**Improved IFFL Robustness Analysis**

Robustness analysis is based on Hafner et al. (2009) *PloS Comput. Biol. 5*, e1000534

Original scripts can be found on: <http://www.ieu.uzh.ch/wagner/publications-software.html>

Robustness analysis is performed in four steps:

1. Global part
2. MC integration
3. Local part
4. Parameter assessment

The global part uses the accepted parameter sets from sampling, and is initiated with glocal.m. See comments for details. Then, MC integration is performed with glocal\_volume.m, vastly increasing the number of viable sets. Each of these viable sets is perturbed locally by local.m. Finally, local\_parameters.m chooses a model based on individual robustness (results from local.m) and assess the effect of perturbing each parameter individually. This choice is sequential: 1 is the most robust set. The values that result from this parameter assessment are used as weighting factors in the DNA strand design algorithm. The files checksetsfunction.m and checksetsfunctionsplit.m do the classifications of the sets. The first one is used by steps 1-3, the second one by step 4.