Code: <https://github.com/Tchanders/NetworkInference.jl#scope>

import Pkg

Pkg.add("NetworkInference")

using Julia NetworkInference.jl package

using NetworkInference

infer\_network("/Users/15145/Desktop/Glioma.txt", PIDCNetworkInference())

nodes = get\_nodes("/Users/15145/Desktop/Glioma.txt")

inferred\_network = InferredNetwork(PIDCNetworkInference(), nodes)

write\_network\_file("/Users/15145/Desktop/PIDGlioma.txt",inferred\_network)

**JULIA CODE**

import Pkg

Pkg.add("NetworkInference")

using NetworkInference

# Paths

base\_path = "C:/Users/uabic/Desktop/Gene sets"

# File names (without extensions)

file\_names = ["selected\_HVGIDHWT", "selected\_HVGK27M", "selected\_TopFeatIDHWT", "selected\_TopFeatK27M", "selected\_scEpathIDHWT", "selected\_scEpathK27M"]

for file\_name in file\_names

input\_file = "$base\_path/$file\_name.txt"

output\_file = "$base\_path/PID\_$file\_name.txt"

# Infer network

infer\_network(input\_file, PIDCNetworkInference())

nodes = get\_nodes(input\_file)

inferred\_network = InferredNetwork(PIDCNetworkInference(), nodes)

write\_network\_file(output\_file, inferred\_network)

end