

mimR – a (small) contribution to gR

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mimR – graphical models in R

- **MIM** (www.hypergraph.dk) is a general (and unique) package for statistical inference (model fitting, model selection etc.) in **Mixed Interaction Models** – a large class of “graphical” models (where conditional independence restrictions are of interest).
- **R** is a general statistical package and programming environment.
- **mimR** integrates the functionality of **MIM** into **R**. **mimR** is available as an **R** package. For additional information, see

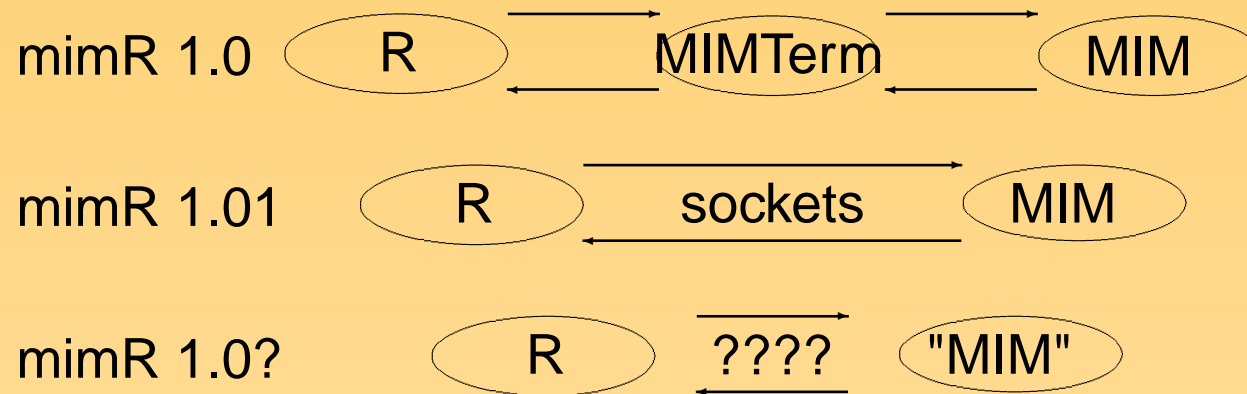
<http://www.jbs.agrsci.dk/~sorenh/mimR/>

Outline of presentation

- Why **mimR**??
 1. In 2000, needed to access **MIM** from Splus
 2. In 2002, the gR-workshop lead to a proper **R** package
- Why the name **mimR**??
- Technicalities: Accessing **MIM** from **R**
- Primitive use of **mimR**
- The object structure of **mimR**:
 - ▶ **mimData**
 - ▶ **mimModel**
- The future of **mimR**
- Example

Technicalities: Accessing MIM from R

Think of **MIM** as the “inference engine” accessed from **R**:



Presumably not the most elegant way one can think of – but it works...

MIM Models – very briefly

Discrete variables d , continuous variables y .

Model: $p(d, y) = p(d)p(y|d)$ where

- $p(d; \theta)$: Log-linear model
- $p(y|d) = N(\mu_d, \Sigma_d)$

Structure of models arise by imposing constraints on $(\theta, \mu_d, \Sigma_d)$.

The *syntax* for a MIM model

$$d_1, d_2, \dots, d_p / l_1, l_2, \dots, d_q / q_1, q_2, \dots, q_r$$

referring to the *d*iscrete, *l*inear and *q*uadratic generators.

“Primitive” use of mimR

1. Direct access to **MIM** via `mim.cmd`–function, e.g.

```
mim.cmd("input d:\mathmark.dat; model //xyz,xzu; fit;")
```

which returns whatever the last **MIM** command returns.

2. **mimR** has a collection of functions mimicing corresponding **MIM** functions but interprets the output in appropriate ways (creates data structures with the output):

mimR function	MIM command
mim.stepwise	stepwise
mim.testdelete	testdelete
mim.print	print
mim.display	display
mim.fit	fit
mim.emfit	emfit

mimR is object-oriented

- Variable names in **MIM** are 1-character, “a”, “b”,..., which is an inconvenient restriction...
- To circumvent this restriction, a mechanism for mapping dataframe-names to **MIM**-names (and vice versa) was established by means of **mimData**-objects.
- From thereof the road was paved for creating **mimModel**-objects etc. such that (at least in principle) the user needs not be concerned with that model fitting, model selection etc. takes place in **MIM**.

mimData-objects

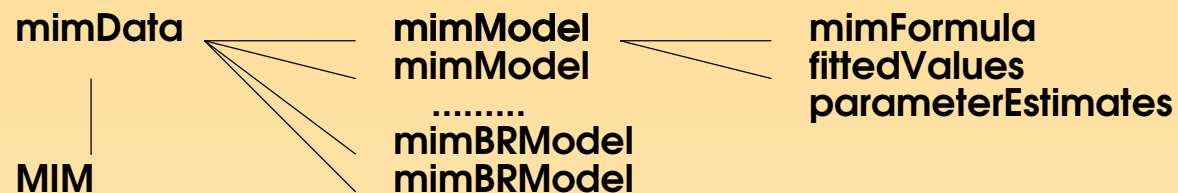
A data frame in **R** is turned into a **mimData**-object, which can be submitted to **MIM**:

```
md <- as.mimData(data=...)
submit(md)
```

mimR keeps track of that **md** is the *current* **MIM** data set (the data set currently loaded into **MIM**). (There can be at most one current data set at the time).

md is an object of class **mimData** to which certain *methods* are associated.

To a **mimData** object several **mimModel** objects can be associated.



`mimModel`-objects

A `mimModel`-object consists of

- A `mimFormula`-object (where the model formula follows **MIM** syntax).
- A (reference to) a corresponding `mimData` object.
- Summary statistics (currently, deviance and DF).
- Slot `is.current` (there can be at most one current model at the time)

```
mm <- mim.model( mim-formula, data=... )
```

The future (if any) of mimR

mimR will hopefully be obsolete in a not too distant future – not because graphical modelling in **R** is not relevant, but because a more coherent approach to graphical modelling in **R** is needed.

– That is the aim of the gR–project.

Until that happens, proceed at slow pace:

- Move functionality from **MIM** to **R**
- Create graph modules
-

Example

```
library(mimR)
data(carcass)
md <- as.mimData(carcass)
submit.mimData(md)

mm1 <- mim.model("//F11:M11:F12:M12:F13:M13,LMP", data=md)
mm2 <- stepwise(mm1,"f")
mm3 <- stepwise(mm2,"ub")

mp <- mim.print("i")
d1 <- display(mm2, "LMP", c("F11:M11:F12:M12:F13:M13"))
d2 <- display(mm2, c("LMP","F11"), c("M11:F12:M12:F13:M13"))
d3 <- display(mm2, c("LMP","F11"))

carcass2 <- carcass
carcass2[, "L"] <- rnorm(nrow(carcass2))
md2 <- as.mimData(carcass2)
submit.mimData(md2)
```

```
mm4 <- mim.model("//L:F11,L:M11,L:F12,L:M12,L:F13,L:M13,L:LMP",
  data=md2, fit=F)
namesTable(md2)
mim.cmd("calc h=ln(0)")
mim.emfit(plot=T)
d4 <- display(mm4, "LMP", c("F11:M11:F12:M12:F13:M13"))

data(rats)
m.rats <- as.mimData(rats)
mm1 <- mim.model("Sex, Drug/Sex:W1,Drug:W1,\
  Sex:W2,Drug:W2/Sex:W1:W2,Drug:W1:W2", data=m.rats)
mm2 <- stepwise(mm1)
```