**For simulation and analyses used for “Murine genetic models of obesity: type I error rates and the power of commonly used analyses as assessed by plasmode-based simulation (Ejima et al., International Journal of Obesity, 2020)”:**

* boot\_perm.r: R code for bootstrap test and permutation test
* descriptive.r: R code to compute descriptive statistics
* type-I-error computation
  + type-I-error-simulation.r: R code for simulating and obtaining p-values
  + type-I-error.r: R code to compute type I error rates based on the obtained p-values.
  + type-I-error-figure.r: R code to create a figure.
* Power computation
  + power-simulation.r: R code for simulating and obtaining p-values
  + power.r: R code to compute power based on the obtained p-values.
  + empirical-power.r: R code to compute reference values of power for each test.
  + power-figure.r: R code to create a figure.