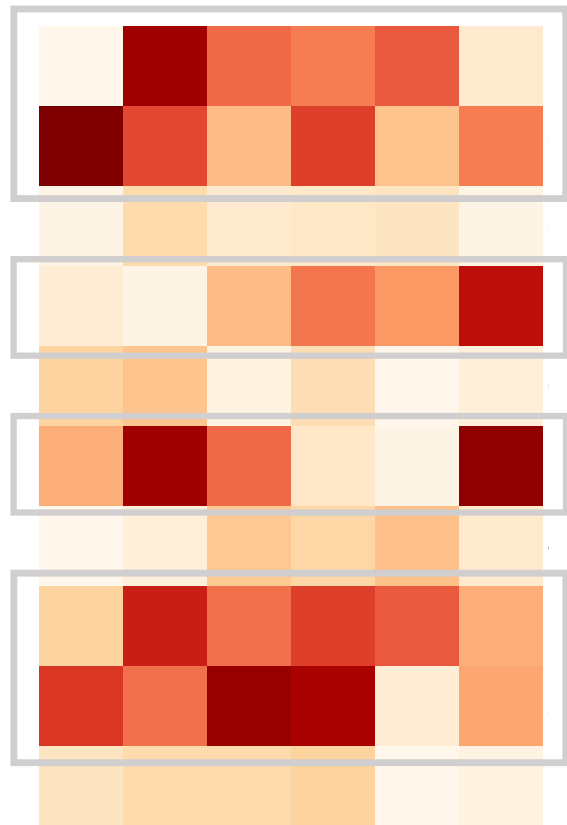


Initial ST data  
n

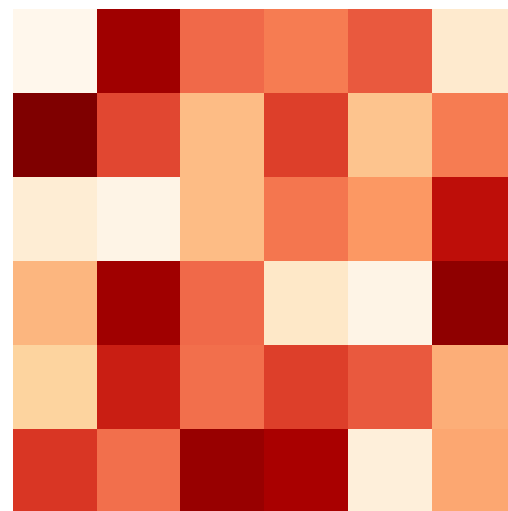


## Deconf

Initial  
feature  
selection

Update  
gene list  
and  
repeat

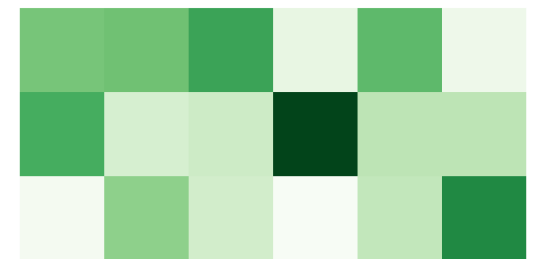
Y  
Reduced ST data



M  
Reference Matrix



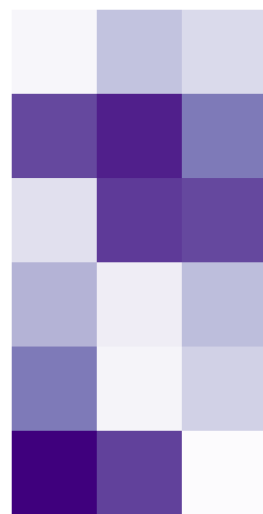
H  
Proportion Matrix



=

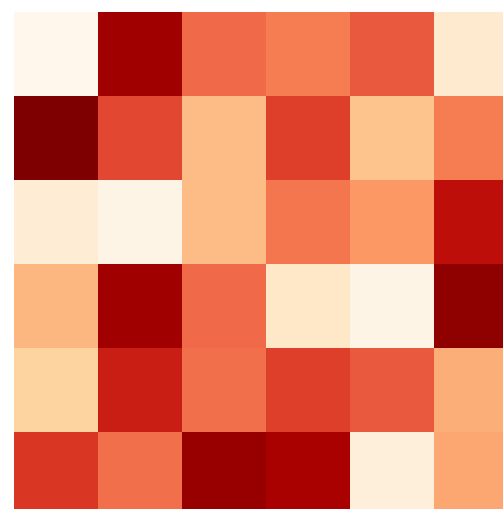
×

Cell-type gene  
expression

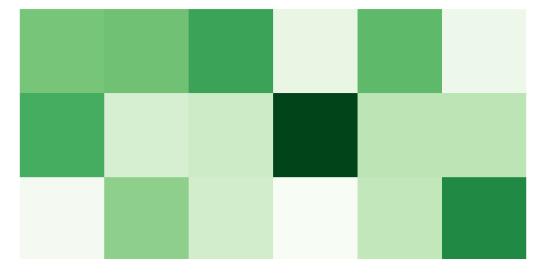


Infer

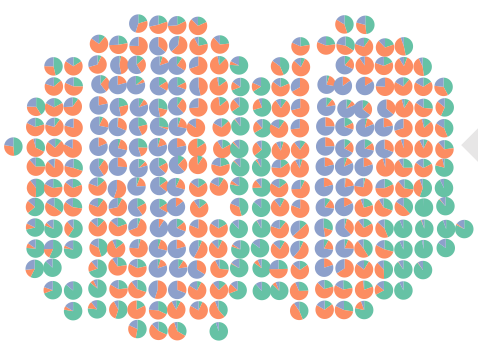
Y  
Reduced ST data



H  
Proportion Matrix



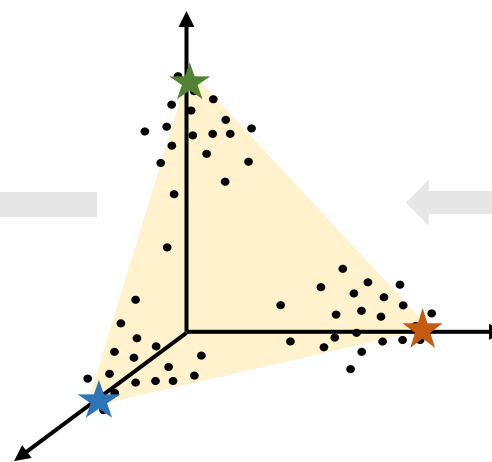
Deconvolution  
result



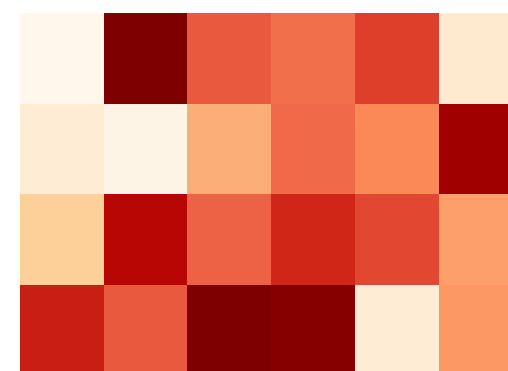
H  
Final Proportion Matrix



SISAL  
Find simplex corner



Y  
Final Reduced ST data



After  
Converge