
gpgraph Documentation

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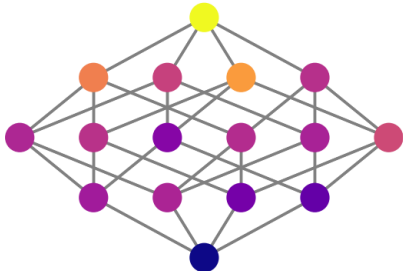
Genotype-phenotype maps in NetworkX

```
from gpmap.simulate import MountFujiSimulation
from gpgraph import GenotypePhenotypeGraph, draw_flattened

# Simulate a genotype-phenotype map
sim = MountFujiSimulation.from_length(4, roughness_width=1)

# Turn the genotype-phenotype map into a networkx object
G = GenotypePhenotypeGraph(gpm)

# Draw the graph
draw_flattened(G, with_labels=False, node_size=100)
```



1.1 Submodules

1.2 gpgraph.base module

1.3 gpgraph.draw module

1.4 gpgraph.matrices module

1.5 gpgraph.models module

1.6 gpgraph.paths module

1.7 Module contents

CHAPTER 2

Indices and tables

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