The following model versions are available:

1. “**TGFb\_ComplexModel\_ModelSelection\_L1**”: Model used for selection of complexes via L1-penalization **(21 parameter)**
   * Naming of the parameters for the initial condition is different from models with genes:  
     init\_S2 “iS2”, init\_S4 "iS4" vs init\_S2 “S2tot”, init\_S4 “S4tot”
   * Steady states of unphosphorylated complexes
2. Two models with genes **(117 parameter)** 
   * Not required complexes have production rates = 0 (here, no steady states are used since this would require a very long time for compiling). Therefore, unphosphorylated complexes have init=0.
   * inits of Smads S2, S3, S4 are termed S2tot, S3tot, S4tot
   1. “TGFb\_ComplexModel\_withGenes“: INcluding all activation and inhibition parameters
   2. “TGFb\_ComplexModel\_withGenes\_Reduced”: Reducde model, however, unnecessary parameters are only set to zero and still in the model.

If compiling time is an issue:   
Use compiler without code-optimization, e.g. with option (-O0 or \od).

If you refit the data using another software, please consider fitting of errors and the Bessel-correction.