



LAB SESSION 3

The goal of this exercise session is to (i) become familiar with the Python syntax in Biogeme and (ii) estimate and interpret a binary logit model. In order to achieve this goal you will specify and estimate mode choice models for the Netherlands case study.

First, download the file `BinaryNetherlands.zip` (under *Case study*). It contains:

1. the `binary_generic_NL.py` file with an example model specification:
 - it is a binary logit model between car and rail, and
 - this is your base model, and you will use it as a template to perform more modeling exercises;
2. the description and interpretation of the base model, as well as some extensions of it that we propose (`Binary_Netherlands_2018.pdf`).

Now, copy the `binary_generic_NL.py` file and use it as a template to perform the following tasks:

1. Follow the description in the `Binary_Netherlands_2018.pdf` file and for each model described there:
 - Try to understand the proposed specification.
 - Try to code the proposed specification. You should create the following files:
 - (a) `binary_specific_NL.py`
 - (b) `binary_socioec_NL.py`
 - Estimate the model specifications. You should obtain the following files:
 - (a) `binary_specific_NL.html`
 - (b) `binary_socioec_NL.html`
 - In order to verify that your code is correct, compare the results that you obtain with the ones that we provide in the description file.

2. Develop new model specifications using your own hypotheses. Estimate these models and interpret the obtained results. Compare with the proposed models to see if there is any improvement in the performance of the model.

Remarks and hints:

- Under the ‘Utilities’ section of the BIOGEME webpage (<http://biogeme.epfl.ch>), you can find an excel file that you can use to perform the statistical test in order to compare two nested models, i.e. the “Loglikelihood ratio test”.
- You will find the Netherlands dataset and its description in:
<http://transp-or.epfl.ch/discretechoice/data.html>

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