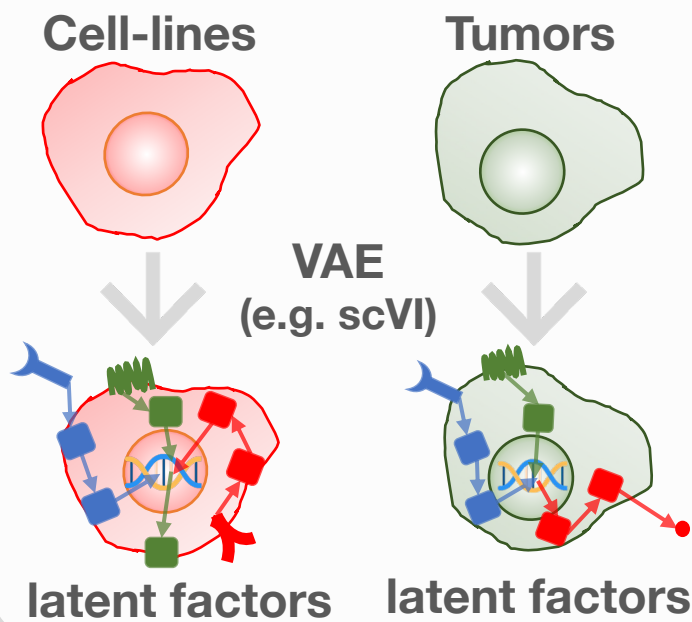
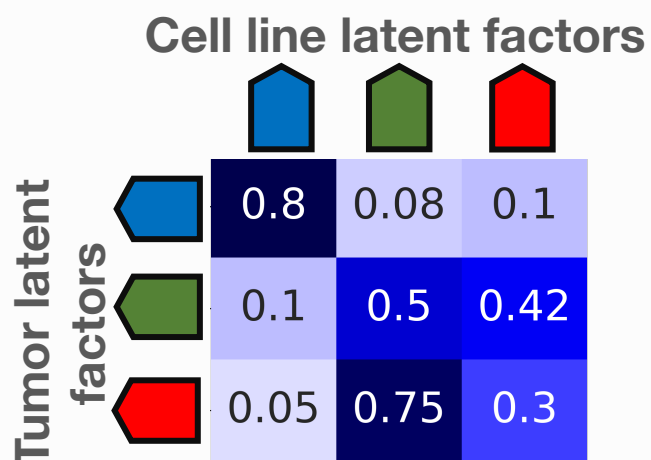


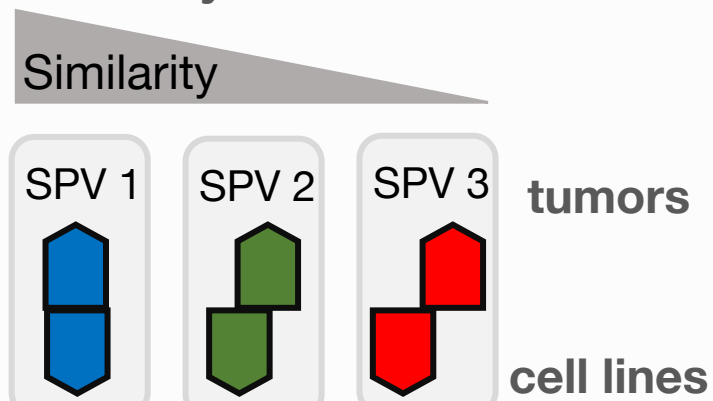
A. Find activated pathways by deep generative modelling.



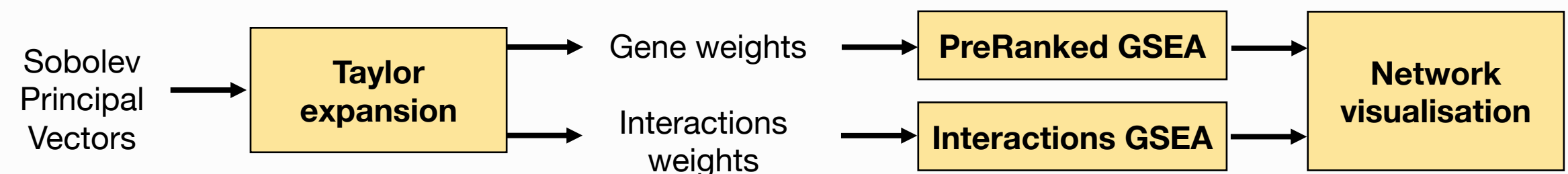
B. Systematically compare latent factors.



C. Rank pathways by similarity.



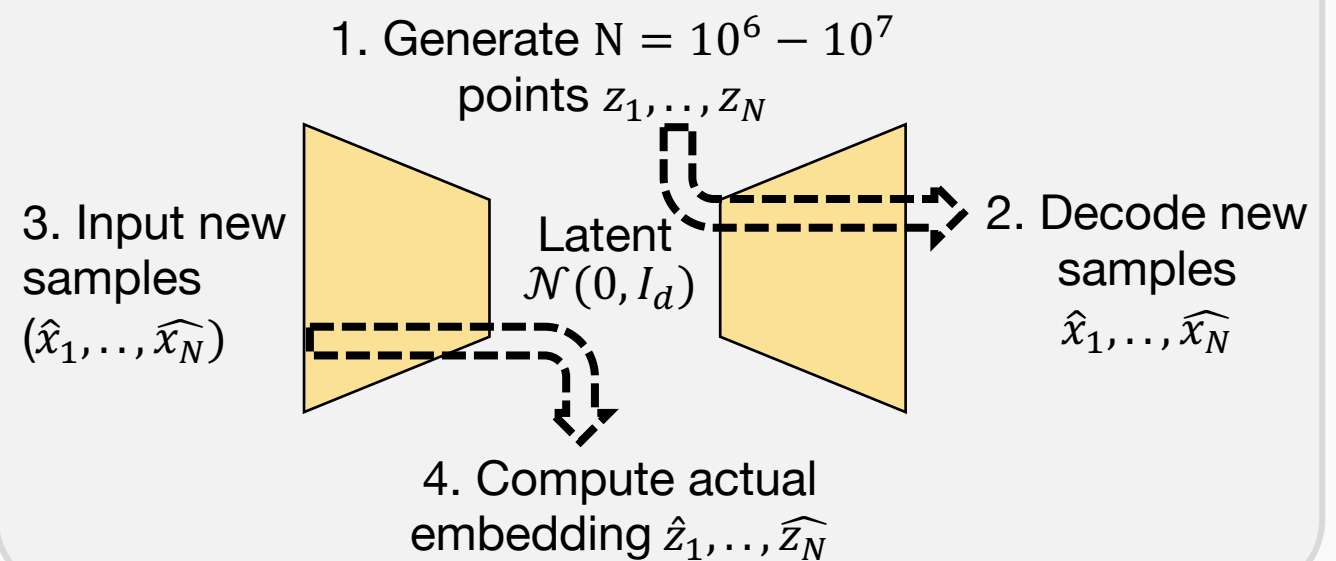
E. Interpretation of factors by Taylor expansion of Matérn kernel.



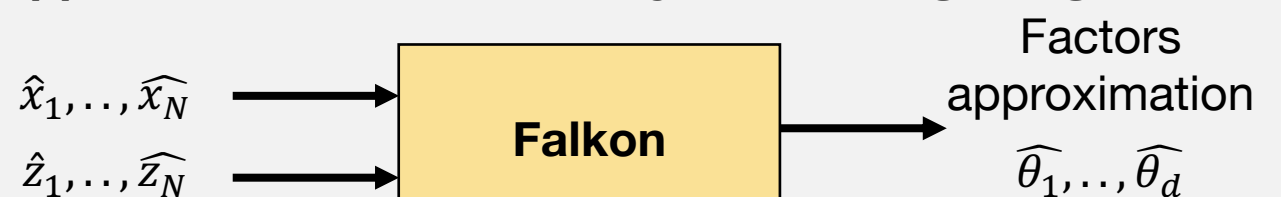
D. Workflow of Sobolev comparison of latent factors.

Approximation (independent on cell lines and tumor VAE)

Create representative training data between input and embedding space.



Approximate latent factors by Kernel Ridge Regression



Compute cosine similarity between KRR directions

