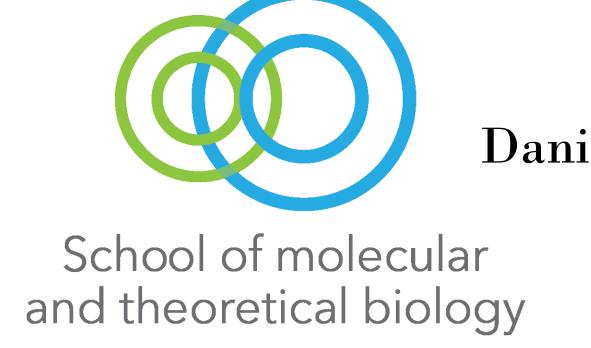
Laboratory of Protein Physics



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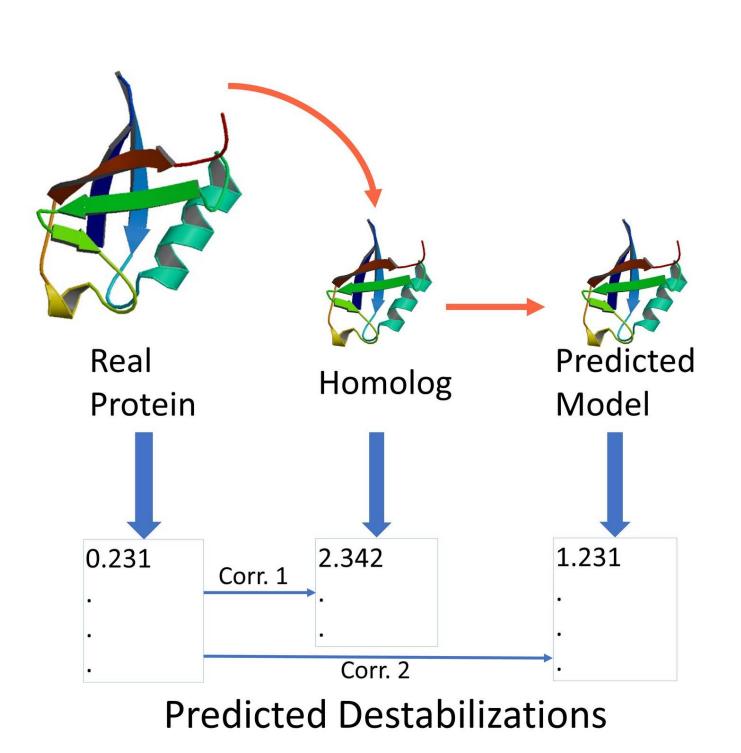
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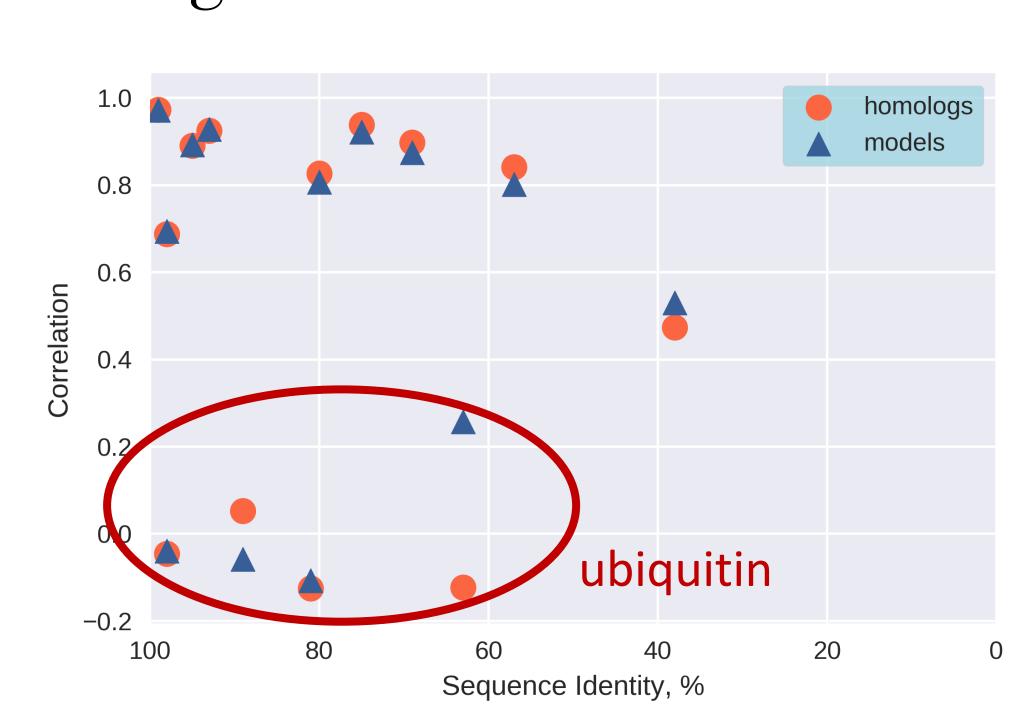
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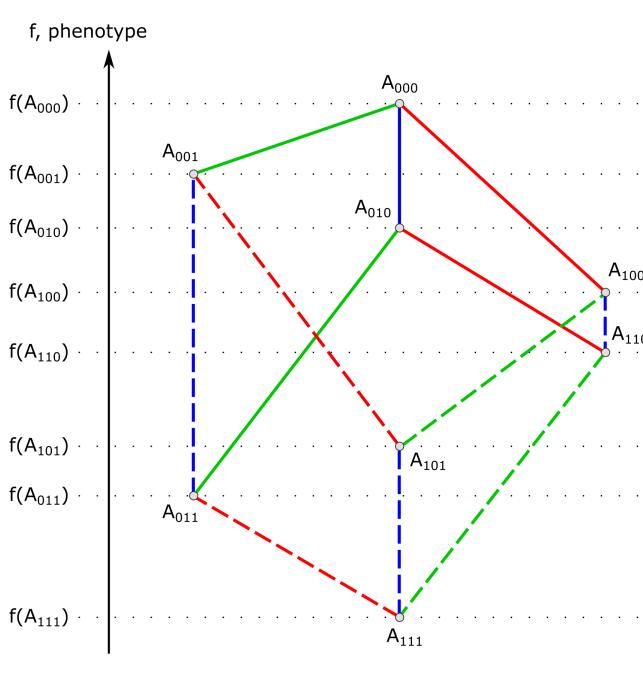
Predicted structure vs homolog structure





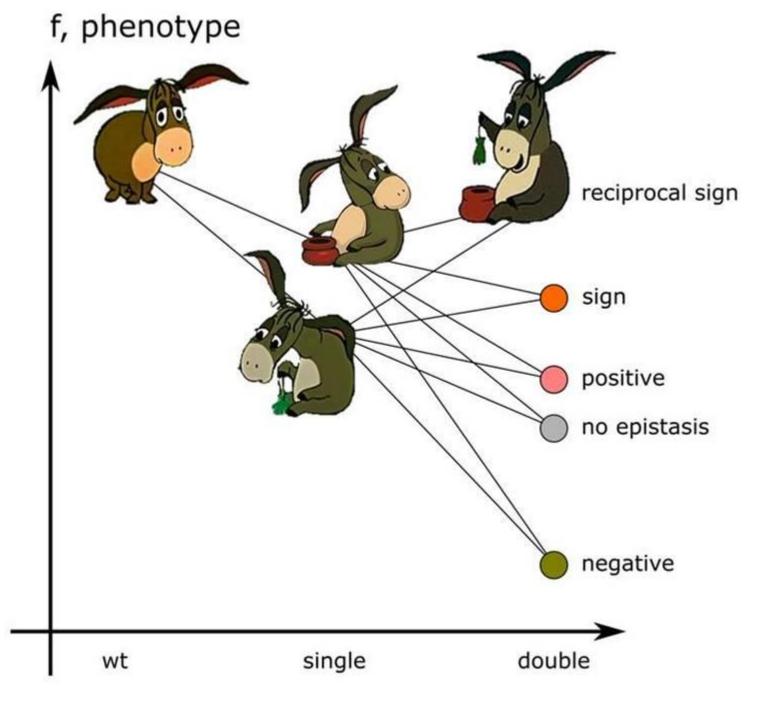
It seems, there is no difference between using homolog and model for destabilization prediction. Although we have some artifacts, we notice that correlation decreases with decrease of similarity.

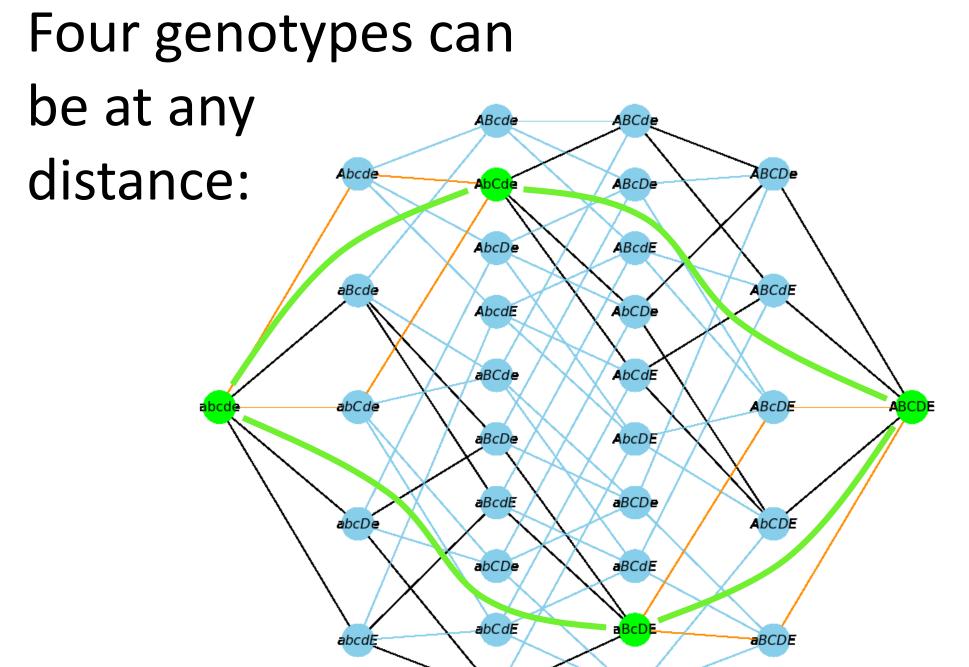
AND IOT DIS



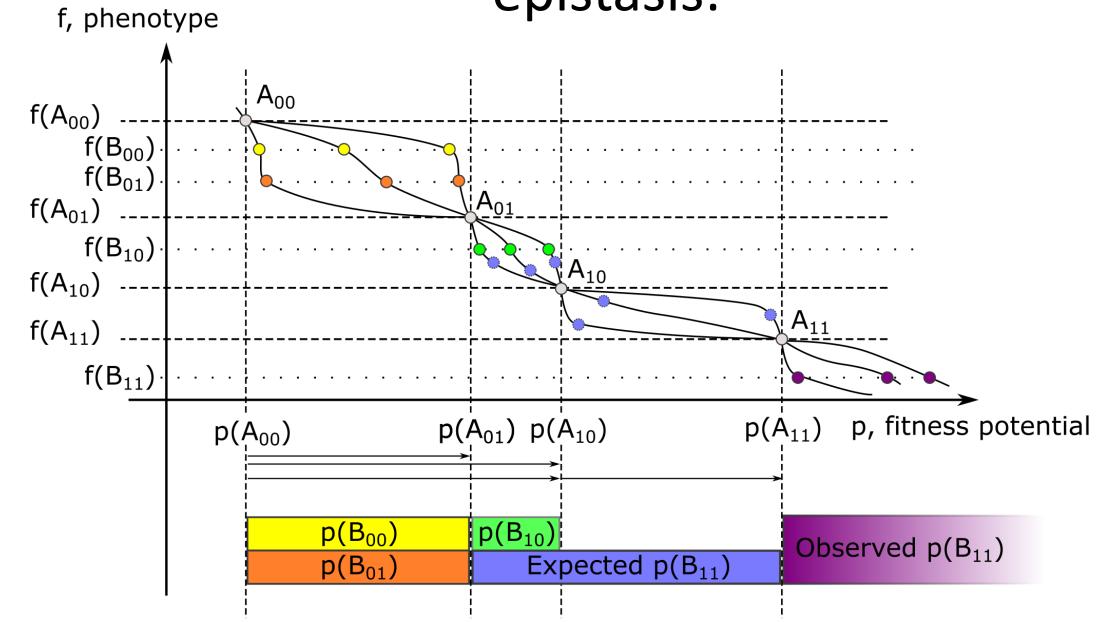
High-order vs multidimensional epistasis

What is epistasis?





"Inconsistency" type of multidimensional epistasis:



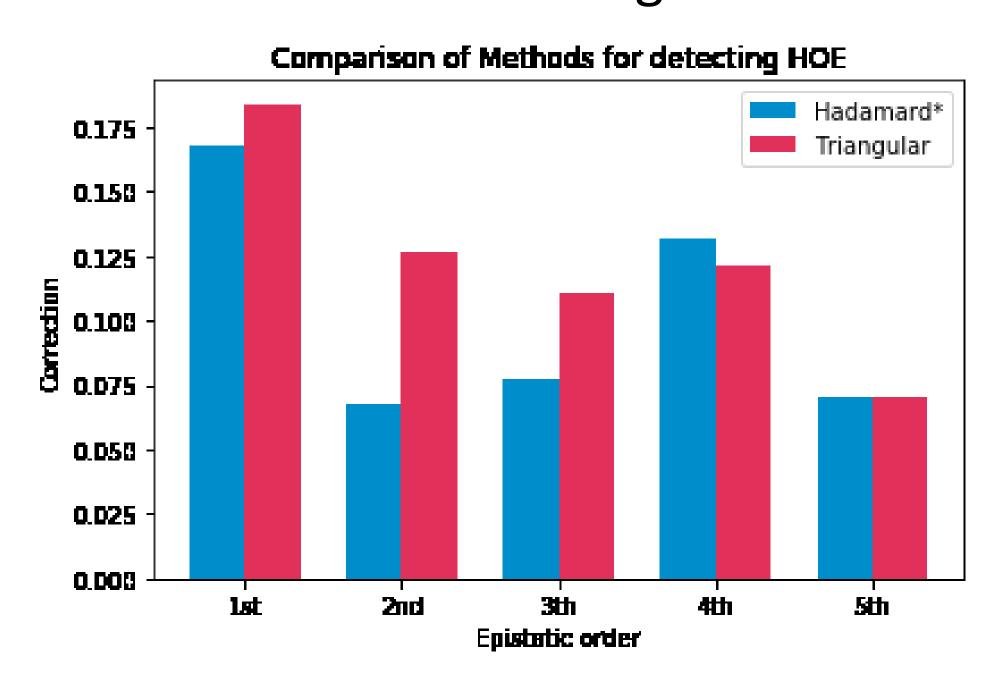
Hadamard high-order epistasis:

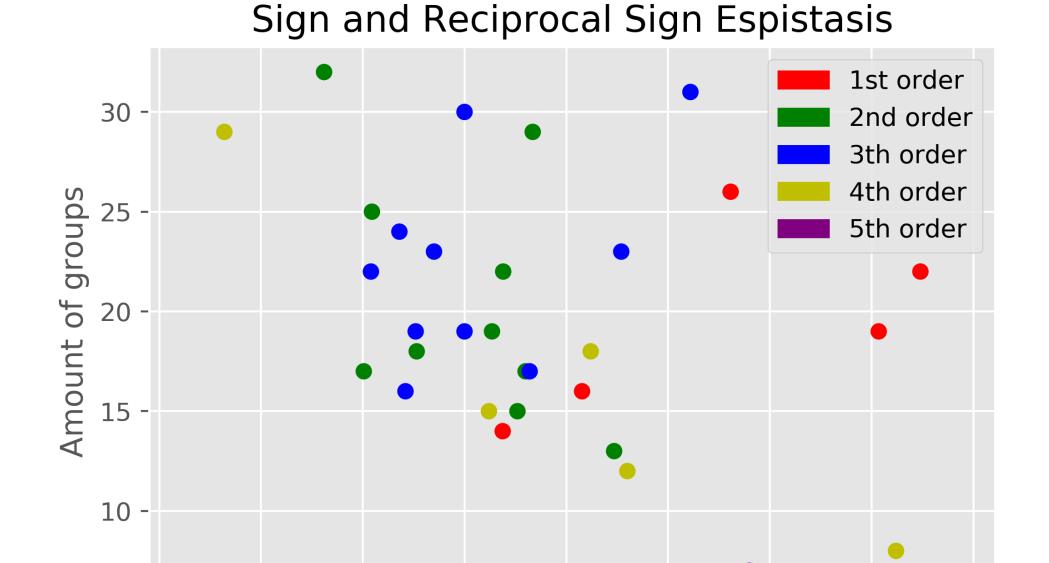
Modified representation (Hadamard*):

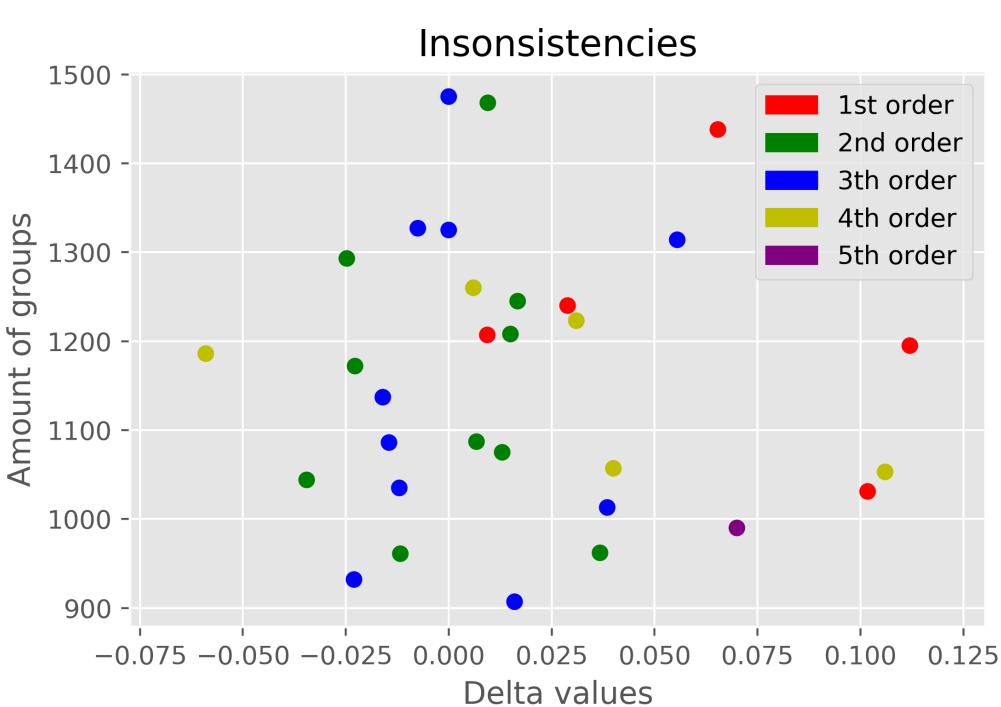
A simpler way to describe high-order epistasis:

$$T^{-1} = \begin{pmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ -1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ -1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & -1 & -1 & 1 & 0 & 0 & 0 & 0 \\ -1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 1 & -1 & 0 & 0 & -1 & 1 & 0 & 0 \\ 1 & 0 & -1 & 0 & -1 & 0 & 1 & 0 \\ -1 & 1 & -1 & 1 & -1 & -1 & -1 & 1 \end{pmatrix}$$

Hadamard* and triangular differ:







We have different methods of representing high-order epistasis. They give different estimates of the amount of high-order epistasis. Multidimensional and high-order types of epistasis do not have to be coupled with each other. Moreover, we see from experimental data that, indeed, they do not relate.

Delta values

-0.075 -0.050 -0.025 0.000







We found no relation between multidimensional and high-order epistasis: