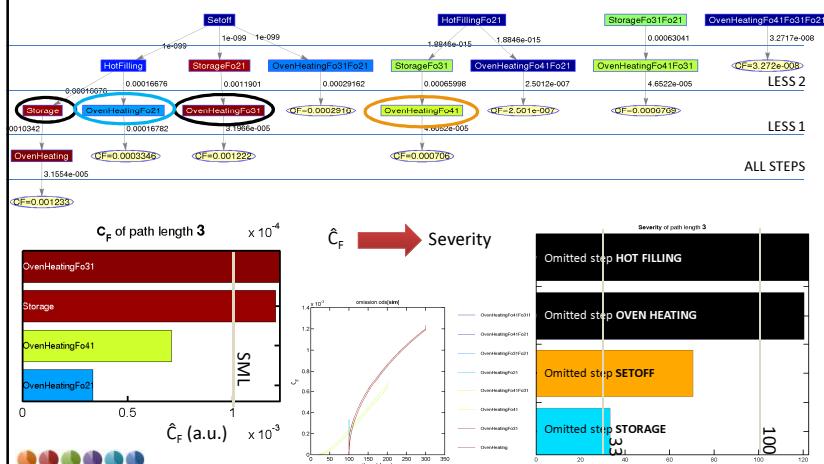
OMISSION_COMPLEX.ODS | 19-MAY-2011 13:23:39 | 16.1
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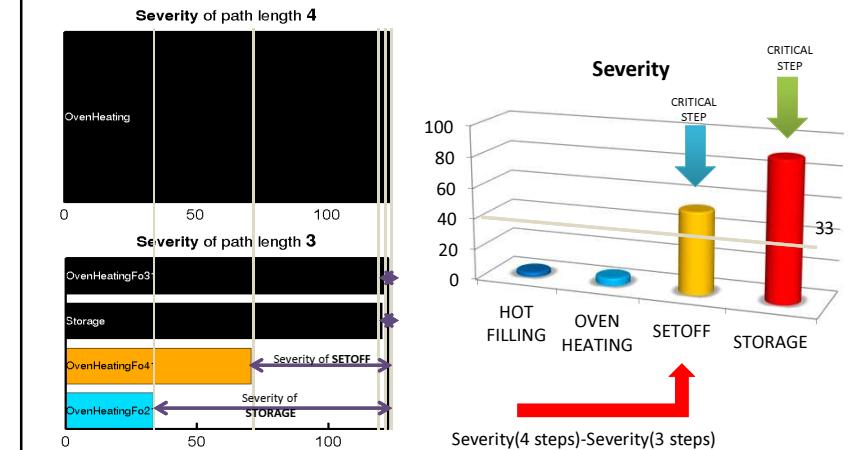




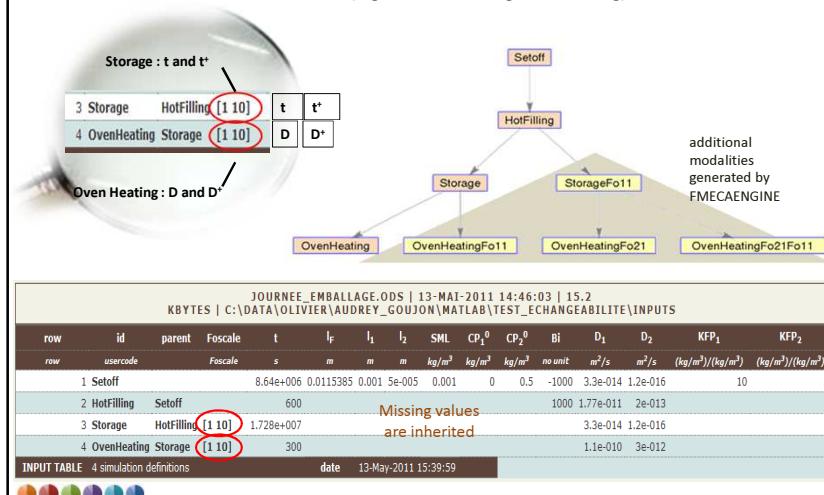
RULE 2: THE MODAL CRITICALITY ASSOCIATED TO ONE OR A COMBINED STEP(S) IS OBTAINED BY OMITTING THE STEP TO ASSESS



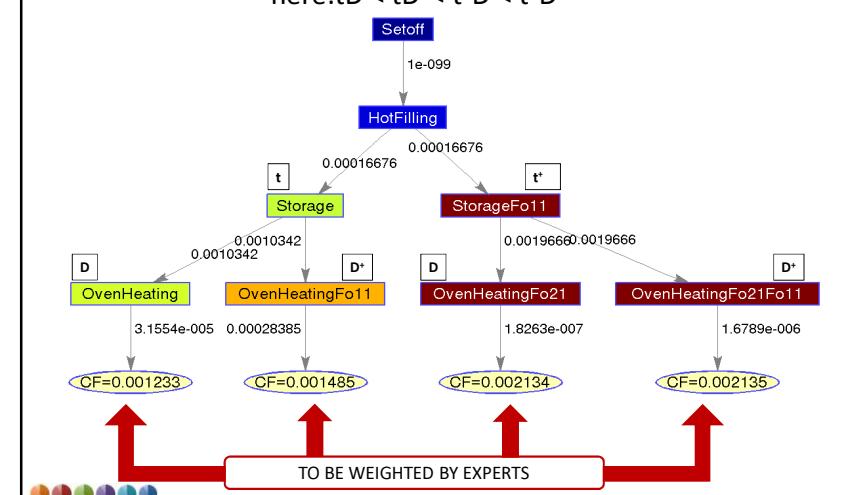
RULE 2: CALCULATION PROCEDURE TO EXTRACT THE SEVERITY OF A SINGLE STEP



RULE 3: RATING COMBINED MODALITIES REQUIRES TO ASSESS THE CUMULATIVE EFFECT OF ALL COMBINATIONS (e.g. excessive storage and heating)

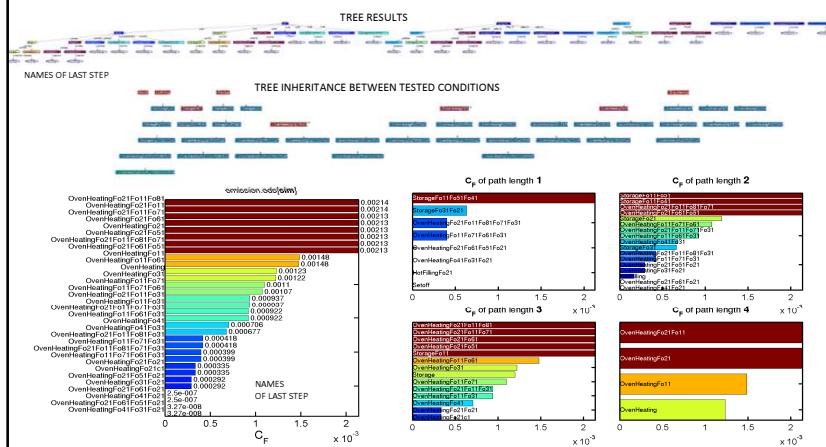


RULE 3: RATING COMBINED EFFECTS here:tD < tD⁺ < t⁺D < t⁺D⁺



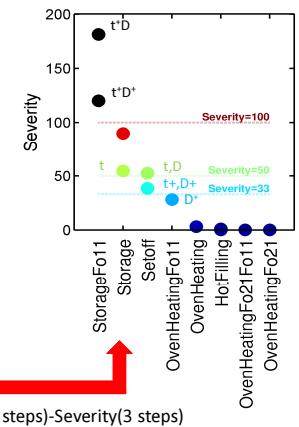
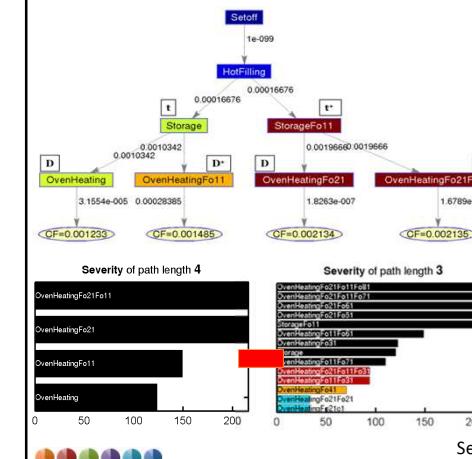
RULE 3: MODAL CRITICALITY ASSOCIATED TO $[t, D] \times [t^+, D^+]$

→ all sequences with omitted steps (1..3) are tested (**43 simulations**!).



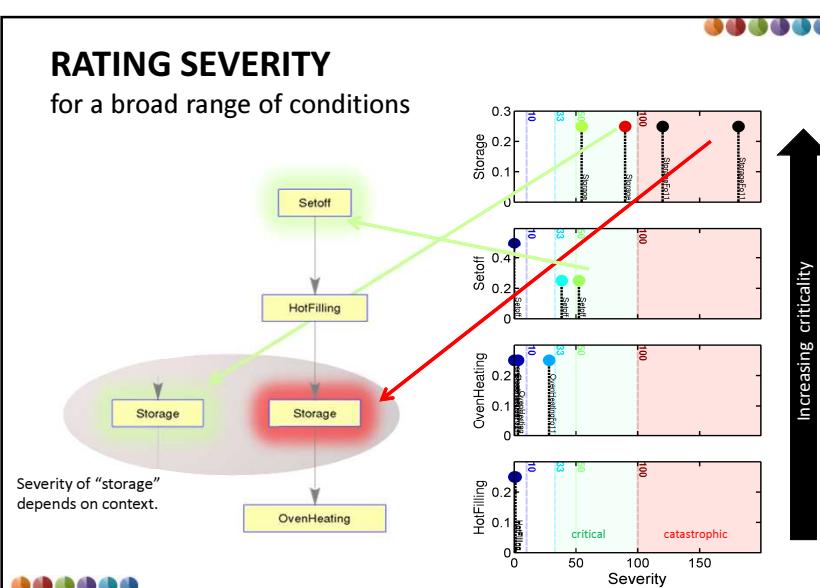
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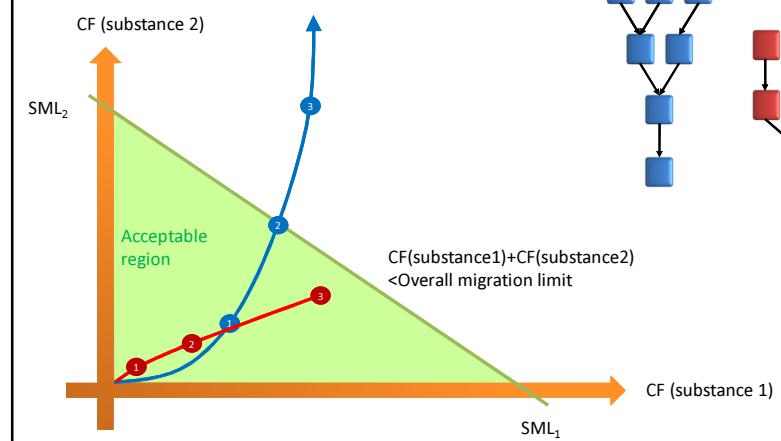


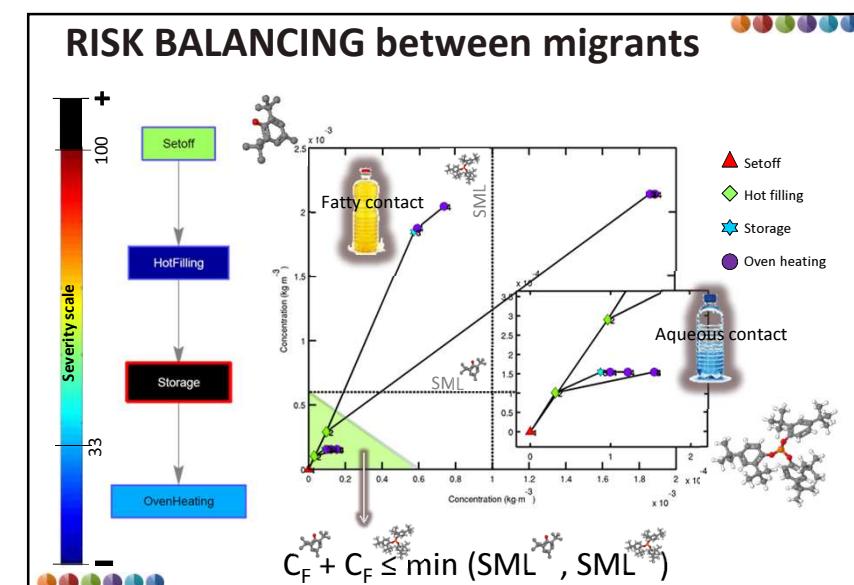
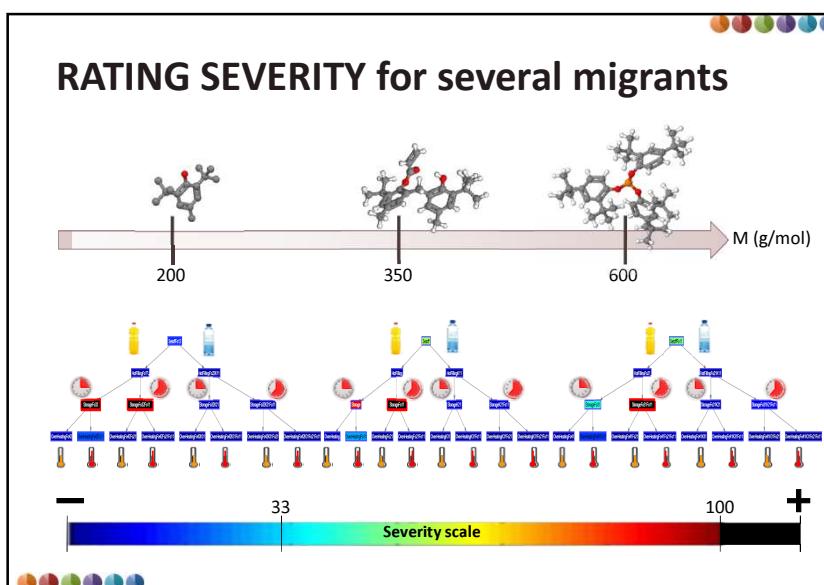
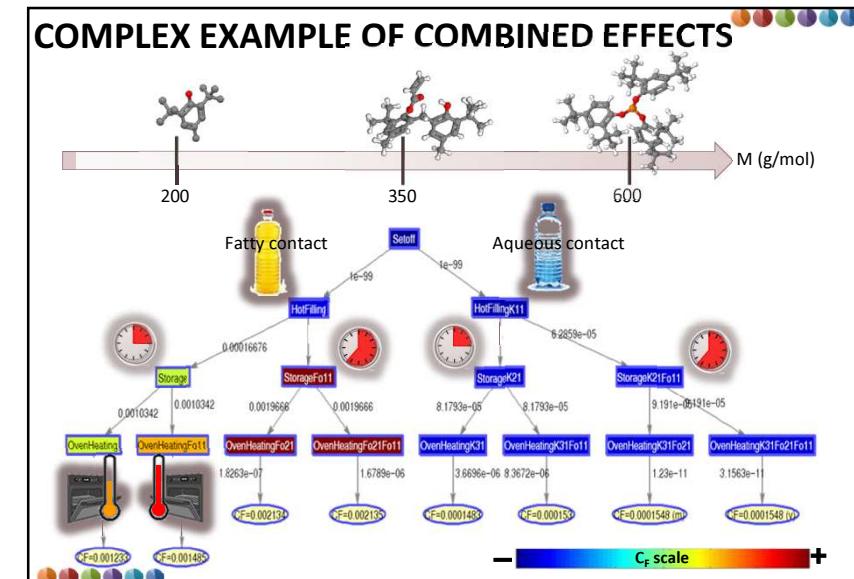
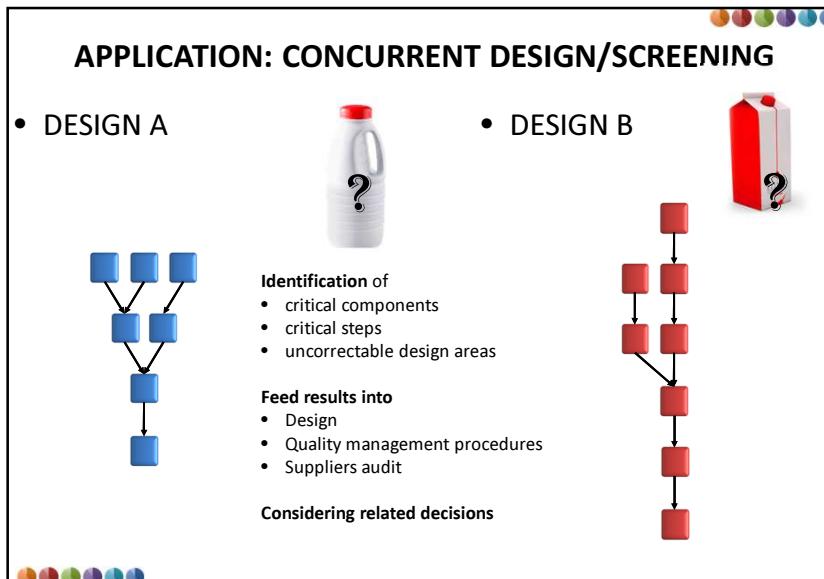
RATING SEVERITY

for a broad range of conditions



HOW DOES IT WORK?







CONNECTING WITH PHYSICO-CHEMICAL DATABASES

Relational databases
Key examples (coding with fmecaengine V 0.41 and later)

IMPLEMENTED RELATIONSHIPS

Implemented relationships include:

- one-to-one relationships
- one-to-many relationships
- many-to-many relationships
- cascading between keys

Operations above are coded using a special syntax (more flexible and concise than SQL) that mimics UML (http://en.wikipedia.org/wiki/Unified_Modeling_Language) :

```
PP:polymer::name->classadditives
PP:polymer::name->classadditives:substance::class->name
PP:polymer::name->classadditives:substance::class->M
```

By default, a UNIQUE operator operator (data reduction) is apply to all relationships involving strings or cell array of strings. The request order is respected only for single requests.

It is worth to notice that final results are also included within a large database that can be resused in future simulations or in subsequent analysis (e.g. for calculating severity).

Background:
[http://en.wikipedia.org/wiki/Many-to-many_\(data_model\)](http://en.wikipedia.org/wiki/Many-to-many_(data_model))
http://en.wikipedia.org/wiki/Junction_table
http://en.wikipedia.org/wiki/Foreign_key
<http://en.wikipedia.org/wiki/Superkey>
http://en.wikipedia.org/wiki/Associative_Entities

RELATIONAL DATABASES

Database = collection of tables including primary, super key and foreign keys

Examples

Monomer		A	B	C	D	E	F	G	H
name	1	2,4,4'-dihydroxy-2,2-diphenylpropyl bisphenol A	PMREF	CAS	M	SML	polymer	class	
C_name	2	4-Caprolactame		134800	80-05-7	228.29	0.6 PA	monomer1	
PMREF	3	4-Ethylene glycol		142000	105-60-2	113.16	15 PA	monomer1	
CAS	4	1-butene		169900	107-21-1	62.07	30 PET/PEN	monomer2	
M	5	1-hexene		169900	74-95-1	28.05	60 LDPE/LD monomer4		
SML	6	1-octene		226600	111-66-0	132.22	15 LDPE monomer5		
polymer	7	Styrene		24610	100-42-5	104.15	60 HIPS/PS monomer6		
class	8	Terephthalic acide		24910	100-21-0	166.13	7.5 PET/PBT monomer7		
	9	1-hexene		18820	592-41-6	84	3 HDPE/LLD monomer8		
	10								

Polymer		A	B
name	1	HDPE	monomer4
composition	2	HDPE	monomer8
	3	HDPE	monomer10
	4	HDPE	monomer11
	5	HDPE	monomer12
	6	HDPE	antioxidant
	7	HDPE	UV_stabilizer
	8	PP	monomer9
	9	PP	antioxidant
	10	PP	UV_stabilizer
	11	PP	UV_stabilizer

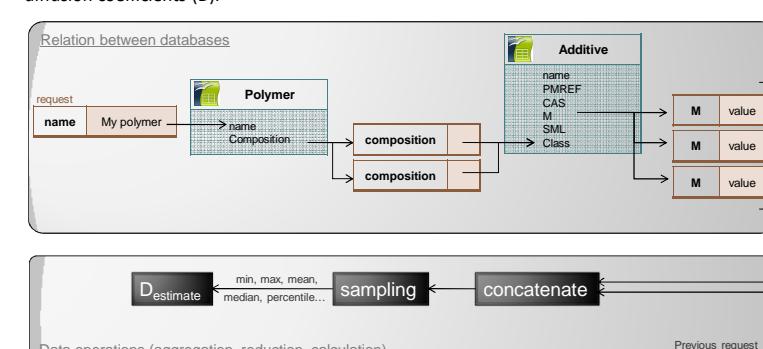
Additive		A	B	C	D	E	F	G	H
name	1	2,2,2-triethyl-4-	PMREF	CAS	M	SML	class		
PMREF	2	2,2,2-triethyl-4-		46880	65140-91-2	694.84	6 antioxidant		
CAS	3	2,2,2-triethyl-4-		66480	119-47-1	340.1	1.5 antioxidant		
M	4	2,2,2-triethyl-4-		66480	119-47-1	340.1	1.5 antioxidant		
SML	5	2,2,2-triethyl-4-		92800	96-69-5	358.54	0.48 antioxidant		
Class	6	2,2,2-triethyl-4-		59200	35074-77-2	638.93	6 antioxidant		
	7	2,2,2-triethyl-4-		60800	65447-77-0	1500	30 UV_stabilizer		
	8	2,2,2-triethyl-4-		60800	65447-77-0	1500	30 UV_stabilizer		
	9	2,2,2-triethyl-4-		60400	3896-11-5	315.8	30 UV_stabilizer		
	10	2,2,2-triethyl-4-		60320	70321-86-7	447.58	1.5 UV_stabilizer		
	11	2,2,2-triethyl-4-							

Affinity		A	B
food	1	aqueous	0.001
	2	fat	1
	3	dairy	1
	4	dairy	0.001
	5		

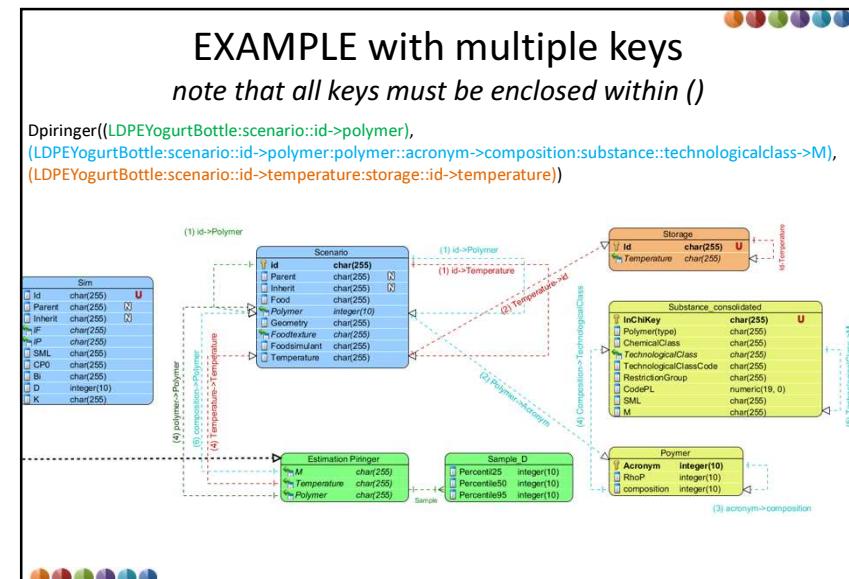
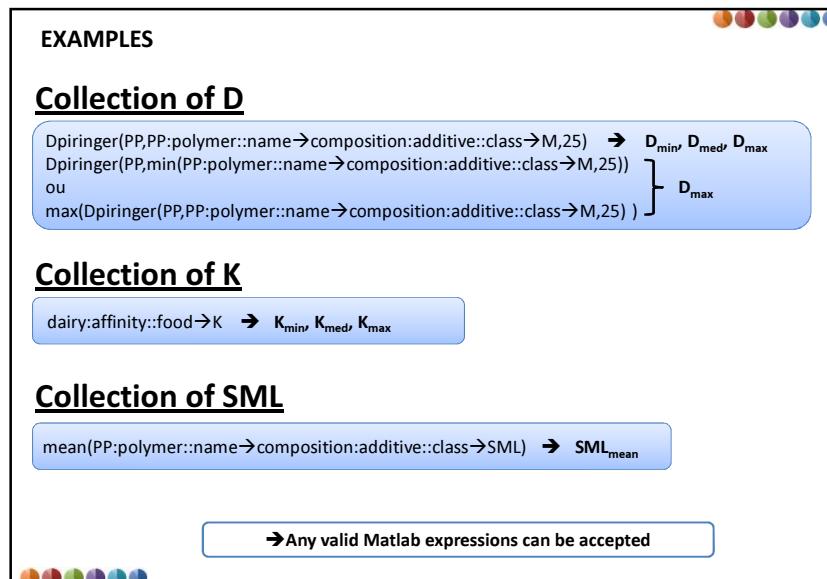
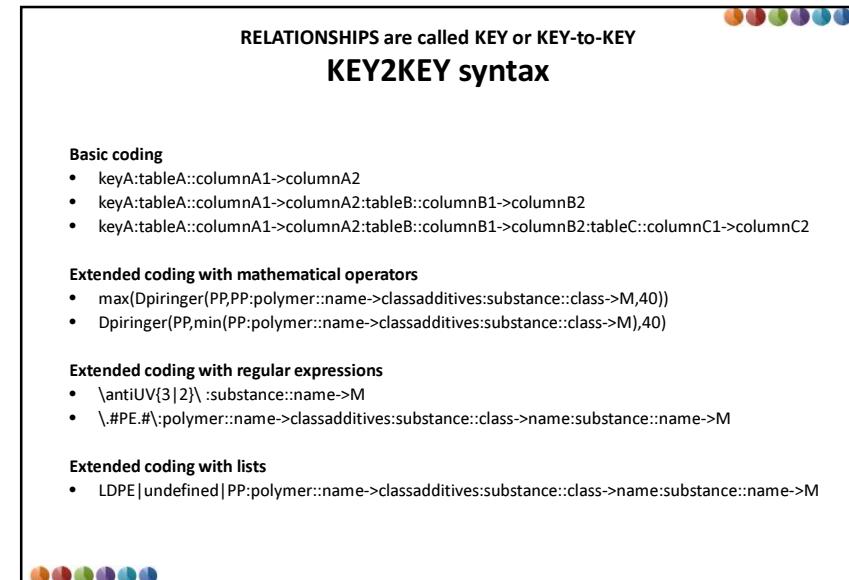
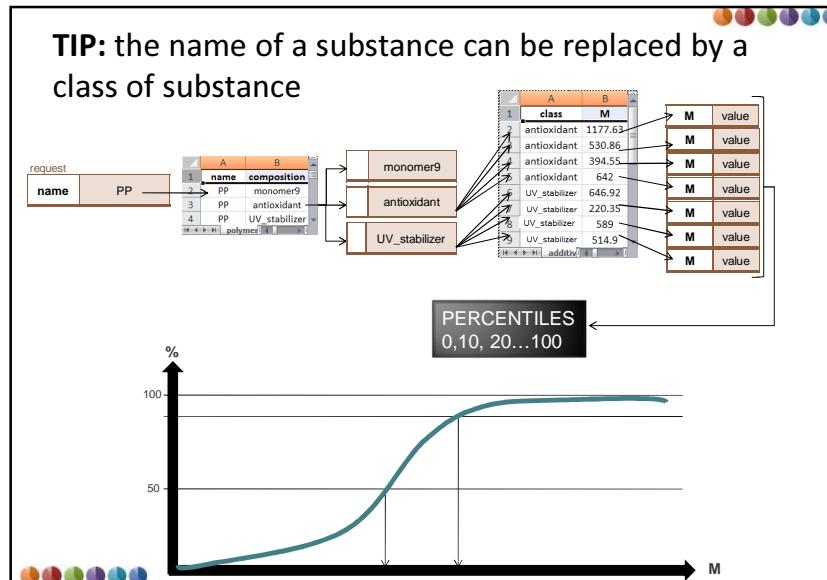
EXAMPLE OF ONE TO MANY RELATIONSHIPS

The example depicts how databases could be used to derive the formulation (substance content) of a common polymer and finally to sample the distribution of molecular mass (M) of possible migrants. These values are finally used for the calculation of some estimates of diffusion coefficients (D).

Relation between databases



Data operations (aggregation, reduction, calculation)





HOW TO BUILD USER DATABASES, RULEBASES, KNOWLEDGE BASES

Database, rulebase, knowledgebase = collection of tables including primary, super key and foreign keys

EXAMPLES: RULE BASES AND KNOWLEDGE BASES

scenario	
Primary key	Id: gobeleTP
Foreign key	Food : hotdrink
List/Foreign key	Foodsimulant: fatty, ethanol50
Foreign key	Material : PP
Foreign key	Geometry : gobele
Foreign key	Step : consumption
Foreign key	Temperature : hot

Geometry	
Primary key	Id: gobele
List/ Foreign key	A: 170
List/ Foreign key	Aut: cm2
List/ Foreign key	mF: 200
List/ Foreign key	PFunit: g
List/ Foreign key	IP: 150
List/ Foreign key	IPunit: µm

Food	
Primary key	Id: hotdrink
List/ Foreign key	Shelflife: 2
List/ Foreign key	Temperature: h
List/ Foreign key	rhof: 1000

Foodsimulant	
Primary key	Id: ethanol50
List	K: 0.1

Consumption	
Primary key	Id : hot
List/ Foreign key	Temperature: 70
List/ Foreign key	Time: 2
List/ Foreign key	Unit: h

Diffusion	
Primary key	InChiKey: NLZUEZXRPGMBCV-UHFFFAOYSA-N
	M: 220.35
	polymer: PP
	rhof: 0.95
	temperature: 40
List	D: 4.6E-15;2.7E-16;5E-15

Examples: Tables of physico-chemical properties

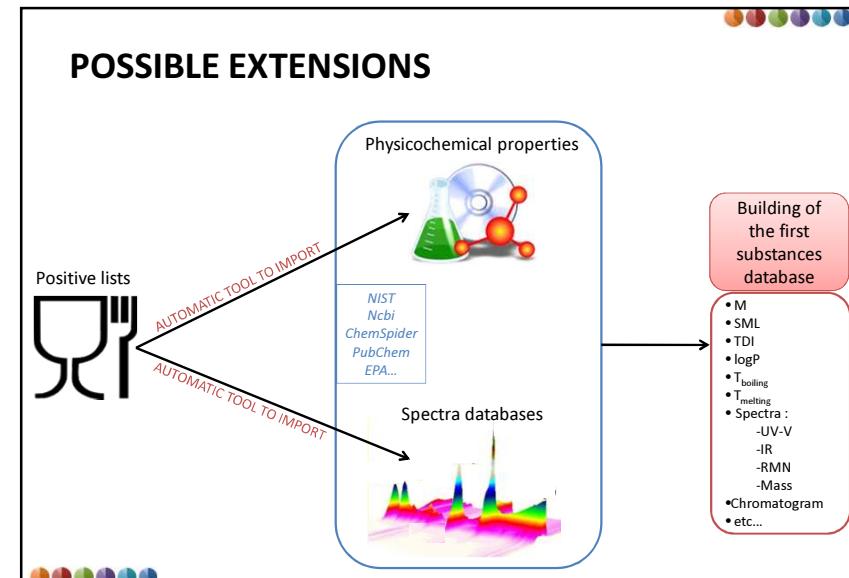
Additive	
InChiKey:string (U)	NLZUEZXRPGMBCV-UHFFFAOYSA-N
Name:string	2,6-Di- <i>t</i> -butyl-4-hydroxytoluene;2,6-di- <i>t</i> -butyl-4-methyl phenol;4-Methyl-2,6-bis(2-methyl-2-propenyl)phenol;4-Methyl-2,6-di- <i>t</i> -butyl-phenol;4-Methyl-2,6-ditributylphenol;BHT;Butylated hydroxytoluene;phenol, 2,6-bis(1,1-dimethylethyl)-4-methyl-2,6-Di- <i>t</i> -butyl-p-cresol;128-37-0;1948-33-0;25377-21-3;50-78-2;26298-56-0;720-39-8;950-56-1;97123-41-6
CAS:list of strings	115-07-1;33004-01-2;676-63-1
PMREF:integer	23980
M:real	42.08
SML:real	60
TDI:real	NaN
logP:real	1.7
Class:string	propylene
Polymer:string	PP

Monomer	
InChiKey:string (U)	QQONPFPPTGQHPMA-UHFFFAOYSA-N
Name:string	name: propene;1- propene;propylene;methylene;1- propylene;prop-1-ene
CAS:list of strings	115-07-1;33004-01-2;676-63-1
PMREF:integer	23980
M:real	42.08
SML:real	60
TDI:real	NaN
logP:real	1.7
Class:string	propylene
Polymer:string	PP

Polymer	
Acronym:string	PP
Name:string	polypropylene
Class:string	PO
Density:real	0.95;0.92
Composition: list of strings	antioxidant, UV_stabilizer, monomer

ALL DATA TYPES ARE RECOGNIZED IMPLICITELY ACCORDING TO THE FOLLOWING RULES	
Empty cell	= Not A Number
Scalar	Any numeric value
List	String containing ";" or ":"
Unique (U)	is enforced for all keys returning an array of strings
Primary/Foreign key	Any key with string/char content (possibly including some lists)

POSSIBLE EXTENSIONS



Positive lists

Automatic tool to import

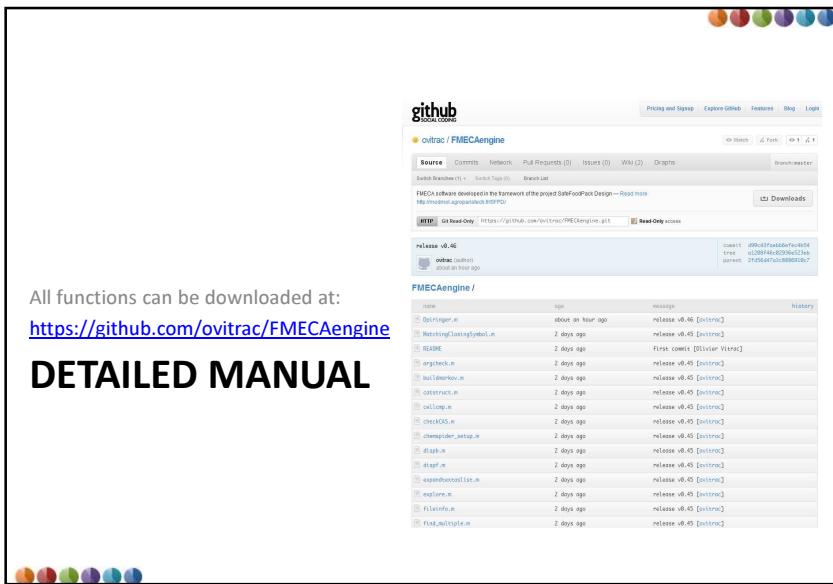
Physicochemical properties

NIST
Ncbi
ChemSpider
PubChem
EPA...

Spectra databases

Building of the first substances database

- M
- SML
- TDI
- logP
- $T_{boiling}$
- $T_{melting}$
- Spectra :
 - UV-V
 - IR
 - RMN
 - Mass
- Chromatogram
- etc...



All functions can be downloaded at:

<https://github.com/ovitrac/FMECAengine>

DETAILED MANUAL

fmecaengine

fmecaengine: advanced script/function (object-oriented) to launch complex FMEA calculations from an OpenOffice Spreadsheet

USAGE AS A SCRIPT (deprecated)

Once the section "path and file definitions" properly defined, you need only to press F5 (i.e. run)
To override default values, define user variables in the workspace

USAGE AS A FUNCTION (recommended)

Syntax: fmecaenfine('variable1','value1','variable2','value2','variable3','value3',...)
fmecaenfine(definition,...) whith definition a structure with fields definition.variable1 = 'value1'

LIST OF USER VARIABLES

local	root directory of all files and folders (default = pwd)
inputpath	folder that contains all inputs (relative to local, default = 'inputs')
outputpath	folder that contains all outputs (relative to local, default = 'outputs')
fmecamainfile	filename of ODSfile (located in inputpath, default = 'fmeca_demo.ods')
	a structure (matching the output data0) can be used instead to link several calls of fmecaengine (use inputpath to setup the pattern for output filenames, it must include an)
fmecadbfile	fmecadbfile of the meta database (default = 'fmecabaseofconditions.mat')
fmecasheetname	name of spreadsheet that (default = 'sim')
	If you use several sheets, do not use same id between sheets as it will be break the consistency of simulation:
database	a database to feed all numeric input values (with statistics if needed) including Foscale, Kscale a structure such database.table.column than can be indexed as valueA:table::columnA->columnB a valid ODS file that code for a similar structure (table=sheetname, column names=first row)
	By default, fmecaengine assumes that fmecamainfile is a such database
severity	vectorized anonymous function to define severity (default = @(CF,SML) 100*99./max(100*SML./CF-1,0)) Alternative, define first NOELfact = 100; @(CF,SML) NOELfact*(NOELfact-1)./max(NOELfact*SML./CF-1,0)
sample	anonymous function to setup how a one->many or a many->many relationship is sampled default = @(x) prctile(x,[5 50 95]) (only 5th, 50th and 95th percentiles are considered)
	versions older than 0.43 used @(x) [min(x) median(x) max(x)] Note that Foscale and Kscale derived from one->many or a many->many relationships are normalized from the median the sample: setdiff(sample,median(sample))/median(sample)
ADDITIONAL PROPERTIES FOR ADVANCED USERS	(change solver performances used in senspatankar and variants, enable linked instances o.
nograph	flag value (default=true) to prevent graphs from being plotted
options	ODESET structure default value = odeset('RelTol',1e-4,'AbsTol',1e-4,'Initialstep',1e-8,'Maxstep',1e3,'Maxorder',2); % note based nmesh number of finite volumes for a layer with a dimensionless thickness of 1 (accurate for most of purposes) default value = 200
fmecamainfile	matching the output structure data0 can be used instead of a filename to link several calls of fmecaengine inputpath (when fmecamainfile is a structure) setups the pattern for output filenames (it must include the extension .ods)

OTHER PROPERTIES (to change the behavior of fmecaengine, mainly for developers, see code for additional details)

headers	number of header lines (default=2) in fmecamainfile:fmecasheetname
databaseheaders	number of header lines (default=1) in database file
regular_l, regular_D, regular_K, regular_C:	regular expressions to identify column titles matching l,D,K,C
print_id, print_parent, print_inherit, print_l, print_D, print_K, print_C, print_t, print_L, print_Bi:	expressions (matching fprintf syntax) to name layers id,parent,inherit,l,D,K,C,t,L,Bi

OUTPUTS

fmecadb	= fmecaenfine(...) returns the global database listing all conditions
[fmecadb,data0,data,options]	= fmecaenfine(...) returns the input parameters as a structure
data0:	initial content of fmecamainfile as a structure
data:	state of data0 after execution of fmecaengine
options:	options used in the current instance of fmecaengine

OUTPUT FILES (located in outputpath)

raw MAT files for post-processing	
HTML report with linked PNG and PDF files (individual simulations, dependence/inheritance/result graphs, Pareto charts)	

DETAILED DESCRIPTION

- > The current script reads the spreadsheet 'sim' from an ODS file (OpenOffice Spreadsheet) to setup complex migration simulations.
- > Possible simulations (possibly combined) include: multilayer, chained scenarios, setoff effect, hot-filling, sterilization...
Titles in the spreadsheet are used to recognize variables/inputs.
- > Please, check closely the structure of the demonstration ODS file (fmeca_demo.ods) before using this script.
- > Each row in the spreadsheet codes for a single simulation. The spreadsheet can contains an arbitrary number of rows.
- > A column "id" is used to identify each simulation inputs and outputs.
- > Complex chaining of simulations is enabled by using the column "parent" that gives the id of the previous result to be used as input for the next simulation.
The script does not post-process the simulations. It stores all intermediate simulations results as a MAT file (id.mat). For routine control, a corresponding id.png and id.pdf, including the concentration profile and concentration kinetic with twice the requested time, are also saved together.
- > A metadatabase 'fmecadb' (data about simulations), whose filename is defined by the variable fmecadbfile, stores all simulation conditions including solver parameters.
- > The script manages the prioritization and history of all simulations regardless their order in the spreadsheet and their chaining complexity (only limitation: a single parent).
- > For dependent simulations, default input inheritance is also accepted so that only modified parameters need to be specified and all other variables/inputs can be left empty.
- > The script detects any change in unputs and restart all dependent simulations in cascade.
- > Removing any id.MAT file or the entire output directory forces corresponding simulations to be restarted.
- > Removing an entry id in 'fmecadb' (with the command rmfield) is the same as removing the corresponding id.MAT (the corresponding MAT file will be rewritten).
- > Inheritance of the sole inputs (while discarding simulations results) is possible via an optional column 'inherit'. All empty or NaN cells are replaced by their equivalent contents from the row with id corresponding to 'inherit'. Complex propagation are allowed for inheritance (e.g. cascading, tree) whatever the dependence enforced by parent. In case of conflicts between inputs inheritance between 'parent' and 'inherit', the later have a higher precedence. As a rule of thumb, use 'parent' to chain simulations and prefer 'inherit' for sensitivity analysis (e.g. to calculate Jacobians).

> Combinatory simulations (Full or pseudo Monte-Carlo [preferred]) are setup via special columns that contain vectors of scaling values. A valid Matlab syntax embedded with a string can be used to define vectors (1:3, [.1 10], logspace(-3,3,10) ...). Note that the scaling value 1 is removed from the list as the original row with defined values is considered to be the reference simulation with a unitary scaling (i.e. no scaling). Tree bifurcations/ramifications induced by multiple values are automatically generated. New id are based on original id by combining the name of scaling variable (e.g. Fo or K) the following tree level (1..m) and the scaling value (1..n). Row vectors (e.g. 1:3) do not propagate scaling values to children (to simulate different contact times at a step). Column vectors (e.g. (1:3)') propagate scaling values to children (to simulate different classes of molecules). Currently, the following scaling parameters are recognized:

- Foscale scale to simulate indifferently variable diffusion time and diffusion coefficients
- Kscale to simulate different chemical affinity.

> To assess the effect of a single setup, use 0 as scaling parameter (non-propagable value). The corresponding step will be removed. When required, new roots are added to the simulation tree.

fmeaengine can be linked with internal and external databases with keyword 'database' and relational syntaxes (see KEY2KEY).

EXAMPLES for fmea_demo3.ods:

```
100*(test_key:sim::id->CP20) to reuse the concentration value of the simulation with the id test_key
1000*min(PP:polymer::name->classadditives:substance::class->SML) replacing a numerical SML value
min(Dpiringer(PP,PP:polymer::name->classadditives:substance::class->M),40) replacing a numerical D value
Dpiringer(PP,max(PP:polymer::name->classadditives:substance::class->M),40) replacing a numerical D value
Dpiringer(PP,PP:polymer::name->classadditives:substance::class->M,40) replacing a numerical D value and setting up Foscale value.
```

ADVANCED SYNTAXES (see key2key examples for further details)

e.g. request based on alternatives

```
HDPE|PP:polymer::name->classadditives:substance::class->M
```

e.g. request based on superclass defined in "polymerfamily": polyolefin = 'LLDPE;LDPE;MDPE;HDPE;PP'

```
polyolefin:polymerfamily::name->polymer:polymer::name->classadditives:substance::class->name:substance::name->M
```

e.g. request based on regular expressions (simple regular expressions are accepted)

```
\antiUV{3|2}\ :substance::name->M
```

> **fmeaengine** is designed to run in parallel (through several instances) on the computing cluster of JRU 1145 on either Windows or Linux (preferred for efficiency) nodes.

> Please write, an additional script or function for complex post-treatment. It was not the intent of this script. Please, note that for accuracy while preserving memory a linear time scale is used for kinetics and time scale proportional to the square root of time is used for concentration profiles.

ADDITIONAL COMMENTS

- Note 1: To add more layers, update the spreadsheet consistently (no need to modify this script/function)
- Note 2: It is expected that simulation chaining is applied to consistent structures (i.e. with a same number of layers)
- Note 3: Any negative Bi value is interpreted as "setoff" simulation (to be placed as a starting node)
- Note 4: Any change in solver parameters is also detected and forces the whole database to be recalculated (use different output folders to store the results from different strategies if required)
- Note 5: For debugging purposes, the structure array s stores all simulation parameters in same order as in the original spreadsheet. Use r = senspatankar(senspatankar_wrapper(s(i))) to restart the ith simulation
- Note 6: Creation of PDF files on the fly may interact with antivirus software on windows systems. If you get randomly messages such as "print at XXX %temp%\tempfile.ps: Cannot open file: permission denied.", restart the script/function and it should solve the issue.

SEE ALSO: FMECASINGLE FMECAROOT BUILDMARKOV KEY2KEY LOADFMECAENGINEDB

DEPENDENCY INFORMATION TO IMPLEMENT THIS SCRIPT/FUNCTION IN OTHER PROJECTS
 > Dependencies to other functions (written by INRA\Olivier Vitrac)

```
DEMO (Fmecaengine v0.25)
fmeaengine(... without auto expansion
  'local','C:\Data\Olivier\INRA\Etudiants & visiteurs\Audrey Goujon\illustration_fmea',...
  'fmecamainfile','illustration_fmeaengine.ods',...
  'inputpath','inputs',...
  'outputpath','tmp' ...
);

fmeaengine(... automatic expansion
  'local','C:\Data\Olivier\INRA\Etudiants & visiteurs\Audrey Goujon\illustration_fmea',...
  'fmecamainfile','illustration2_fmeaengine.ods',...
  'inputpath','inputs',...
  'outputpath','tmp2' ...
);

DEMO (Fmecaengine v0.27)
fmeaengine...
  'local','C:\Data\Olivier\INRA\Etudiants & visiteurs\Audrey Goujon\illustration_fmea',...
  'fmecamainfile','illustration3_fmeaengine.ods',...
  'inputpath','inputs',...
  'outputpath','tmp3' ...
);

fmeaengine...
  'local','C:\Data\Olivier\INRA\Etudiants & visiteurs\Audrey Goujon\illustration_fmea',...
  'fmecamainfile','illustration4_fmeaengine.ods',...
  'inputpath','inputs',...
  'outputpath','tmp4' ...
);
```

CONTACT

Any question to this script/function must be addressed to: olivier.vitrac@agroparistech.fr
 The script/function was designed to run on the cluster of JRU 1145 Food Process Engineering (admin: Olivier Vitrac)

Migration 2.1 (Fmecaengine v0.45) - 10/04/2011 - INRA\Olivier Vitrac - Audrey Goujon - rev. 26/08/2011

See also

[argcheck\(\)](#), [buildmarkov\(\)](#), [cellcmp\(\)](#), [dispb](#), [dispf](#), [Dpiringer\(\)](#), [fileinfo](#), [find_multiple\(\)](#), [formatfig](#), [formatax](#), [key2key\(\)](#), [localname](#), [loadods\(\)](#), [LOADFMECENGINEDB\(\)](#), [MatchingClosingSymbol](#), [matcmp\(\)](#), [nearestpoint\(\)](#), [print_pdf](#), [print_png](#), [rgb](#), [senspatankar\(\)](#), [senspatankarC\(\)](#), [setoffatankar\(\)](#), [structcmp\(\)](#), [subplots](#), [wraptex\(\)](#) indispensable functions ([shared](#) between toolboxes [migration](#) and [MS](#)) > Commercial toolboxes required: Bioinformatics Toolbox (only [for](#) Graph plotting)

key2key

key2key returns the values related to keyA

SCOPE key2key is a multivalued function (in a Mathematical sense) that implements cardinality operations also known as relationships between tables via primary key, super key and foreign keys. Implemented relationships include:

- one-to-one relationships
- one-to-many relationships
- many-to-many relationships
- cascading between keys

Operations above are applied via an intuitive syntax, different of SQL for concision.

By default, a UNIQUE operator operator is apply to all relationships involving strings or cell array of strings. The request order is respected only for single requests.

Examples of relationships in connection with FMECAENGINE

```
PP:polymer::name->classadditives
PP:polymer::name->classadditives:substance::class->name
PP:polymer::name->classadditives:substance::class->M
```

Background:

```
http://en.wikipedia.org/wiki/Many-to-many\_\(data model\)
http://en.wikipedia.org/wiki/Junction\_table
http://en.wikipedia.org/wiki/Foreign\_key
http://en.wikipedia.org/wiki/Superkey
http://en.wikipedia.org/wiki/Associative Entities
```

Basic syntax: val = key2key(db, key)

INPUTS

db: structure such as db.tableX.columnY = numerical value or string
alternatively a structure coding for an ODS file such as: db=struct('filename',..., 'headers',...)

key: string or a 1xn/nx1 string cell array coding for
keyA

keyA

keyA

key can contain be combined with numbers or can contain Matlab expressions (see examples for details)

NOTE 1: about lists embedded in strings

db.tableX.columnY and keys can include list of strings.

Values are separated by symbols: ';' (semi-colon) or '!' (vertical bar)

As a rule of thumb, '!' must be preferred in keys as they mimic the behavior or operator OR.

NOTE 2: about extra spaces

Spaces are tolerated within key values but note that they are trimmed around ';' and '!'.

Do not use spaces without checking the reliability of the database content.

NOTE 3: about regular expressions

Regular expressions are partly implemented (see the rules below).

A regular expression must start with symbol '!' and end with '!'.

Symbol '*' must be replaced by '#' (* is reserved for multiplications).

Symbols '(' and ')' must be replaced by '{' and '}' respectively

Quantifiers {} must be replaced by {{}}.

Quantifier ? is available

Operators | . \d \D \s \W are implemented

Operators [] ^ \$ \< \> (?< (?= and quantifiers + are not implemented !!!

NOTE 4: about multiple keys

When multiple keys are combined in expressions, they must be enclosed within ()

NOTE 5: about mathematical expressions

Almost any valid Matlab expressions can be combined with keys.

Diringger() has been implemented within a syntax simpler than with Matlab conventional one

Dpiringer(polymercode, key:table1::columnA1->columnB1:table2::columnA2->columnB2 ...->M)

Dpiringer(polymercode, key:table1::columnA1->columnB1:table2::columnA2->columnB2 ...->M, temperature)

OUTPUTS

val: array of values as stored in db when key is a string
a nx3 array as [min(values median(values) maximum(values)]

Advanced syntax: [val, dbout] = key2key(...)
dbout: database (loaded if needed)

Internal syntax: val = key2key(db, key, interpreterflag, recursionflag)
interpreterflag (default = true) executes keys as possible Matlab expressions
recursionflag (default=false) forces key2key to drop the recursion

Syntax with specific statistical analysis (works only with cell array of keys)
val = key2key(db, keyarray, [],[], percentiles)
default percentiles = 5th, 50th, 100th

TOY EXAMPLES, execute lines between {} with F9 (evaluate)

```
%{
% EXAMPLE 1 (full toy example)
key = 'PP:polymer::name->classadditives:substance::class->name';
db.polymer = ...
    struct('name', {'LLDPE' 'LLDPE' 'LDPE' 'LDPE' 'MDPE' 'MDPE' 'HDPE' 'HDPE' 'PP' 'PP'}),...
    'classadditives', {'antioxidants' 'antiUV' 'antioxidants' 'antiUV' 'antioxidants' 'antiUV' 'antioxidants' 'antiUV' 'antioxidants'});
db.substance = ...
    struct('class', {'antioxidants' 'antioxidants' 'antioxidants' 'antiUV' 'antiUV' 'antiUV'},...
        'name', {'antiox1' 'antiox2' 'antiox3' 'antiUV1' 'antiUV2' 'antiUV3'}),...
        'M', [ 101      102      103      201      202      203 ]',...
    );
key2key(db, key)

%}
%{
% EXAMPLE 2: Variation based on example 1 (not very useful but illustrate the jump between multiple tables)
key2 = 'PP:polymer::name->classadditives:substance::class->name:substance::name->M';
key2key(db, key2)

%}
%{
```

```

% EXAMPLE 3: Variation based on example 2 (use of superclass as key)
key3 = 'polyolefin:polymerfamily::name->polymer:polymer::name->classadditives:substance::class->name:substance::name->M';
db.polymerfamily = struct...
    'name', {'polyolefin' 'polystyrene'}, ...
    'polymer', {'LLDPE;LDPE|MDPE;HDPE;PP' 'HIPS;PS'} ...
);
key2key(db, key3)
%}
%{
% EXAMPLE 4: Variation based on example 3 (behavior in presence of missing values)
key4 = 'LDPE|undefined|PP:polymer::name->classadditives:substance::class->name:substance::name->M';
key2key(db, key4)
%}
%{
% EXAMPLE 5: Variation based on example 4 (alternative values, note that extra spaces can be included arround operator '| ')
key5 = 'antiUV2 | antiox1 | antiUV3 :substance::name->M';
key2key(db, key5)
%}
%{
% EXAMPLES 6: Variation based on example 5 (search all anitUVi with i=0..9)
key6a = '\antiUV\d\ :substance::name->M';
key6b = '\antiUV\d\{1\}\ :substance::name->M';
key6c = '\antiUV\d\{1,1\}\ :substance::name->M';
key6d = '\antiUV\d?\ :substance::name->M';
key2key(db, key6a)
key2key(db, key6b)
key2key(db, key6c)
key2key(db, key6d)
%}
%{
% EXAMPLES 7: Variation based on example 6 (to illustrate the difference beween regular expressions)
key7a = '\antiUV\{3|2\}\ :substance::name->M';
key7b = '\antiUV\{2\}\ :substance::name->M';
key7c = '\.#\#PE.\#:polymer::name->classadditives:substance::class->name:substance::name->M';
key7d = '\PE\:polymer::name->classadditives:substance::class->name:substance::name->M';
key7e = '\PE:\polymer::name->classadditives:substance::class->name:substance::name->M';
key2key(db, key7a) % interpreted as containing antiUV3 or containing antiUV2
key2key(db, key7b) % interpreted as containing antiUV3 or containing 2
key2key(db, key7c)
key2key(db, key7d)
key2key(db, key7e)
%}
%{
% EXAMPLES 8: with mathematical formula
key8a = 'Dpiringer(PP,PP:polymer::name->classadditives:substance::class->M)';
key8b = 'min(Dpiringer(PP,PP:polymer::name->classadditives:substance::class->M,40))';
key8c = 'Dpiringer(PP,max(PP:polymer::name->classadditives:substance::class->M))';
key8d = 'min(Dpiringer(PP,PP:polymer::name->classadditives:substance::class->M,100))';
key8e = 'Dpiringer(LDPE,\antiUV\{3|2\}\:substance::name->M)';
key8f = 'Dpiringer(LDPE,[\antiUV\{3|2\}\:substance::name->M];(\antiUV1\:substance::name->M))';
key2key(db, key8a)
key2key(db, key8b)
key2key(db, key8c)
key2key(db, key8d)
key2key(db, key8e)
key2key(db, key8f)
%}
%{
% EXAMPLE 9: example 8a with double and triple keys
db.contact = struct('condition', {'cond1' 'cond2' 'cond3'}), 'temperature', [25 40 110];
key9a = 'Dpiringer(PP,(PP:polymer::name->classadditives:substance::class->M),(cond3:contact::condition->temperature))';
key2key(db, key9a)
db.scenario = struct('id', {'scenarioA' 'scenarioB' 'scenarioC'}), 'polymer', {'PP' 'LDPE' 'PS'});
key9b = 'Dpiringer((scenarioA:scenario::id->polymer),(PP:polymer::name->classadditives:substance::class->M),(cond3:contact::con...
key2key(db, key9b)
key9c = 'Dpiringer((scenarioA:scenario::id->polymer),(scenarioA:scenario::id->polymer:polymer::name->classadditives:substance::...
key2key(db, key9c)
%}

```

See also

[fmecaengine](#) [fmecasing](#) [ismemberlist](#) [expandtextaslist](#) [loadfmecaenginedb](#)

fme casingle

fme casingle calculate the migration contribution of single steps from FMECA simulations including omitted steps (e.g. Foscale = [0 0])

SYNTAX res = fme casingle(db ,ref,proba)
[res,resunique] = fme casingle(...)

INPUTS

- db: database generated by FMECAENGINE with Foscale=[0 0] forced to all steps
All considered simulations (possibly independent) must have originally a similar number of steps.
Simulations can be derived from a previous simulation with modalities (several Foscale or Kscale values possibly combined)
- ref: names or indices of reference steps (by default they are derived from inherit information)
Reference simulations - simulations before omission/deletion with Foscale = [0 0]
- default = []

proba: probability of terminal nodes (their sum must be equal to 1)
It can be an array in the same order as terminal nodes in db
or a structure such as proba.node = value
The structure assignment must be preferred when the order is unknown.
default = [] assigns 1/n where n is the number of terminal nodes

OUTPUTS

- res: structure with fields coding for all steps used as input (identified from res.(step) - {dcF values})
- resunique: multiple structure that match only steps without modalities
resunique.value.(step0)=[dcF values]
resunique.id.(step0)=[corresponding names]
resunique.proba.(step0)=[corresponding probabilities]

Example (used for development):

```
load('C:\Data\Olivier\Communications\LNE2011\drafts\fme cabaseofconditions.mat')
res = fme casingle(db);
SM=1e-3; severity=(CF*100*99.*max(100*SML./CF-1,0));
hfig=figure; forntfig(hfig,'filename','omission_dseverity','paperposition',[ 5.0467    7.2245   10.8907   15.2284]);
ha = subplot([1.2 1],[1.6 4],[],[],'allive',3);
subplot(hs), hold on, i = 0;
for step=fieldnames(res)
    i=i+1;
    res.(step{1}) = struct('dCf',res.(step{1}), 'severity',severity(res.(step{1})), 'col',interp1(linspace(0,1,64),jet(64),severity(res.(step{1}))'/100 ) );
    res.(step{1}).severity(res.(step{1}).severity==0)=NaN;
    res.(step{1}).col(isnan(res.(step{1}).col))=0;
    plotp([i*ones(size(res.(step{1}).severity)),res.(step{1}).severity,'markerfacecolor',res.(step{1}).col,'markeredgecolor',res.(step{1}).col,'linestyle','none','markersize',12,'marker','o']);
    text(1,0,[step{1}{1}],'fontsize',16,'rotation',90,'HorizontalAlignment','right','VerticalAlignment','middle');
end
hr = resline(0,100); set(hr,'color','r','LineWidth',2,'LineStyle','');
hr = resline(0,33); set(hr,'color','c','LineWidth',2,'LineStyle','');
formatax(hs,'FontSize',18,'XickLabel',''); ylabel('Severity','FontSize',16);
print_png(300,get(gcf,'filename'),'O:\Data\Olivier\Communications\LNE2011\drafts');
```

SEE ALSO

[fme engine](#) [fmecaroot](#) [key2key](#) [buildmarkov](#) [loadfmeengine](#) [nd](#)

fmecaroot

fmecaroot returns the root (according to prop) of each node (to be created with FMECAENGINE)

syntax: root = fmecaroot(fmecadb [,prop])

fmecadb: output object of FMECAengine

prop: 'parent' (default) or 'inherit'

See also

[fmecaengine](#), [fmecasingle](#), [buildmarkov](#), [loadfmecaenginedb](#), [key2key](#)

buildmarkov

buildmarkov builds a Markov chain based on a list keywords or values and a list of parent

```
[treename,treeind] = buildmarkov(list,parent)
treename: nx1 cell array giving all possible n paths as names (taken from list)
           structure generated by fmecaengine
treeind: nx1 cell array giving all possible n paths as indices
[treename,treeind,map,succ] = buildmarkov(list,parent,'property',value)
    Implemented properties/values
        sort = 'none' (default), 'ascend' or 'descend'
    map: mxn array (m=max path depth) matching treeind but coded as find_multiple does with format=1
    succ: 1xn array (l=max number of children) coding for the list of children (coded as find_multiple does with format=1)
```

example

```
list = {'A1' 'B1' 'C1' 'A2' 'A3' 'A4' 'C3' 'C2' 'AA1' 'AA2' 'AB1' 'AB2'}
parent = {'' '' '' 'A1' 'A2' 'A3' 'C2' 'C1' 'A1' 'AA1' 'AA1' 'AB1'}
[pathsnames,pathsind]=buildmarkov(list,parent)
pathsnames{::}
ans =
    'A1'      'A2'      'A3'      'A4'
ans =
    'A1'      'AA1'     'AA2'
ans =
    'A1'      'AA1'     'AB1'     'AB2'
ans =
    'B1'
ans =
    'C1'      'C2'      'C3'
```

SEE ALSO

[fmecaengine](#), [fmecasingle](#), [loadfmecaenginedb](#), [key2key](#), [ismemberlist](#)