Use:
chmod +x generate_files.sh
chmod +x sensitivity_analysis_all.sh
./generate_files.sh
./sensitivity_analysis_all.sh

Notes:
File "Ex2Task_Work_Space.mat" has to be created.
The file must contain:
- ithIndex: vector with the indexes of the Excahnge reactions that will be tested in the sensitivity analysis
- Model Annotation: COBRA model (iEC3006)
- Model_Baseline: COBRA Baseline model. This variable structure contains:
  - S: Stoichiometric Matrix: size: metabolites x reactions
  - b: Vector of zeros, lenght = metabolites
  - c: Vector of lenght = reactions. All values are zero except for the objective function (tipically in the index of biomass reaction = 1)
  - csense: lenght = metabolites
  - lb and ub: upper and lower boundaries. lenght = reactions
- Task Table: Table with the tasks to be evaluated:

1 ID	2 SYSTEM	3 SUBSYSTEM	4 DESCRIPTION	5 IN	6 INLB	7 INUB	8 OUT	9 OUTLB	10 OUTUB
1	'LIPIDS METABOLISM'	'CHOLESTEROL METABOLISM'	'Cholesterol synthesis'	'o2[c]'	9	13	'nadp[c]'	10	15
1	'LIPIDS METABOLISM'	'CHOLESTEROL METABOLISM'	'Cholesterol synthesis'	'nad[c]'	0	2	'h2o[c]'	7	11
1	'LIPIDS METABOLISM'	'CHOLESTEROL METABOLISM'	'Cholesterol synthesis'	'fadh2[c]'	1	1	'nadh[c]'	0	2
1	'LIPIDS METABOLISM'	'CHOLESTEROL METABOLISM'	'Cholesterol synthesis'	''	NaN	NaN	'co2[c]'	2	2
1	'LIPIDS METABOLISM'	'CHOLESTEROL METABOLISM'	'Cholesterol synthesis'	''	NaN	NaN	'fad[c]'	1	1
2	'ENERGY METABOLISM'	'KREBS CYCLE'	'Krebs cycle - NADH generation'	'accoa[m]'	1	1	'coa[m]'	1	1
2	'ENERGY METABOLISM'	'KREBS CYCLE'	'Krebs cycle - NADH generation'	'gdp[m]'	1	1	'fadh2[m]'	1	1
2	'ENERGY METABOLISM'	'KREBS CYCLE'	'Krebs cycle - NADH generation'	'fad[m]'	1	1	'gtp[m]'	1	1
2	'ENERGY METABOLISM'	'KREBS CYCLE'	'Krebs cycle - NADH generation'	'nad[m]'	3	3	'nadh[m]'	3	3
2	'ENERGY METABOLISM'	'KREBS CYCLE'	'Krebs cycle - NADH generation'	'pi[m]'	NaN	NaN	'co2[m]'	2	2
2	'ENERGY METABOLISM'	'KREBS CYCLE'	'Krebs cycle - NADH generation'	'h2o[m]'	2	2	'h[m]'	2	3
3	'AMINO ACIDS METABOLISM'	'ASPARTATE METABOLISM'	'Conversion of aspartate to arginine'	'asp_L[c]'	1	1	'arg_L[c]'	1	1
3	'AMINO ACIDS METABOLISM'	'ASPARTATE METABOLISM'	'Conversion of aspartate to arginine'	'citr_L[c]'	1	1	'fum[c]'	1	1
3	'AMINO ACIDS METABOLISM'	'ASPARTATE METABOLISM'	'Conversion of aspartate to arginine'	'atp[c]'	1	1	'amp[c]'	1	1
3	'AMINO ACIDS METABOLISM'	'ASPARTATE METABOLISM'	'Conversion of aspartate to arginine'	''	NaN	NaN	'ppi[c]'	1	1
3	'AMINO ACIDS METABOLISM'	'ASPARTATE METABOLISM'	'Conversion of aspartate to arginine'	''	NaN	NaN	'h[c]'	1	1

- TXTUrxn1: list of Exchange reaction ids to be tested in the sensitivity analysis