Building a computational model for complex biological systems is an iterative process. It starts from an abstraction of the process and then incorporates more details regarding the specific biochemical reactions which results in the change of the model fit. Meanwhile, the model's numerical properties such as its numerical fit and validation should be preserved. However, refitting the model after each refinement iteration is computationally expensive resource-wise.

There is an alternative approach which ensures the model fit preservation without the need to refit the model after each refinement iteration. And this approach is known as quantitative model refinement.

The aim of this thesis is to develop and implement a tool called ModelRef which does the quantitative model refinement automatically. It is both implemented as a stand-alone Java application and as one of Anduril framework components.

ModelRef performs data refinement of a model and generates the results in two different well known formats (SBML and CPS formats). The development of this tool successfully reduces the time and resource needed and the errors generated as well by traditional reiteration of the whole model to perform the fitting procedure.

Keywords: Reaction-based models, ODE-based models, Quantitative model refinement, Heat shock response, Data refinement, ModelRef, Anduril