
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

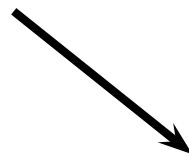
How does BIOGEME work?

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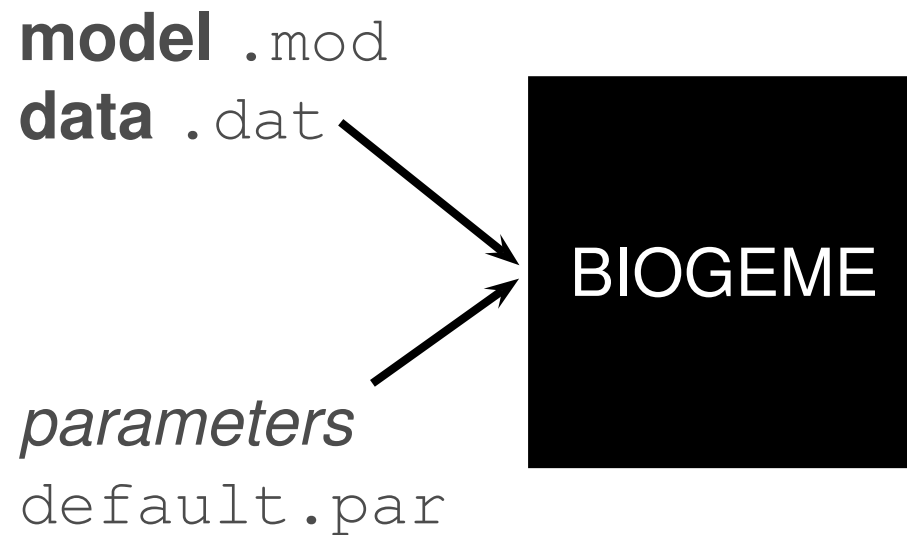
BIOGEME

How does BIOGEME work?

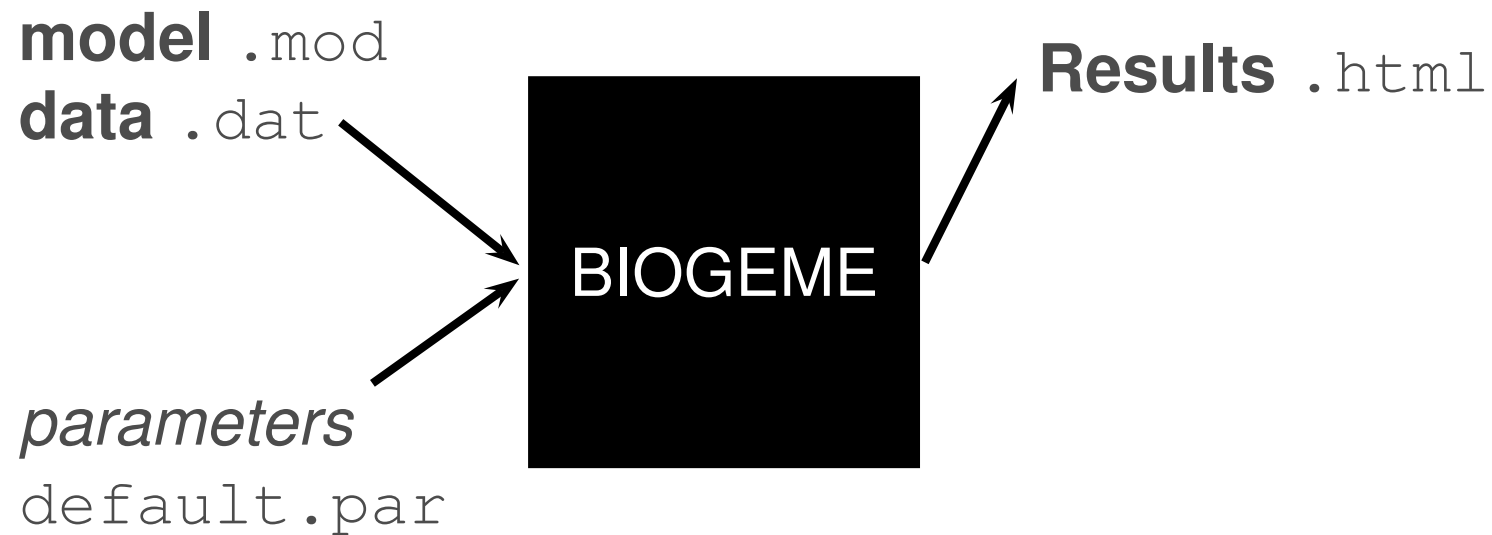
model .mod
data .dat



How does BIOGEME work?



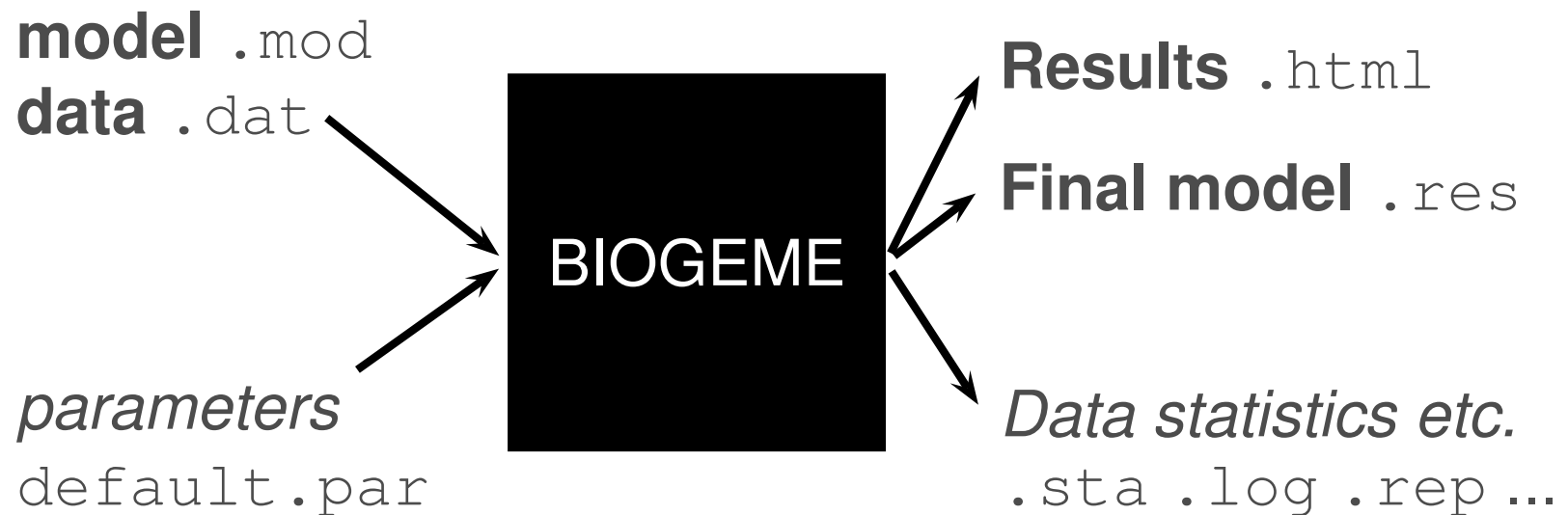
How does BIOGEME work?



How does BIOGEME work?



How does BIOGEME work?



BIOGEME - Data file

- File extension `.dat`
- First row contains column / variable names
- One observation per row
- Each row 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

netherlands.dat

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Unique identifier of observations

BIOGEME - Data file

netherlands.dat

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1	0	40	2.5	5	1.167
2	0	35	2.016	9	1.517
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Choice indicator, 0: car and 1: train

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?

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

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

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
```


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 +
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1 Rail one ASC_RAIL * one + BETA_COST * rail_cost +
BETA_TIME * rail_time
```

BIOGEME - Model file

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[Choice]
```

```
choice
```

```
[Beta]
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// Name      DefaultValue LowerBound UpperBound  status
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```

```
[Utilities]
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      BETA_TIME * rail_time
```

BIOGEME - Model file

```
[Choice]
```

```
choice
```

What is one?

Which is the type of model?

```
[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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BIOGEME - Model file

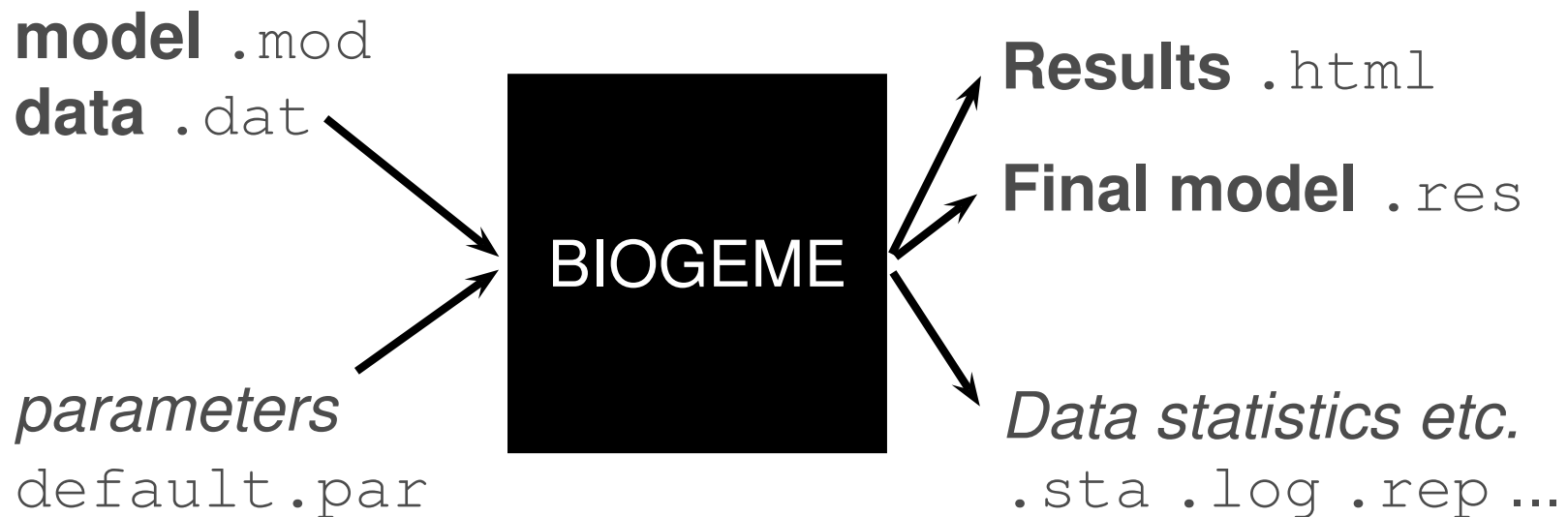
```
[Expressions]
```

```
// 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
```

How does BIOGEME work?



Model and Data Files

- How to read and modify model files?
How to read data files?
 - GNU Emacs, vi, TextEdit (Mac) or Wordpad (Windows)
 - **Notepad (Windows) should not be used!**

BIOGEME - Results - Netherlands dataset

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

```
Terminé
```

BIOGEME - Results

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Terminé

General model information

BIOGEME - Results

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Terminé

Coefficient estimates

Today

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

Binary Logit Case Study

- Available datasets:
 - Airline itinerary choice (Boeing)
 - Choice-Lab marketing
 - Mode choice in Netherlands
 - Residential Telephone Services
 - Mode choice in Switzerland (Optima)
- Descriptions available on the course web site
- Optima dataset does not contain `.mod` files. A specification has to be proposed as an assignment (next lab session).

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

Course website

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

Today's plan

1. Independent work on 2-3 Case Studies
 - choose case
 - estimate
 - interpret
2. Group work
 - gather in groups
 - generate .mod file (base)
 - test an idea / hypothesis

Specifying models: Recommended steps

- Formulate a-priori hypothesis:
 - Expectations and intuition regarding the explanatory variables that appear to be significant for mode choice.
- Specify a minimal model:
 - Start simple;
 - Include the main factors affecting the mode choice of (rational) travelers;
 - This will be your starting point.
- Continue adding and testing variables that improve the initial model in terms of *causality*, and *efficiency* with respect to what actually happened in the sample.

Evaluating models

The main indicators used to evaluate and compare the various models are summarised here:

- Informal tests:
 - *signs* and *relative magnitudes* of the parameters β values (under our a-priori expectations);
 - *trade-offs* among some attributes and ratios of pairs of parameters (e.g. reasonable value of time).
- Overall goodness of fit measure:
 - *adjusted rho-square* (likelihood ratio index): takes into account the different number of explanatory variables used in the models and normalizes for their effect → suitable to compare models with different number of independent variables. We check this value to have a first idea about which model might be better (among models of the same type), but it is not a statistical test.

Evaluating models (cont.)

- Statistical tests:
 - *t-test values*: statistically significant explanatory variables are denoted by t-statistic values remarkably higher/ lower than ± 2 (for a 95% level of confidence);
 - *final log-likelihood* for the full set of parameters: should be remarkably different from the ones in the naive approach (null log-likelihood and log-likelihood at constants); we ask for high values of likelihood ratio test $[-2(LL(0) - LL(\beta))]$ in order to have a model significantly different than the naive one.
- Test of entire models:
 - *likelihood ratio test* $[-2(LL(\hat{\beta}_R) - LL(\hat{\beta}_U))]$: used to test the null hypothesis that two models are equivalent, under the requirement that the one is the restricted version of the other. The likelihood ratio test is X^2 distributed, with degrees of freedom equal to $K_U - K_R$ (where K the number of parameters of the unrestricted and restricted model, respectively).