ALaSCA: A novel *in silico* simulation platform to untangle biological pathway mechanisms in Type 1 Diabetes progression

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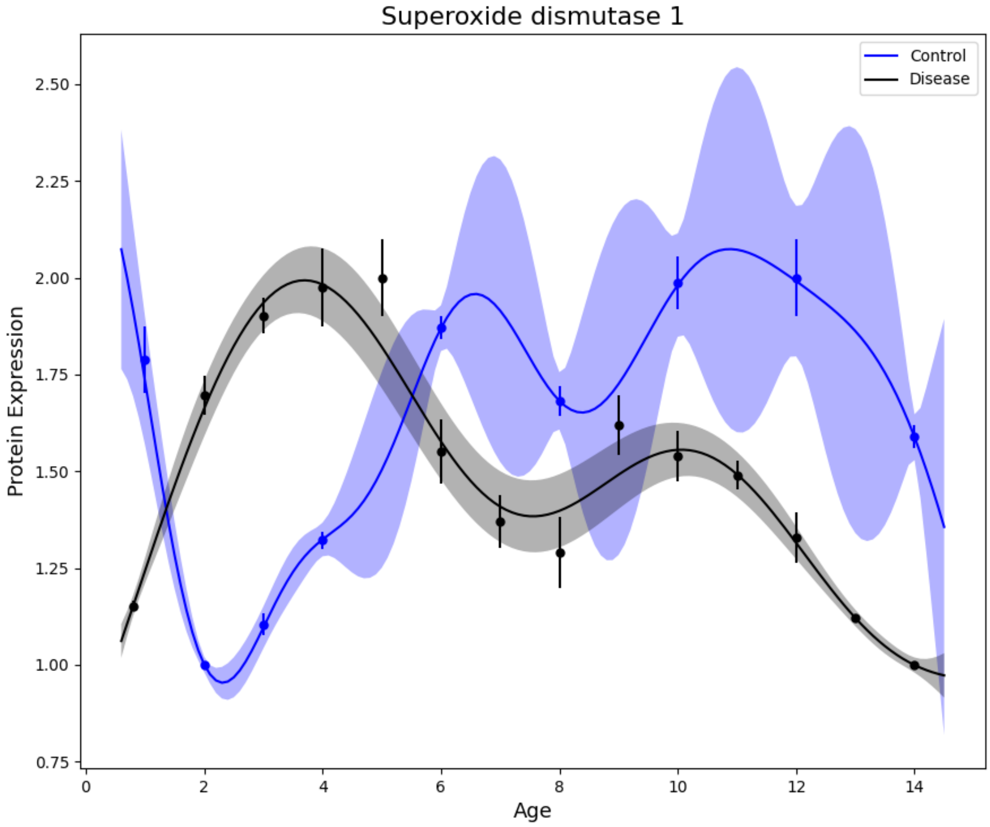

Figure 4: Inferred protein expression using Gaussian Process Regression of the protein Superoxide dismutase 1 from the dataset of Liu, *et al.* [Liu2018]. The solid line and shaded area represent the mean and 95% credibility interval of the protein expression distribution, while markers with error bars show measurement means ± standard deviation. The blue and black lines represent the inferred levels of the protein in control and diseased patients respectively.

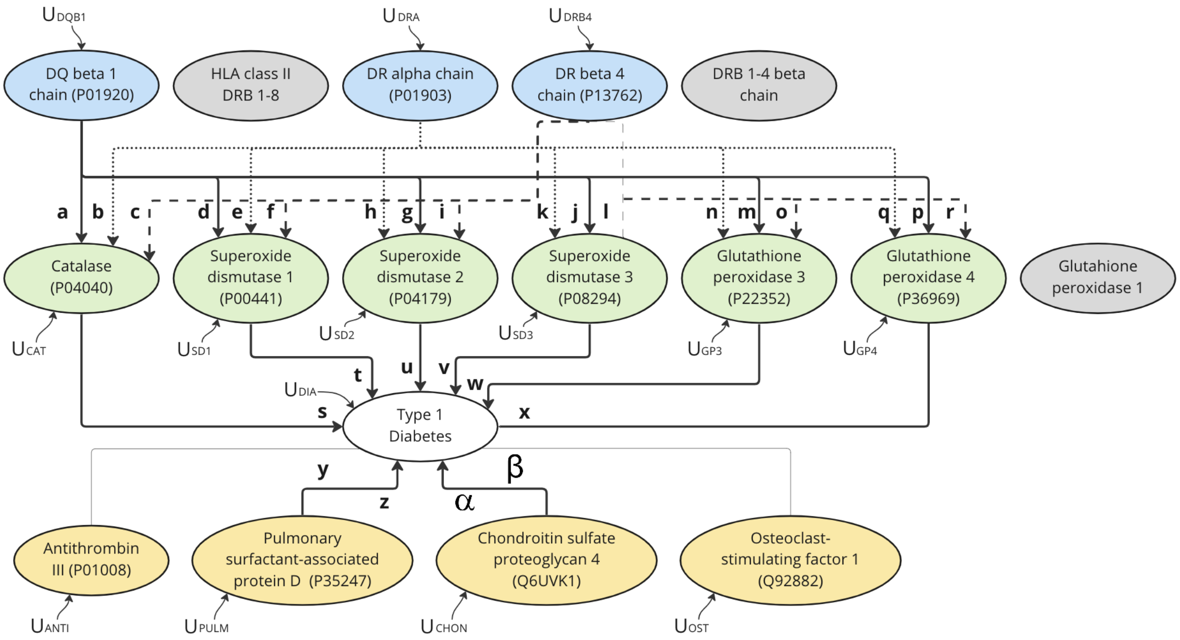

Figure 5: The mechanism DAG shows the HLA proteins (blue) which affect Type 1 Diabetes (T1D) via free radical metabolism, represented by the antioxidant proteins (green). Proteins for which either disease or control data could not be collected are shown in grey. Proteins known to not be drivers of T1D are shown in yellow. The T1D disease progression is represented by the white node. The causal effects a - β are shown on the respective DAG edges, while the exogenous variable of each node is shown as U_i.

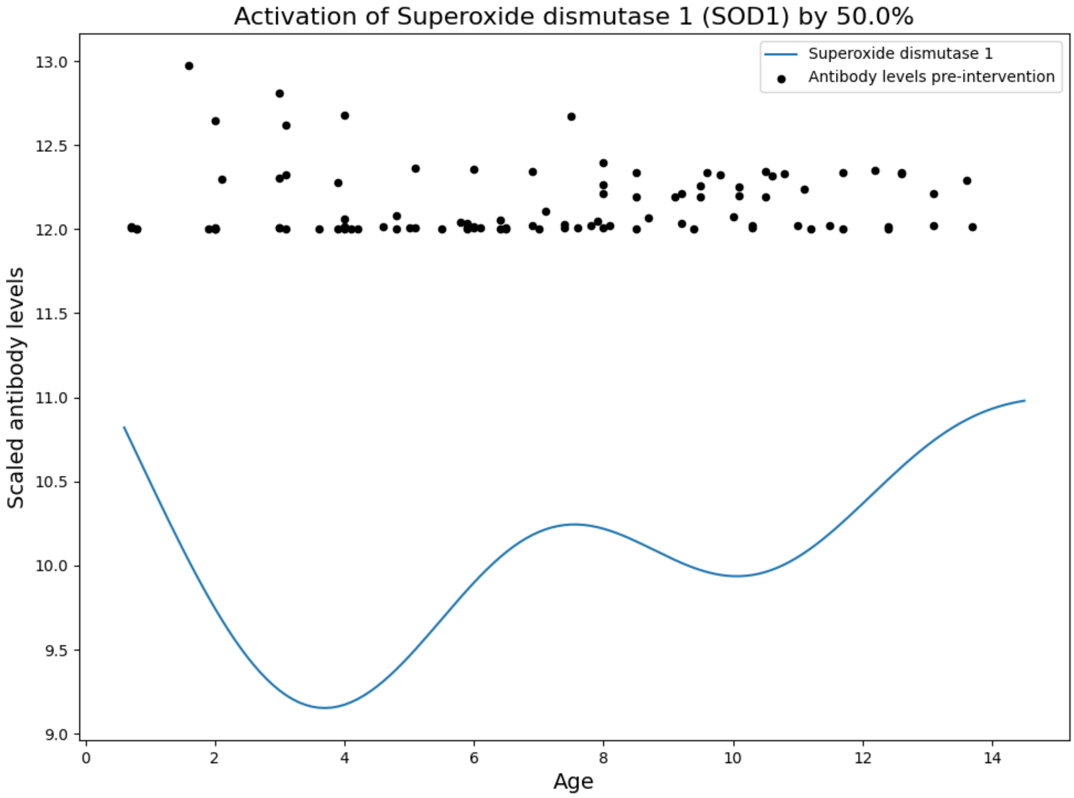

Figure 6: Simulation of the full disease mechanism model shows that the activation of Superoxide dismutase 1 protein has a decreasing effect on Diabetes (antibody levels). This is similar to the trend seen in literature [Lei2011].

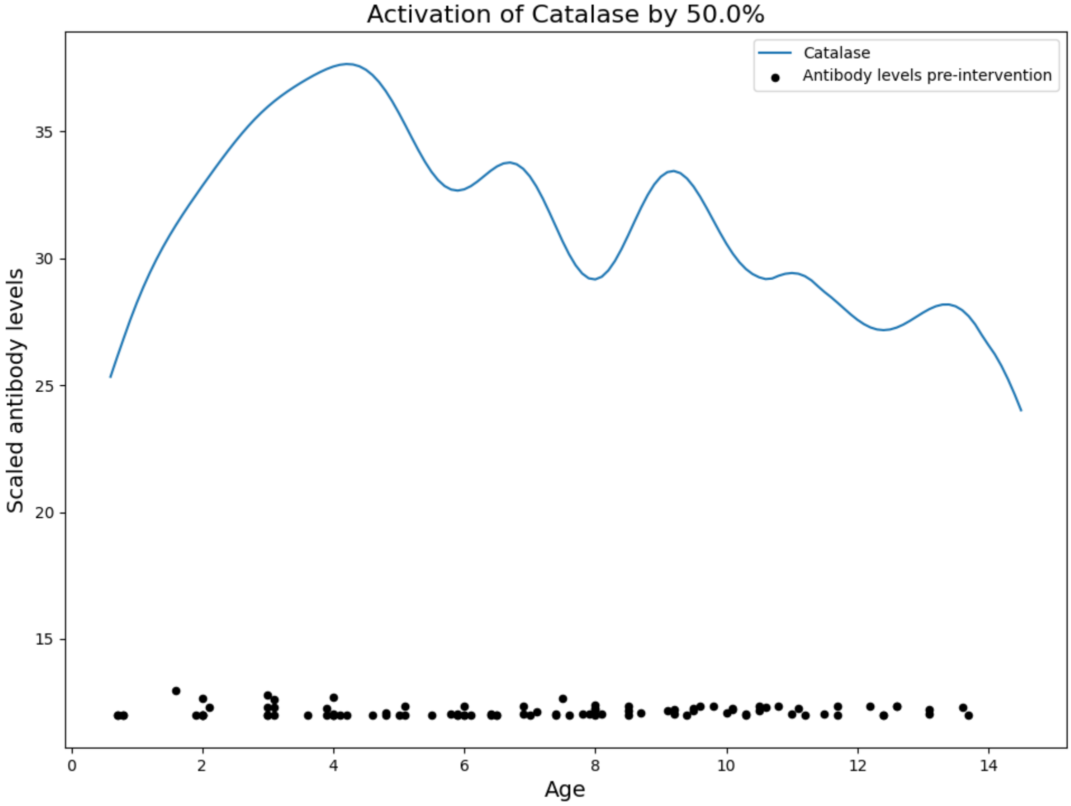

Figure 7: Simulation of the Li *et al.* experimental model shows that the activation of Catalase has an increasing effect on Diabetes (antibody levels). This is qualitatively comparable with the results seen in the Li study [Li2006].