**Introduction**

Quality Diversity (QD) algorithms seek to find a diverse collection of distinct high quality solutions to a problem. QD algorithms find different solutions to the same problem, diversifying and finding many unique good solutions.

**MAP-Elites**

Multi-dimensional Archive of Phenotypic Elites (MAP-Elites [1]), is a QD algorithm that maps solutions to an archive divided up by features of a solution.

- Each bin in the archive represents solutions with a particular set of features.
- Each solution has features corresponding to exactly one bin.
- The quality of the solution is evaluated. There are three cases:
  - fills an empty bin,
  - improves an older, worse solution
  - is discarded for being worse

**Binning Schemes**

Binning schemes consider the features of a solution and output the bin that the solution corresponds to.

**Comparing Binning Schemes**

To evaluate a binning scheme, every elite solution from an archive is re-evaluated with respect to a different binning scheme, and survivors and fill percentage are recorded. If many bins were filled and the percentage is high, the target scheme is successfully capturing the diversity in the source scheme.

**GAN Level Generation**

Using existing Generative Adversarial Networks, or GANs, created by past SCOPE students [2,3], we use the GANs to map input vectors to game levels for evaluation.

**Results, Conclusions, and Observations**

- In Mario, the general schemes (KL Div and Latent Variable) were not able to effectively transfer, but in MegaMan, Latent Variable nearly filled 50% of the other archives.
- The schemes are not all equal sizes. When the sizes differ, there are either less bins than possible to fully fill the target archive, or too many bins that it becomes easy to fill. If our archives were all the same size, comparison would be easier.
- In MegaMan, our “Novelty, Verticality, Connectivity” and “Distinct Segments, Verticality, Connectivity” schemes both share Verticality and Connectivity, yet the scheme with novelty did terrible compared to the one with distinct segments

**References**