Sensitivity analysis

Sensitivity analysis methodology is described in supplement material A4 in a work of Schirm et al [1]. The parameters were increased or decreased by 2.5 % and the change of the sum of the fitness functions as percentage is plotted as bar diagrams. Values of the fitness functions of different scenarios are added.

In our implementation it can be realized as follows:

1. main\_struct (or main\_struct0) is the main structure, which includes entire information for implementation of the COVID-19 project.
2. xtot structure includes individual information for simulation for every German state
   1. ID of Germany together is ind\_indiv=1.
   2. ID of Saxony is ind\_indiv=9.
3. The field xtot$phiopt$indiv is a list of vectors of all 17 individual transformed parameters’ sets phi. These vectors are fitted.
4. The model’s parameters are saved in a structure param\_, whose fields are parameters values, named accordingly.
5. ConstructParam(x,ind\_indiv,main\_struct) is a function, which updates param\_ given ID ind\_indiv, list of individual phis (xtot$phiopt) and the main structure of the project main\_struct.
6. PerturbPar(x,delt,ind\_indiv,par\_name,main\_struct,transform\_opt,rel\_opt) perturb parameter named par\_name from an individual phi vector x (xtot$phiopt$indiv[[ind\_indiv]] by perturbation delt.
   1. transform\_opt whether perturbation value relates directly to the transformed parameter phi (1) or to the final parameter param\_ (0)
   2. rel\_opt whether parameter is relatively perturbed (multiplied by delt) or absolutely perturbed (+/- delt)
   3. In order to provide analysis as described in [1], it is necessary to choose rel\_opt=1, transform\_opt = 0, delt = 1.025 or 0.975.
7. Sensitivanalysis (xtot,delt,ind\_indiv,main\_struct,transform\_opt,rel\_opt) is a function, which provides sensitivity analysis for all parameters together.
8. CompareLimits(x=x,ind\_indiv,main\_struct) is a function, checking how far each estimated parameter is from its limit. Perturbations should not bring the parameters beyond their limits!

References

1 Schirm S, Engel C, Loeffler M, et al. A biomathematical model of human erythropoiesis under erythropoietin and chemotherapy administration. PloS one 2013;**8**(6):e65630. doi:10.1371/journal.pone.0065630.