Computer Lab II

Further introduction to Biogeme
Binary Logit Model Estimation

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Today

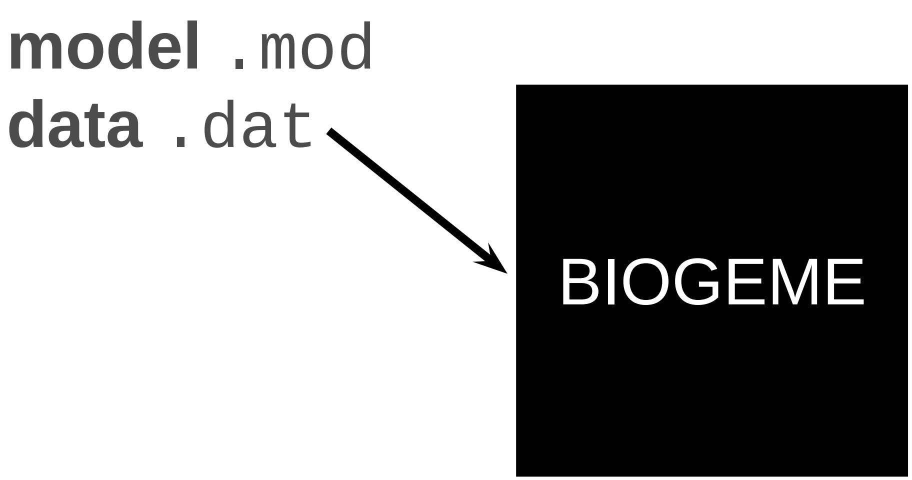
- **Further introduction to BIOGEME**
- Estimation of Binary Logit models

How does BIOGEME work?

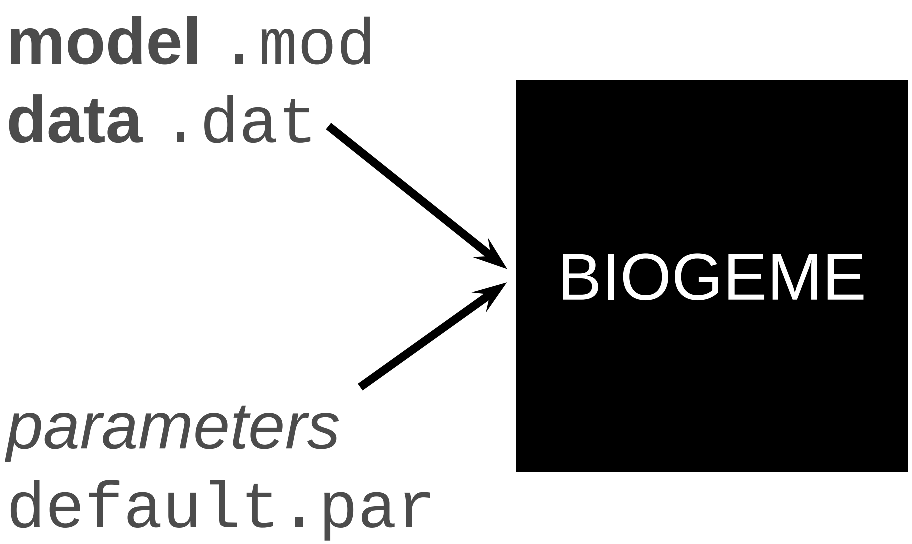
How does BIOGEME work?

BIOGEME

How does BIOGEME work?



How does BIOGEME work?



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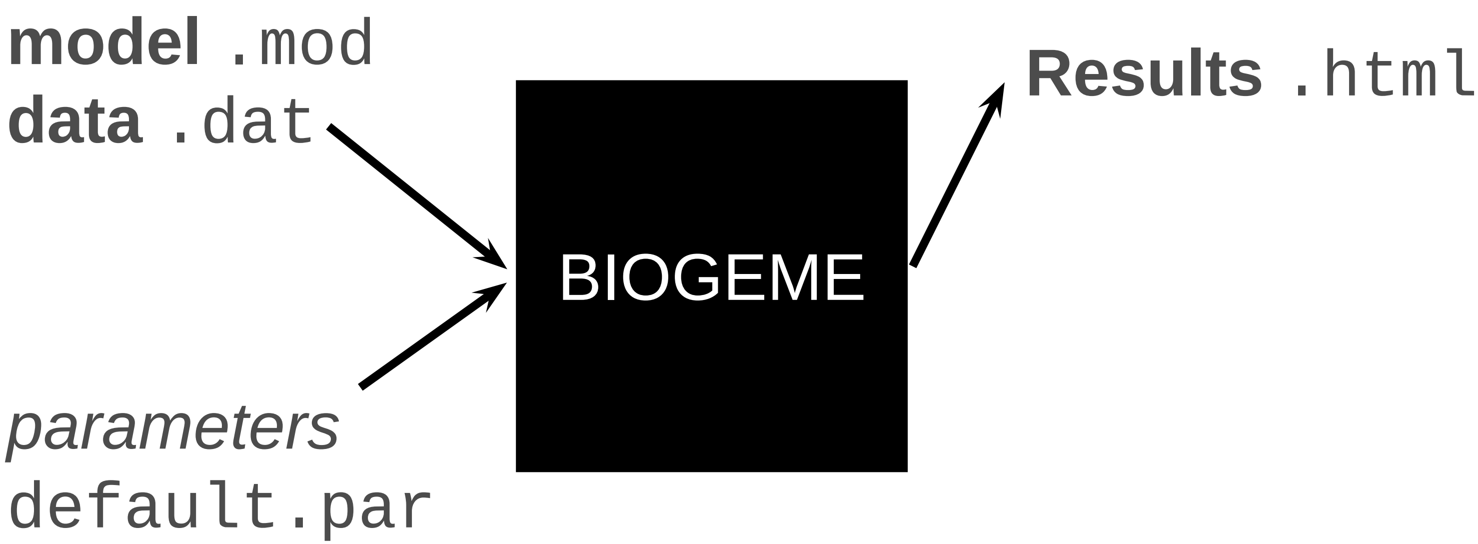

How does BIOGEME work?

How does BIOGEME work?

model `.mod`
data `.dat`

parameters
`default.par`

BIOGEME

Results `.html`

Final model `.res`

Data statistics etc.
`.sta` `.log` `.rep` ...

BIOGEME - Data file

- File extension `.dat`
- First row contains column / variable names
- One observation per row
- Each line must contain a choice indicator

- Example with the Netherlands transportation mode choice data: choice between car and train

BIOGEME - Data file

netherlands.dat

id	choice	rail_cost	rail_time	car_cost	car_time
1	0	40	2.5	5	1.167
2	0	35	2.016	9	1.517
3	0	24	2.017	11.5	1.966
4	0	7.8	1.75	8.333	2
5	0	28	2.034	5	1.267
...					
219	1	35	2.416	6.4	1.283
220	1	30	2.334	2.083	1.667
221	1	35.7	1.834	16.667	2.017
222	1	47	1.833	72	1.533
223	1	30	1.967	30	1.267

BIOGEME - Data file

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Unique identifier of observations

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BIOGEME - Data file

netherlands.dat

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Choice indicator, 0: car and 1: train

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BIOGEME - Model file

- File extension `.mod`
- Must be consistent with data file
- Contains deterministic utility specifications, model type etc.
- The model file contains different *sections* describing different elements of the model specification

BIOGEME - Model file

- How can we write the following deterministic utility functions for BIOGEME?

$$V_{\text{car}} = \text{ASC}_{\text{car}} + \beta_{\text{time}}\text{car}_{\text{time}} + \beta_{\text{cost}}\text{car}_{\text{cost}}$$

$$V_{\text{rail}} = \beta_{\text{time}}\text{rail}_{\text{time}} + \beta_{\text{cost}}\text{rail}_{\text{cost}}$$

BIOGEME - Model file

```
[Choice]
choice

[Beta]
// Name       DefaultValue LowerBound UpperBound  status
ASC_CAR       0.0          -100.0     100.0         0
ASC_RAIL      0.0          -100.0     100.0         1
BETA_COST     0.0          -100.0     100.0         0
BETA_TIME     0.0          -100.0     100.0         0

[Utilities]
//Id Name Avail linear-in-parameter expression
0    Car  one   ASC_CAR * one + BETA_COST * car_cost +
                BETA_TIME * car_time
1    Rail one   ASC_RAIL * one + BETA_COST * rail_cost +
                BETA_TIME * rail_time
```

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BIOGEME - Model file

```
[Choice]
choice

[Beta]
// Name       DefaultValue LowerBound UpperBound  status
ASC_CAR       0.0          -100.0     100.0         0
ASC_RAIL      0.0          -100.0     100.0         1
BETA_COST     0.0          -100.0     100.0         0
BETA_TIME     0.0          -100.0     100.0         0

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BIOGEME - Model file

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```

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BIOGEME - Model file

What is one?

Which is the type of model?

```
[Choice]
choice

[Beta]
// Name       DefaultValue LowerBound UpperBound  status
ASC_CAR       0.0          -100.0     100.0         0
ASC_RAIL      0.0          -100.0     100.0         1
BETA_COST     0.0          -100.0     100.0         0
BETA_TIME     0.0          -100.0     100.0         0

[Utilities]
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0    Car  one   ASC_CAR * one + BETA_COST * car_cost +
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1    Rail one   ASC_RAIL * one + BETA_COST * rail_cost +
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```

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BIOGEME - Model file

```
[Expressions]
// Define here arithmetic expressions for name that are not directly
// available from the data
one = 1

[Model]
// Currently, only $MNL (multinomial logit), $NL (nested logit), $CNL
// (cross-nested logit) and $NGEV (Network GEV model) are valid keywords
//
$MNL
```

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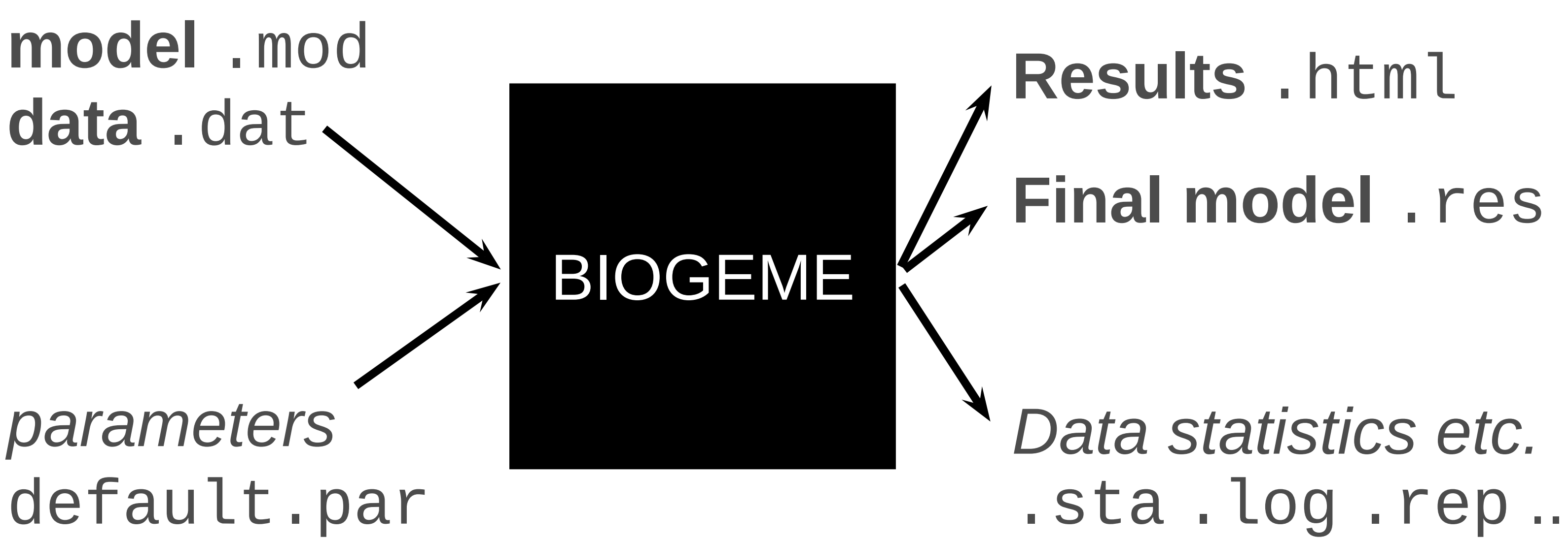
How does BIOGEME work?



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Model and Data Files

- How to read and modify model files?
  How to read data files?
  - GNU Emacs or Wordpad
  - Notepad should not be used!

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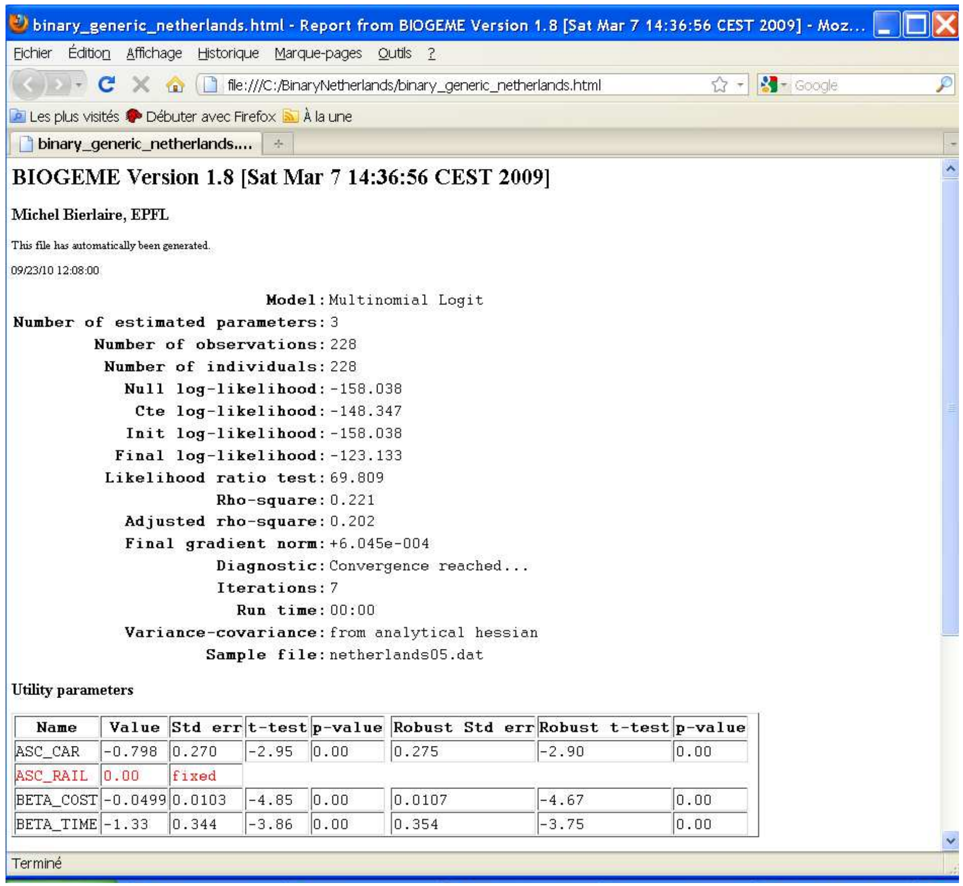
BIOGEME - Results - Netherlands dataset



BIOGEME Version 1.8 [Sat Mar 7 14:36:56 CEST 2009]

Michel Bierlaire, EPFL

This file has automatically been generated.

09/23/10 12:08:00

Model:	Multinomial Logit
Number of estimated parameters:	3
Number of observations:	228
Number of individuals:	228
Null log-likelihood:	-158.038
Cte log-likelihood:	-148.347
Init log-likelihood:	-158.038
Final log-likelihood:	-123.133
Likelihood ratio test:	69.809
Rho-square:	0.221
Adjusted rho-square:	0.202
Final gradient norm:	+6.045e-004
Diagnostic:	Convergence reached...
Iterations:	7
Run time:	00:00
Variance-covariance:	from analytical hessian
Sample file:	netherlands05.dat

Utility parameters

Name	Value	Std err	t-test	p-value	Robust Std err	Robust t-test	p-value
ASC_CAR	-0.798	0.270	-2.95	0.00	0.275	-2.90	0.00
ASC_RAIL	0.00	fixed					
BETA_COST	-0.0499	0.0103	-4.85	0.00	0.0107	-4.67	0.00
BETA_TIME	-1.33	0.344	-3.86	0.00	0.354	-3.75	0.00

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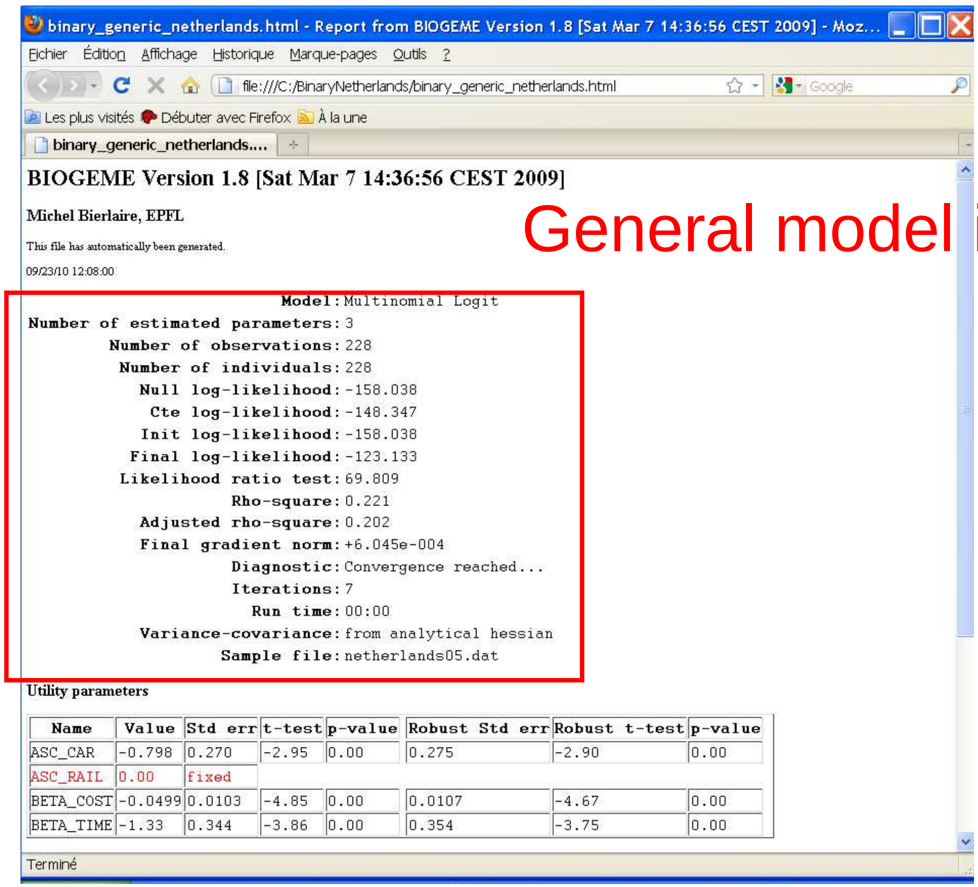
BIOGEME - Results



binary_generic_netherlands.html - Report from BIOGEME Version 1.8 [Sat Mar 7 14:36:56 CEST 2009] - Moz...

Fichier Édition Affichage Historique Marque-pages Outils ?

file:///C:/BinaryNetherlands/binary_generic_netherlands.html

Les plus visités Débuter avec Firefox À la une

binary_generic_netherlands....

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BETA_TIME	-1.33	0.344	-3.86	0.00	0.354	-3.75	0.00

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General model information

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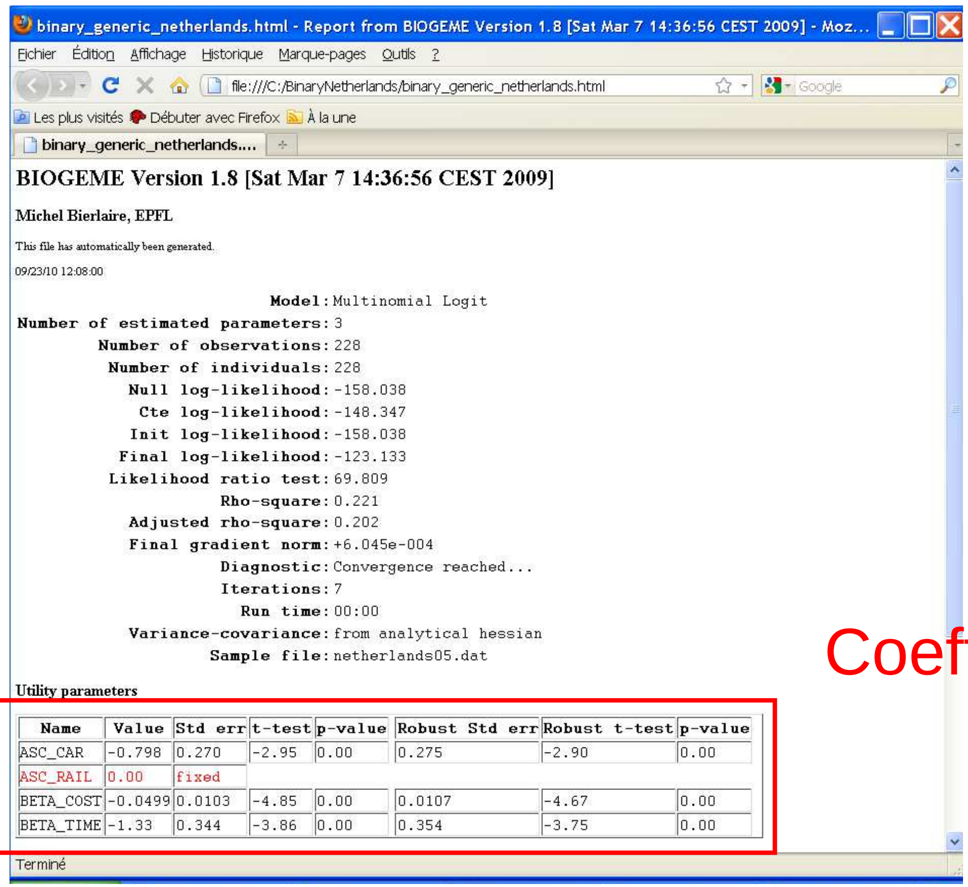
BIOGEME - Results



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Terminé

Coefficient estimates

Today

- Further introduction to BIOGEME
- **Estimation of Binary Logit models**

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Binary Logit Case Study

- Available datasets:
  - Airline itinerary choice (Boeing)
  - Netherlands mode choice
- Descriptions available on the course web site

How to go through the Case Studies

- Choose a dataset to work with (data descriptions are available on the course website)
- Copy the files related to the chosen dataset and case study from the course website.
- Study the `.mod` files with the help of the descriptions
- Run the `.mod` files with BIOGEME
- Interpret the results and compare your interpretation with the one we have proposed
- Develop other model specifications

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Course website

- `http://transp-or.epfl.ch/` $\rightarrow$ Teaching $\rightarrow$ Mathematical modeling of behavior $\rightarrow$ Laboratories
- BIOGEME software
  (including documentation and utilities)
- For each Case Study
  - Data files for available datasets
  - Model specification files
  - Possible interpretation of results

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Running Biogeme

In the MXF014

- accessing your folder My Documents:
  type `L:` in the DOS command window

To run Biogeme on your own computer

- download GUI from the course web site:
  - `BIOGEME v2.0: Windows executables.zip`
  - put `biogeme.exe` in `C:\Program Files`
  - **OR:** put `winbiogeme.exe` in the folder where you would like to work
    - run it by double clicking on the icon

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