MACH 0.94 (subsonic)

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1 Introduction

The Model Analysis and Checker (MACH) tool is an experimental tool to deploy and test advanced algorithms for analyzing UML models. MACH is a flexible and lightweight framework for the loose integration of independent tools, and a set of tools integrated this way under a common UI. All parts of MACH are implemented using SWI-Prolog [5]. Many of its more advanced parts have been subject to previous research publications.

MACH is targeted at modelers that already have a fairly good understanding of UML as a modeling language. Given its purpose and intended audience, MACH puts little focus on UI, making it somewhat challenging to use. MACH is more of a tool demonstrator rather than a high-productivity CASE tool.

2 Getting started

2.1 Obtaining and installing MACH

MACH requires SWI Prolog to be installed. To the best of our knowledge, MACH works with any recent version of SWI-Prolog. SWI Prolog can be downloaded from www.swi-prolog.org and is available for many platforms. The installation is easy, but takes a a few minutes. MACH can be downloaded for free from www.compute.dtu.dk/~hsto/tools. Installing MACH amounts to unpacking the zip and placing the executable in the directory that also contains the swipl.dll (or equivalent thereof on other platforms). Start MACH by running the executable (i.e., double-clicking or similar). MACH will open a console window. In the console window, it's probably best to first set the path to the directory with samples that comes with MACH. It is placed inside MACH, so you just have to say "cd "samples". See below for a sample session.

2.2 First steps

Conventions Commands are entered at the prompt and terminated by the $\langle CR \rangle$ character. Names containing special symbols like spaces, slashes, hash, or dollar signs must be enclosed in double quotes. There are some problems with long file names, and it is thus recommended to use short and simple names when working with MACH. The MACH command line has a history function, that is, the cursor keys $\langle UP \rangle$ and $\langle DOWN \rangle$ recall the previous commands. MACH is exited by typing "quit". There is currently only a rudimentary help function, help for specific commands is not implemented. Similarly, the commands "magic" and "pray" are not yet implemented. Observe that MACH is case sensitive.

Issues Every now and then, a command fails and MACH terminates unexpectedly. For instance, this happens when model names that are supposed to be enclosed by double quotes are not properly closed, i.e., the trailing quotes are omitted. While inconvenient, the user can often recover from this fault quite easily by restarting MACH (saying "mach." at the PROLOG command line). This allows the user to carry on exactly where MACH exited: the environment (such as the current working directory and the opened models) are maintained. At this point, MACH has only been tested with the XMI produced by MD 16.9 to 17.0.3. Since commercial and academic UML modeling tools tend to deviate from the XMI standard, using other file formats might result in incompatibilities.

Getting help The command "help" reminds you of some basic commands and conventions. The command "help commands" lists the available commands alphabetically and provides a short description. The command "help X" will provide a more detailed description for the command X. Any characters after X are ignored so that if a command fails, one can simply recall the previous command from the command history by CURSOR UP, go to its beginning by POS1, and insert "help" to obtain help on the respective command.

```
Welcome to MACH 0.93 ("Subsonic") (C) 2013-2014, H. Strrle
no warranties whatsoever
MACH is case sensitive - exit by saying "quit"
> pwd
h:/_arbeitsbereich/projekte/momat/
> cd "mach/samples"
> pwd
h:/_arbeitsbereich/projekte/momat/mach/samples/
> ls -m
       LMS_2011_2.mdxml
                              m2.mdxml
                                           IE1.mdxml IE2.mdxml
> open "LMS_2011_2"
% LMS_2011_2.pl compiled into LMS_2011_2 0.22 sec, 2,586 clauses
> size "LMS_2011_2"
Model LMS_2011_2 has 2584 elements with 7568 attributes.
This is magnitude 4, a medium model.
> frequency "LMS_2011_2" width 60 min 25 sort alphabetical
                    activity 33 ++
            activityFinalNode 26 ++
            activityPartition 69 +++++
                 association 120 +++++++
           callBehaviorAction 231 +++++++++++++
            centralBufferNode 26 ++
                      class 30 ++
         componentRealization 26 ++
                connectorEnd 32 ++
                 dataStoreNode 26 ++
                decisionNode 58 ++++
           enumerationLiteral 37 ++
                    forkNode 27 ++
                     include 60 ++++
                 initialNode 31 ++
                    inputPin 39 +++
              literalInteger 38 +++
messageOccurrenceSpecification 39 +++
                  objectFlow 105 +++++++
                   operation 58 ++++
                   outputPin 35 ++
                     package 37 ++
                   receiveOperationEvent 43 +++
                      state 38 +++
                  transition 62 ++++
                     trigger 45 +++
                     useCase 32 ++
```

>

3 Working with directories

MACH offers some commands to navigate directory trees. The syntax is vaguely reminiscent of a UNIX shell, but offers only a very small number of the most basic options. Recall that using some special characters such as white spaces will require that you enclose your path expression in double quotes.

pwd

Shows the current working directory ("print working directory").

cd PATH

Move to the directory indicated by the parameter ("change directory"). Accepts a relative path separated by "/", and using ".." for the upper level directory. E.g. cd subdir changes the working directory to the subdir subdirectory of the current working directory. Path names have to be enclosed by double quotes.

ls OPTION

Shows the contents of the current working directory. Accepts the following values for ${\tt OPTION}:$

- m : list only models
- ${\tt a}$: list all files
- p : list all Prolog files

4 Working with Models

The following commands are used to access existing models in MACH. Models are assumed to be stored as files conforming to the MagicDraw MDXML format (based on the standard XMI model interchange format), having the *.mdxml* file extension.

open FILE

Accesses FILE and tries to interpret it as a model. The *.mdxml* file extension should be omitted when specifying FILE. E.g.: The command open testmodel opens the model stored in the file *testmodel.mdxml*.

open FILE as \$ALIAS

Accesses FILE and tries to interpret it as a model. Assigns the name **\$ALIAS** as a shorthand for the file. This alias may be used instead of a model file name in all subsequent commands. When using an alias, it must be preceded by the dollar sign. The *.mdxml* file extension should be omitted when specifying FILE. E.g.: The command open testmodel as \$x opens the model stored in the file *testmodel.mdxml* and assigns \$x as a shorthand for it.

show all aliases

List all currently defined aliases.

show alias \$ALIAS

Show details of the specified alias.

clear all aliases

Remove all alias declarations.

clear alias \$ALIAS

Remove the specified alias declaration.

models

show all opened models

List all the models currently opened.

5 Querying and inspecting models

The following commands are used to search for specific patterns or elements in models, and to ispect parts of models in detail.

dump all of MODEL

Show a tabular overview of all elements in MODEL. E.g.: The command dump all of x shows a tabular overview of all elements in the model previously associated with the alias x, while the command dump all of testmodel shows a tabular overview of all elements in the model stored in the file *testmodel.mdxml*.

dump #ID of MODEL in (detail|summary|overview)

Show a tabular overview of the element with identifier ID in MODEL, providing several levels of details. E.g.: The command dump #mdx123 of \$x in detail shows a detailed tabular overview of the element with ID = mdx123 of the model previously associated with the alias \$x, while the command dump #mdx123 of testmodel in summary shows a summary tabular overview of the element with ID = mdx123 of the model stored in the file testmodel.mdxml.

find exactly QUERY in MODEL

Looks for the string QUERY in MODEL, as an exact match.

find QUERY in MODEL

Looks for the string QUERY in MODEL, with a degree of vagueness in the matching (e.g., to correct for typos and the like).

6 Model differences and versions

difference between MODEL1 and MODEL2

Compute the difference between MODEL1 and MODEL2 and list the result in a table. The algorithms applied in this command and its options explained below are published as [1, 2, 3].

difference between E1 of MODEL1 and E2 of MODEL2

Compute the difference between the sub-model below the element E1 in MODEL1 and element E2 in MODEL2. The result is presented in a table by default.

difference between MODEL1 and MODEL2 aggregated

After computing the difference between the two models, this option instructs MACH to try and aggregate the (large) number of low-level changes into a smaller number of high-level changes that make more sense to modelers (cf. [3]). By default, the result is presented in a table. Aggregation only works for class models.

diff MODEL1 and MODEL2 as text

Present the difference as prose rather than in a table. This feature works only for class models, and it is not very reliable.

7 Model similarity

similarity of MODEL1 and MODEL2 by identifiers

Compute the overlap of the identifiers between the two models. This metric only makes sense when applied to successive versions of a models. If the modeling tool used creates identifiers in a deterministic way, high similarity scores may be indicated for dissimilar models.

similarity of MODEL1 and MODEL2 by edits

Compute the similarity between MODEL1 and MODEL2 as correlated to the inverse of the edit distance. The values range from 1 to 0, where larger values represent models of greater similarity. Identical models have an edit distance of 0, which we interpret as a similarity of 1. The edit distance yields a more sensitive similarity metric than spectral comparison, but is limited to comparing models with a (close) common ancestor, such as one of the two models to be compared. Comparing models without a (close) common ancestor will yield edit distances larger than the target model size. This metric only makes sense when applied to successive versions of a models.

similarity of MODEL1 and MODEL2 by length

Compute the similarity of the two models purely based on their length. This metric may be applied to models that are not successive versions of each other, but is a very coarse approximation of true similarity.

similarity of MODEL1 and MODEL2 by spectrum

Compute the (scaled) cosine-similarity of the meta-class spectra of MODEL1 and MODEL2. The values range from 1 to 0, where larger values represent models of greater similarity. Identical models receive a value of 1. This metric may be applied to models that are not successive versions of each other. It is a better approximation to "similarity by length".

similarity of MODEL1 and MODEL2 by plgind

Compute the likelihood that the two models are successive versions of each other. If the two models score high on this similarity without being proper versions of each other, this is an indication of plagiarism.

8 Model size and quality

The following commands are used to perform model manipulation tasks.

size of MODEL

Provide a rough measure of the size of MODEL. E.g.: The command size x computes the size of the model previously associated with the alias x, while the command size testmodel computes the size of the model stored in the file *testmodel.mdxml*.

frequency of MODEL

Show a histogram of the frequency distribution of meta classes in MODEL. E.g.: The command frequency x shows a histogram of the frequency distribution of meta classes in the model previously associated with the alias x, while the command frequency testmodel shows a histogram of the frequency distribution of meta classes in the model stored in the file *testmodel.mdxml*.

frequency difference of MODEL_1 MODEL_2

Show a histogram of the frequency distribution of meta classes in MODEL. Both this and the previous command offer a free combination of the following options attached to their end.

...sort DIRECTION

Sort the entries by increasing or decreasing size, or alphabetically by the name of the meta-class.

...width INT

Scale the output to fit on INT columns.

...scale FACTOR

Scale the output by the given factor (may result in visually empty bars).

...min VALUE

Clip all entries smaller than the given value.

...max VALUE

Clip all entries greater than the given value.

clones of MODEL

Computes and lists clone candidates in MODEL. E.g.: The command clones x shows clone candidates in the model previously associated with the alias x, while the command clones testmodel shows clone candidates in the model stored in the file testmodel.mdxml. The algorithms applied in this command are published as [4].

A Cheat Sheet

Notation inspired by EBNF.

```
pwd
cd PATH
ls [-m|-a|-p]
open FILE [as $ALIAS]
show all aliases
show alias $ALIAS
clear all aliases
clear alias $ALIAS
dump all of MODEL
dump #ID of MODEL in (detail|summary|overview)
find [exactly] QUERY in MODEL
similarity of MODEL1 and MODEL2
                       [by (spectrum|edits|identifiers|length|plgind)]
diff [E1 of] MODEL1 and [E2 of] MODEL2 [ aggregated |as text]
size MODEL
frequency MODEL
frequency difference A B
clones MODEL
```

References

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