Computer Lab II
Introduction to Biogeme

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Outline

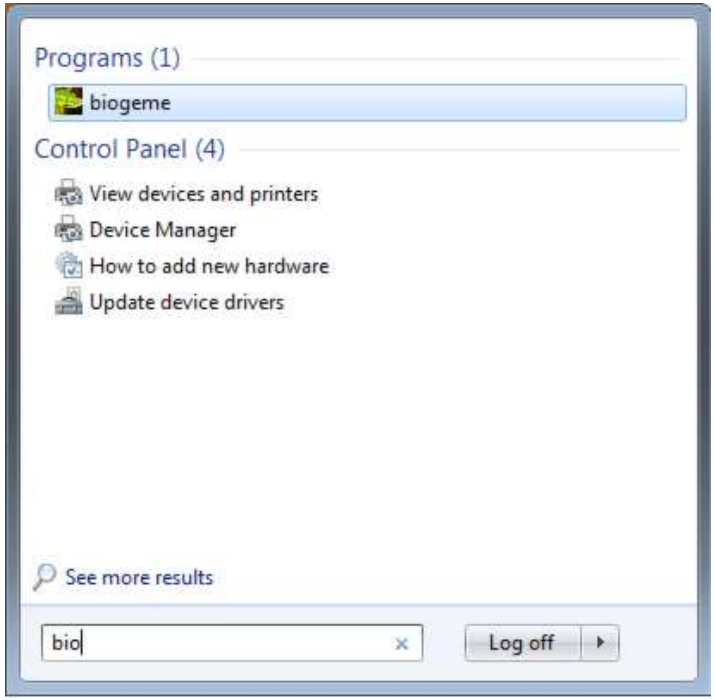
1. Installation of biogeme
2. How does biogeme work?
3. Your work in today's lab

Outline

BIOGEME

- Created by Michel Bierlaire.
- State of the art software for estimating models in the field of discrete choice analysis.
- Open source.
- All models presented in this course can be estimated with BIOGEME.
- webpage: http://biogeme.epfl.ch

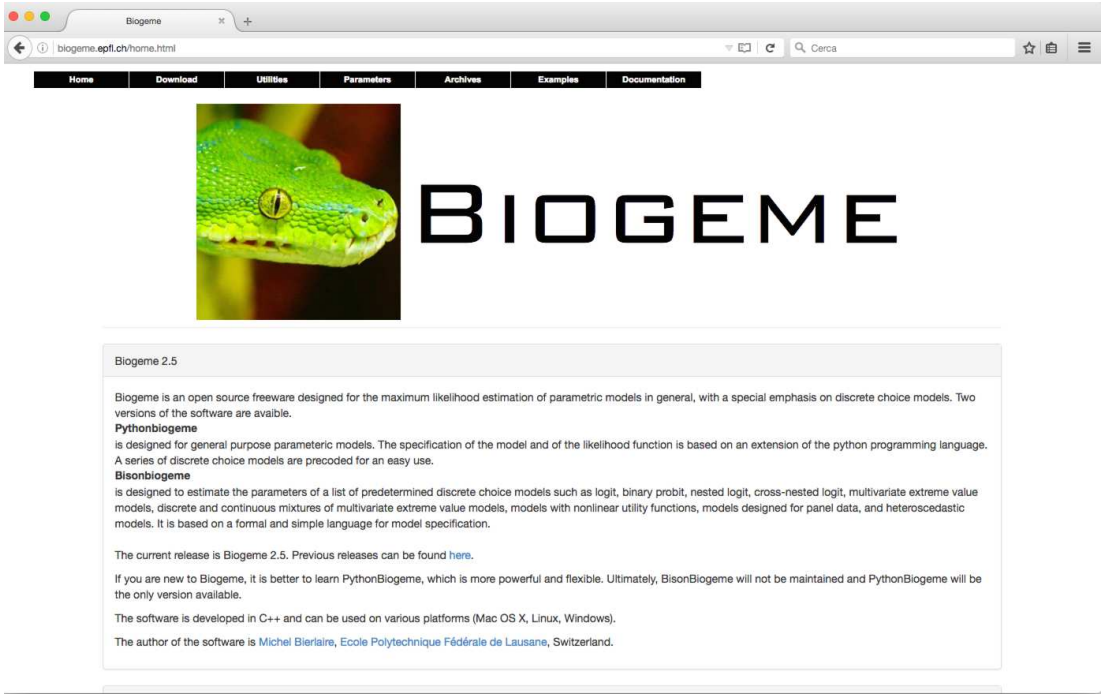
During the labs...



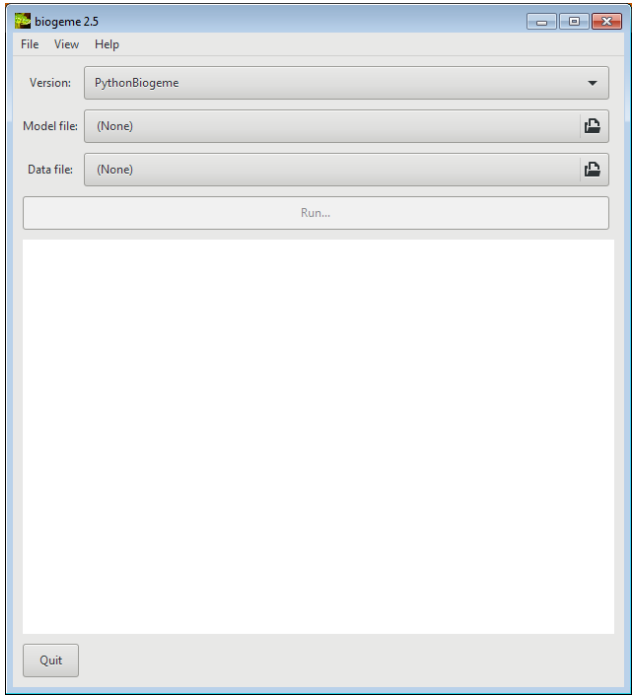
- Biogeme is already installed.
- Look for it and click on it.

Download biogeme on your own computer

- Download the program from the **Download** tab
- Follow the instructions under **Documentation** → **Install**



How does the interface look like?



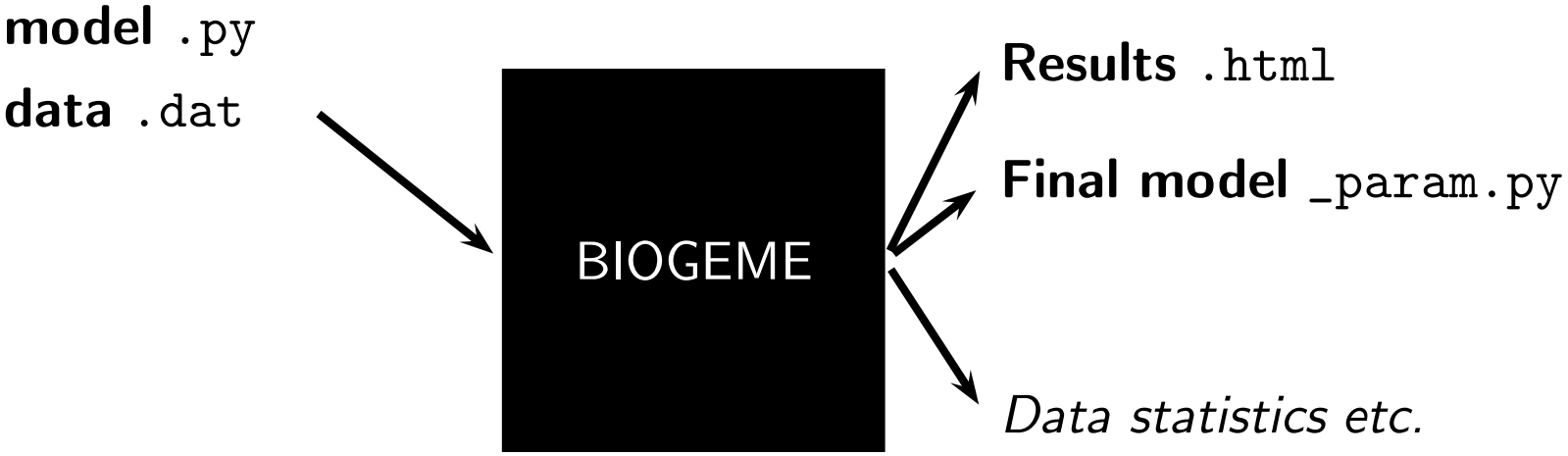
If you work with Mac you can also use the terminal.

Outline

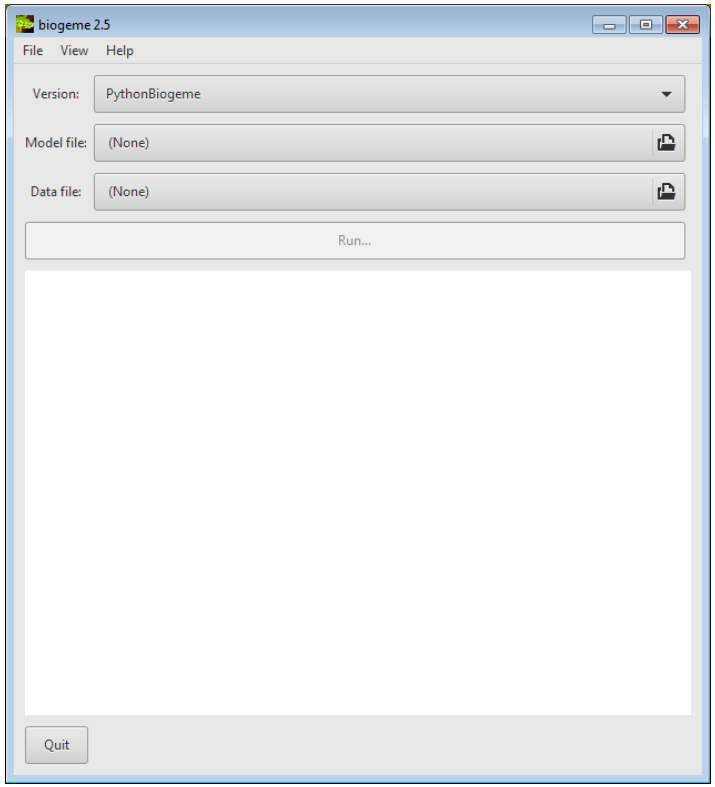
How does BIOGEME work?

- BIOGEME reads:
  - a file containing the model specification `model_file.py`
  - a file containing the data `sample_file.dat`
- BIOGEME automatically generates:
  - A file containing the results of the maximum likelihood estimation: `model_file_param.py`
  - The same file in HTML format: `model_file.html`

How does BIOGEME work?



How to invoke Biogeme?



1. Load the .py file in the **Model file** tab
2. Load the .dat file in the **Data file** tab
3. Press **Run..**

Example

- Netherlands mode choice
- Choice between rail and car
- 228 observations
- Travel times and travel costs are used as explanatory variables for the model, and the deterministic utility specifications are

$$
\begin{aligned}
V_{\text{car}} &= \text{ASC}_{\text{car}} + \beta_{\text{cost}}\text{cost}_{\text{car}} + \beta_{\text{time}}\text{time}_{\text{car}} \\
V_{\text{rail}} &= \beta_{\text{cost}}\text{cost}_{\text{rail}} + \beta_{\text{time}}\text{time}_{\text{rail}}.
\end{aligned}
$$

- Model is specified in `model_file.py`

BIOGEME: Data file

- File extension `.dat`
- It contains the data, what we call observations.
- One observation per row.
- First row contains column (variable) names.
- 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

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Unique identifier of observations

BIOGEME: Data file

netherlands.dat

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Choice indicator, 0: car and 1: train

BIOGEME: Model file

- File extension `.py`
- Must be consistent with data file.
- Contains deterministic utility specifications, model type etc.

BIOGEME: Model file

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

$$
\begin{aligned}
V_{\text{car}} &= \text{ASC}_{\text{car}} + \beta_{\text{time}}\text{time}_{\text{car}} + \beta_{\text{cost}}\text{cost}_{\text{car}} \\
V_{\text{rail}} &= \beta_{\text{time}}\text{time}_{\text{rail}} + \beta_{\text{cost}}\text{cost}_{\text{rail}}
\end{aligned}
$$

BIOGEME: Model file (parameters' section)

```
#Parameters to be estimated
# Arguments:
#   1  Name for report. Typically, the same as the variable
#   2  Starting value
#   3  Lower bound
#   4  Upper bound
#   5  0: estimate the parameter, 1: keep it fixed
ASC_CAR  = Beta('ASC_CAR',0,-100,100,0)
ASC_RAIL  = Beta('ASC_RAIL',0,-100,100,1)
BETA_COST  = Beta('BETA_COST',0,-100,100,0)
BETA_TIME  = Beta('BETA_TIME',0,-100,100,0)

# Define here arithm. expressions that are not directly available from data
one  = DefineVariable('one',1)
rail_time  = DefineVariable('rail_time', rail_ivtt   +  rp_rail_ovt  )
car_time  = DefineVariable('car_time', car_ivtt   +  rp_car_ovt  )
```

BIOGEME: Model file (utilities' section)

```
#Utility functions
__Car = ASC_CAR * one + BETA_COST * car_cost + BETA_TIME * car_time
__Rail = ASC_RAIL * one + BETA_COST * rail_cost + BETA_TIME * rail_time

#Which utility functions corresponds to each value of choice in the data file
__V = {0: __Car, 1: __Rail}

#Availability conditions for each alternative
__av = {0: one, 1: one}

#Excluded observations
BIOGEME_OBJECT.EXCLUDE =  (rp   ==  0 )

# The choice model is a logit, with availability conditions. The likelihood is:
prob = bioLogit(__V,__av,choice)
```

BIOGEME: Model file (estimation and output)

```
#And the loglikelihood:
__l = log(prob)
# Defines an itertor on the data
rowIterator('obsIter')
# Defines the likelihood function for the estimation
BIOGEME_OBJECT.ESTIMATE = Sum(__l,'obsIter')
#This is the optimization algorithm used (to compute maximum likelihood)
BIOGEME_OBJECT.PARAMETERS['optimizationAlgorithm'] = "CFSQP"

# Print some statistics:
nullLoglikelihood(__av,'obsIter')
choiceSet = [0,1]
cteLoglikelihood(choiceSet,choice,'obsIter')
availabilityStatistics(__av,'obsIter')
BIOGEME_OBJECT.FORMULAS['Car utility'] = __Car
BIOGEME_OBJECT.FORMULAS['Rail utility'] = __Rail
```

Estimate your first model

- Download the two files from the course webpage to a directory of your choice (e.g. Desktop).
- Invoke BIOGEME.
- Open the HTML file `model_file.html`.

BIOGEME: Output (Netherlands dataset)

Estimation report

```
          Number of estimated parameters: 3
                            Sample size: 228
                   Excluded observations: 1511
                     Init log likelihood: -158.038
                    Final log likelihood: -123.133
Likelihood ratio test for the init. model: 69.809
          Rho-square for the init. model: 0.221
      Rho-square-bar for the init. model: 0.202
                    Final gradient norm: +4.941e-05
                             Diagnostic: Normal termination. Obj: 6.05545e-06 Const: 6.05545e-06
                             Iterations: 10
                   Data processing time: 00:00
                               Run time: 00:00
                         Nbr of threads: 1
```

Estimated parameters

Click on the headers of the columns to sort the table [Credits]

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
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

Correlation of coefficients

Click on the headers of the columns to sort the table [Credits]

Coefficient1	Coefficient2	Covariance	Correlation	t-test	p-value		Rob. cov.	Rob. corr.	Rob. t-test	p-value	
ASC_CAR	BETA_TIME	0.0455	0.491	1.67	0.09	*	0.0464	0.476	1.60	0.11	*
ASC_CAR	BETA_COST	0.00192	0.693	-2.84	0.00		0.00210	0.713	-2.79	0.01	
BETA_COST	BETA_TIME	0.000295	0.0833	3.72	0.00		0.000311	0.0822	3.61	0.00	

Smallest singular value: 6.79119

Model and Data Files

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

Outline

Binary Logit Case Study

- Available datasets:
  - Airline itinerary choice (Boeing)
  - Mode choice in Netherlands
  - Mode choice in Switzerland (Optima)
- Descriptions available on the course webpage.
- Optima dataset does not contain `.py` files. A specification has to be proposed for the assignment.

How to go through the Case Studies

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

For the assignment

Form groups of ideally four people (groups of three and five will also be accepted).