1 Likelihood Computation

To determine the relationship between organs, particularly their potential dynamics against different genetic backgrounds, an organ-organ likelihood comparison was carried out using correlation datasets between organs among four distinct genetic backgrounds, including AJ, BL, NOD and SJL. Up to 13 organs from each of the four strains were first characterized by their individual proteomes. Each oorgan type also included sets of biological and technical replicates varied from 2 to 14. A pairwise comparison was carried out for every organ proteome, and the obtained Pearson correlation coefficient matrix was used as the input for the described organ dynamic network analysis herein. For each organ pair (e.g. bone and brain), the input dataset consists of replicated pairwise correlations across different mouse strains.

The overall likelihood between two organs is computed in steps that involve first computing likelihoods for different strain combinations, and then aggregating the results. Considering an organ pair (o_i and o_j), a matrix $D_{o_i-o_j}$ consists of the correlation values between the organs i and j across different strains. Then for each strain pair, a and b, a likelihood value $L_{S_{ab}}$ is obtained from $D_{o_i-o_j}(a)$ and $D_{o_i-o_j}(b)$ which are subsets of $D_{o_i-o_j}$ corresponding to strains a and b respectively.

$$L_{S_{ab}} = \prod_{i=1}^{N} (e^{-(\frac{(X_{ai}-\mu_b)^2}{2\sigma_b^2})})^{1/N} \tag{1}$$

where N is the number of individual correlation values, $X_{ai} = D_{o_i-o_j}(a)$ which is the subset of the organ-organ correlation values specific to strain a, and μ_b and σ_{sb} represent the mean and standard deviation of the elements in $D_{o_i-o_j}(b)$. The overall likelihood for organ pairs i and j, $L_{o_i-o_j}$ is obtained by taking an average of the individual $L_{S_{ab}}$ obtained for all strain combinations,

$$L_{o_i-o_j} = \frac{1}{N_{S_{ab}}} \sum_{a \neq b, \in S} L_{S_{ab}} \tag{2}$$

where $N_{S_{ab}}$ is the number of unique strain combinations. A table of likelihood values between organs is then obtained by computing $L_{o_i-o_j}$ for all possible organ pairs. Since the likelihood results between organs are symmetric ($L_{o_i-o_j} = L_{o_j-o_i}$), only the upper or lower diagonal is considered.