1. Calculate Z scores between each pair of conditions (α, β)
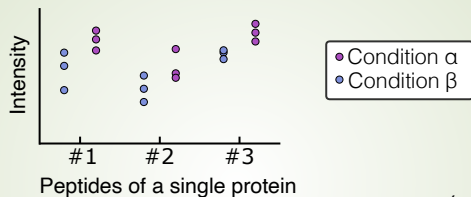

$$Z_{(\alpha,\beta)} = \text{sgn}(\log_2(\text{FC}(\alpha,\beta))\Phi^{-1}\left(\frac{p_{(\alpha,\beta)}}{2}\right)$$ (eq. 1)

Underlying algorithm: MS-EmpiRe calculates p-values (p) & fold changes (FC) from peptide intensities

2. Merge Z scores of pairs of conditions that are from the same data set i

$$Z_i^D = \frac{1}{\sigma_{\mathcal{C}}} \sum_{(\alpha,\beta)\in\mathcal{C}} Z_{(\alpha,\beta)}$$ (eq. 2)

$$\mathcal{C} = \{(c1,c2), (c1, c2), (c2,c3), ... \}$$

$$\sigma_{\mathcal{C}} = \sum_{(\alpha,\beta)\in\mathcal{C}} \sum_{(\gamma,\delta)\in\mathcal{C}} \text{cov}((\alpha,\beta),(\gamma,\delta))$$

3. Merge Z scores of of all data sets that are tested the same perturbation j

$$Z_j^P = \frac{1}{\sigma_{\mathcal{D}}} \sum_{i\in\mathcal{D}} Z_i^D$$ (eq. 3)

$$\mathcal{D}_{\text{C}} = \{\text{C}_{\text{carbon sources}}, \text{C}_{\text{chemostat}}, \text{C}_{\text{titration}}\}$$
$$\mathcal{D}_{\text{A}} = \{\text{A}_{\text{titration}}\}$$
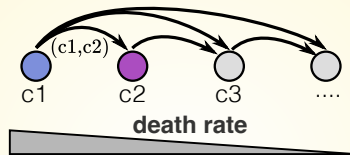$$\mathcal{D}_{\text{R}} = \{\text{R}_{\text{titration}}\}$$
$$\mathcal{D}_{\text{L}} = \{\text{L}_{\text{rich media}}\}$$
$$\mathcal{D}_{\text{S}} = \{\text{S}_{\text{houser}}, \text{S}_{\text{schmidt}}\}$$

$$n_{\mathcal{D}} = |\mathcal{D}|$$
$$\sigma_{\mathcal{D}} = \sqrt{n_{\mathcal{D}}}$$

4. Merge Z scores of perturbations

$$\text{Survival score: } Z^{\text{S}} = \frac{1}{\sigma_{\mathcal{P}}} \sum_{j\in\mathcal{P}} Z_j^P$$ (eq. 4)

$$\mathcal{P} = \{\text{C, A, R, L, S}\}$$

$$\sigma_{\mathcal{P}} = \sqrt{n_{\mathcal{P}}}$$
$$n_{\mathcal{P}} = |\mathcal{P}|$$