

# 1 Error Model for Mass Spectrometry

## 1.1 Context

In order to understand the Nf- $\kappa$ B signaling pathway of the cell a good model has to be obtained. The state of the art aproche is used which is to define a structure of the model with certain parameters left to be atjusted such that the model agrees with the messured data. This structure is generated by pure thought and prior knowleg of similar systems. A vital part of this pursuite is to determine the functional dependencies of values in the model and there degree of freedome represented by the number of parameters that can ajust these dependencies. Also it is of high interesst to limit this number of paramters to a minimum that just allows the model to fit all realistic systems of the kind it is suppose to model but not more as it could be “overfitted” what results in unrealistic predictions. Since messured data is not free of noise this nois has to be accounted for when trying to fit the model. Thus the model should not predict the messured data exactly but the messured data should be destributed arround the prediction just as the messurment is distributed arround the real values due to its noise. Since these destributions are not know they have to be fittet as part of the model. The right type of destribution has to be picked and the parameters fittet such that it fits the destribution of the messured data arround the prediction thus the destribution of the measurements arround the real value.

## 1.2 Goal

Here we want to analyze the mechanics of the procedure to messure the data in order to obtain an understanding of the noise which is produced relative to the real values. We hope to derive a general functional depedency of the messured values to their errors with only a few paramters to be found. Experirience in this field of science has shown that such mechanistic aproches ussually do not work perfectly due to the lack of accurate knowlege of the process.

## 1.3 Mechanic Description