Decoding Nature with Nature's Tools

String Pheno 2023 - Daejeon

Thomas Harvey
Collaborators: Steve Abel, Andrei Constantin, Andre Lukas & Luca Nutricai

Based On: 2306.03147

Motivation

- The String Landscape is vast
  - Ashok & Douglas (2004) ~ 10^{500}
  - Taylor & Wang (2015) ~ $10^{272,000}$
- Extreme difficulty identifying points of physical interest
  - Constantin, He and Lukas (2019) ~ 10^{700} standard models
- Here we use Genetic Algorithms (GA) and Quantum Annealing (QA) to search the space of line bundle sum models
  - “Nature’s tools” - Evolution and Quantum Mechanics

Genetic Algorithms

- Has been used for constructing other physics models
    - S. Abel, A. Constantin, TRH, A. Lukas - Monad Bundles (2021) and Inflation (2022)
    - A. Cole, S. Krippendorf, A. Schachner, G. Shiu - Flux Vacua (2019, 2021)
- Each model is given by a genotype (string of bits) and phenotype (physics)
- 1. Randomly generate a population (e.g 100 random bit strings) and rank by fitness
- 2. Select individuals for breading based on fitness, then crossover pair
- 3. Small probability of mutation
- 4. Repeat with new population
- Based on evolution and survival of the fittest

$$\begin{array}{c}(0,1,1,0\|1,1,\dots)\\(1,1,1,1\|0,0,\dots)\end{array}\longrightarrow\begin{array}{c}(1,1,1,1\|1,1,\dots)\\(0,1,1,0\|0,0,\dots)\end{array}$$

$$P_k = \frac{2}{(1+\alpha)N_{\text{pop}}}\left(1+\frac{N_{\text{pop}}-k}{N_{\text{pop}}-1}(\alpha-1)\right)$$

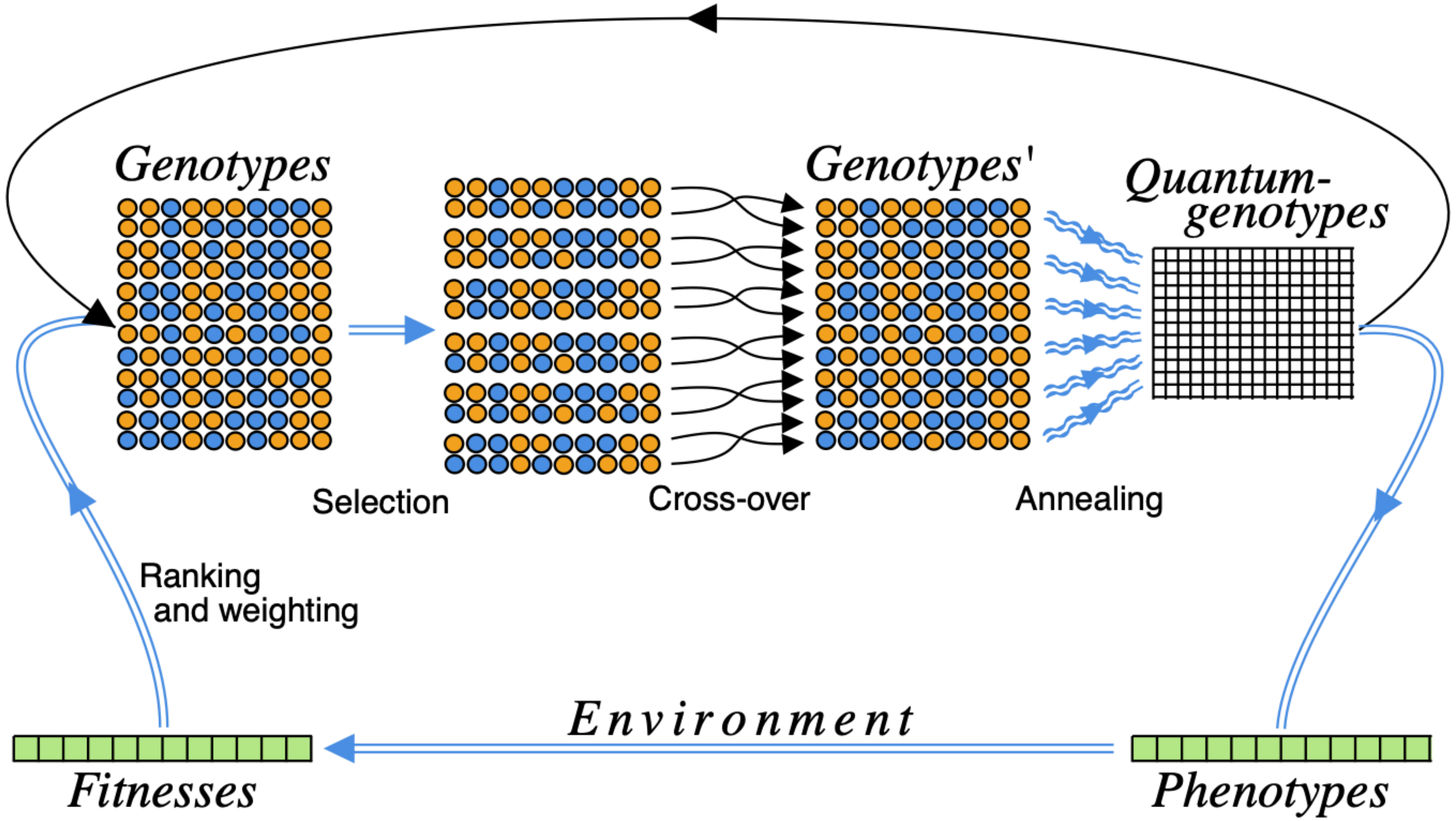
Quantum Annealing

- “A Genetic Quantum Annealing Algorithm” (GQAA)
  - S.Abel, L.Nutricati, M.Spannowsky - GQAA (2022)
  - D-Wave’s Advantage_system4.1
- Form of quantum computing to find ground state of Ising Model
- Start with a system of free-spins in ground state
- Smoothly change to Ising model of interest
  - Adiabatic Theorem -> Should end up in new ground state

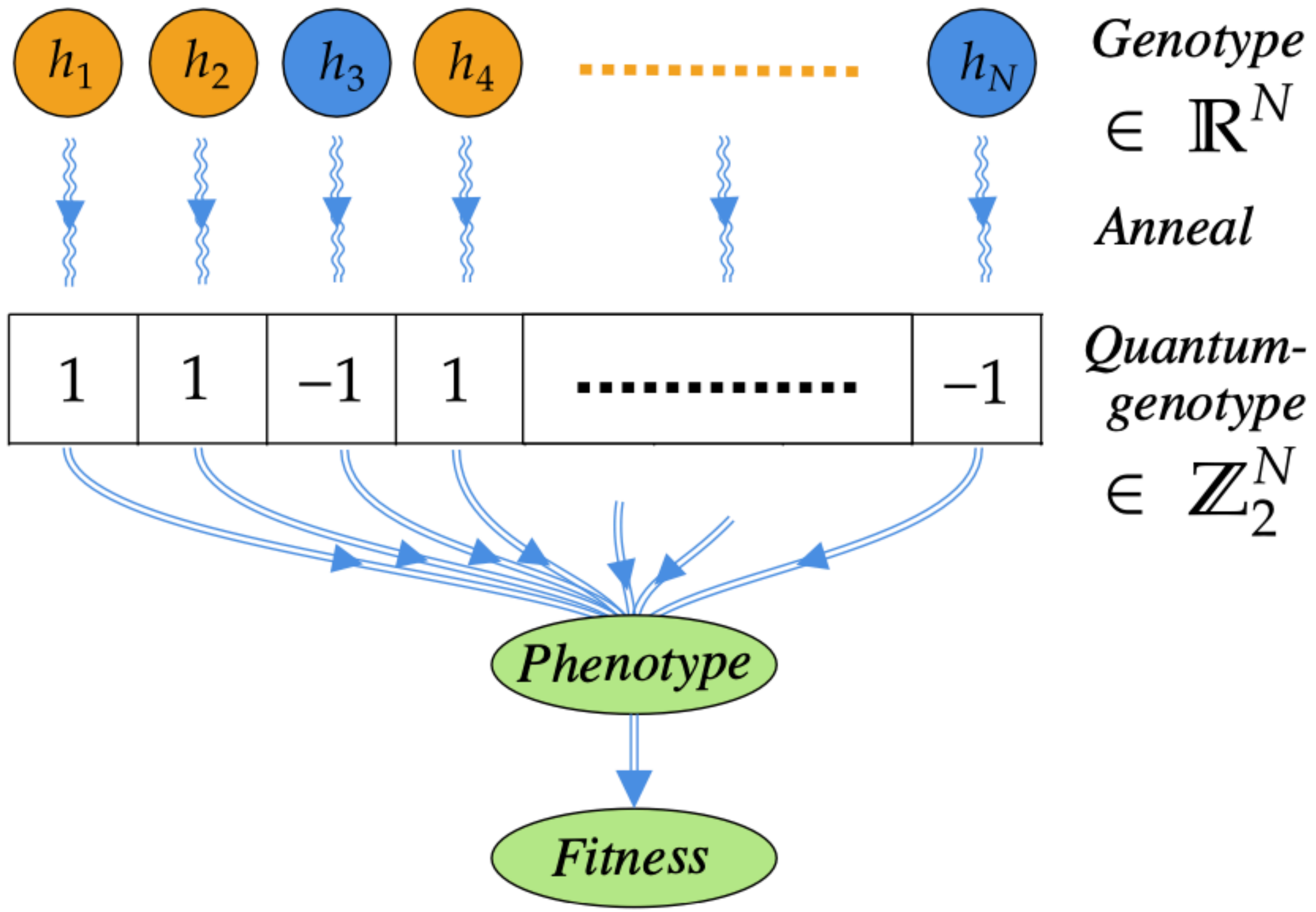
$$H(s=0) = \sum_l \tilde{h}_l \sigma_l^{(x)} \quad \Rightarrow \quad H(s=1) = \sum_l h_l \sigma_l^{(z)} + \sum_{lm} J_{lm} \sigma_l^{(z)} \sigma_m^{(z)}$$

GQAA

1. Replace mutation stage with annealing

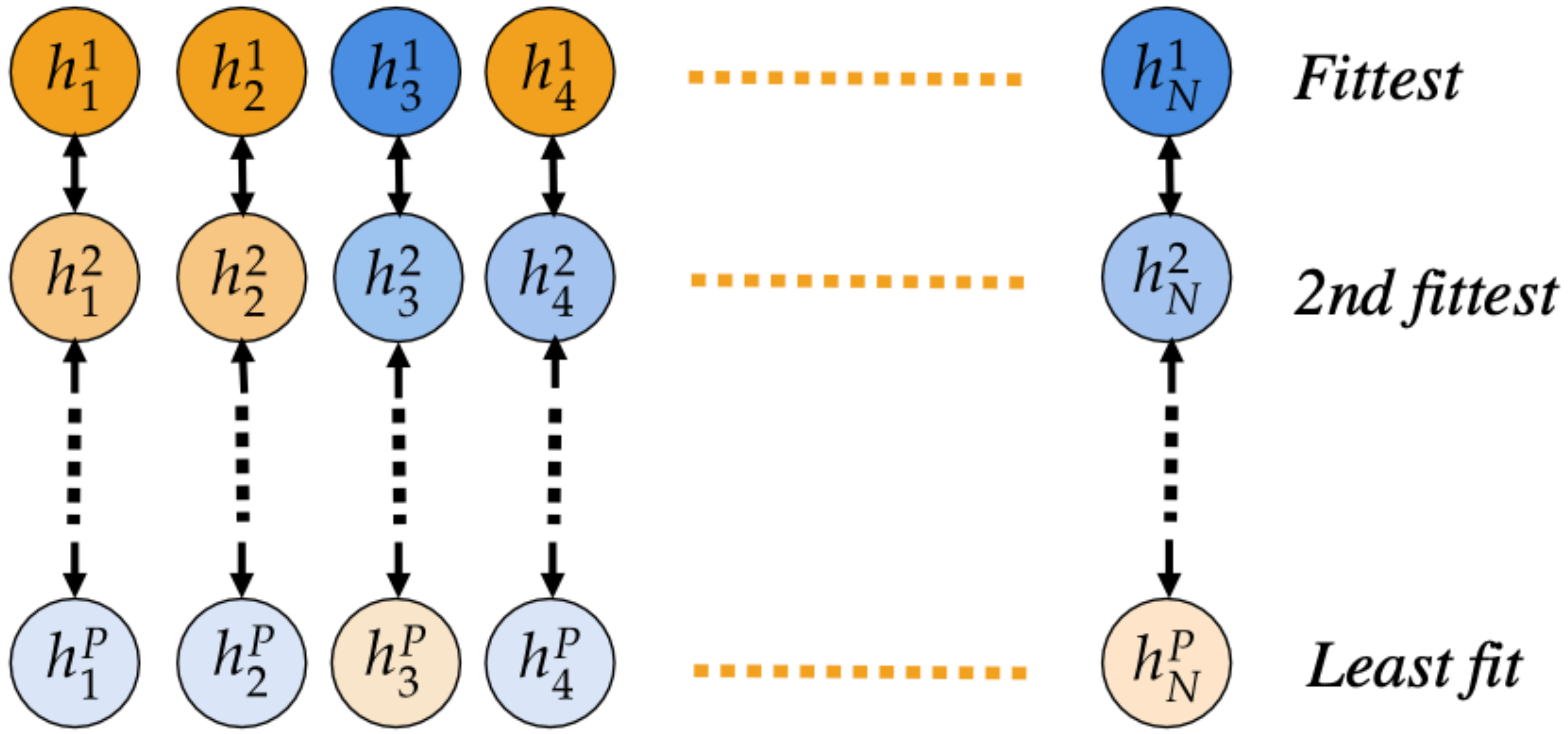


4. Get the new individual by measuring the final spins



2. Linear couplings are the original individual
Magnitude of position in fitness ranking
Sign +/- from 1/0

3. Quadratic couplings from considering the full population



Line Bundle Sums

- Start with E8xE8 Heterotic String Theory
- Need to specify a CY3 M, with vector-bundle V
  - Favourable configuration: Gray Wang (2021)

$$X^{(4,68)}_{7862} = \begin{array}{c} \mathbb{P}^1 \\ \mathbb{P}^1 \\ \mathbb{P}^1 \\ \mathbb{P}^1 \end{array} \left[\begin{array}{c} 2 \\ 2 \\ 2 \\ 2 \end{array} \right] \,, \quad X^{(5,45)}_{7447} = \begin{array}{c} \mathbb{P}^1 \\ \mathbb{P}^1 \\ \mathbb{P}^1 \\ \mathbb{P}^1 \\ \mathbb{P}^1 \end{array} \left[\begin{array}{cc} 1 & 1 \\ 1 & 1 \\ 1 & 1 \\ 1 & 1 \\ 1 & 1 \end{array} \right]$$

$$X^{(6,30)}_{5302} = \begin{array}{c} \mathbb{P}^1 \\ \mathbb{P}^1 \\ \mathbb{P}^1 \\ \mathbb{P}^1 \\ \mathbb{P}^1 \\ \mathbb{P}^1 \end{array} \left[\begin{array}{ccc} 0 & 1 & 1 \\ 0 & 1 & 1 \\ 1 & 1 & 0 \\ 1 & 1 & 0 \\ 1 & 0 & 1 \\ 1 & 0 & 1 \end{array} \right] \,, \quad X^{(7,27)}_{4071} = \begin{array}{c} \mathbb{P}^1 \\ \mathbb{P}^2 \\ \mathbb{P}^1 \\ \mathbb{P}^1 \\ \mathbb{P}^1 \\ \mathbb{P}^2 \\ \mathbb{P}^3 \end{array} \left[\begin{array}{cccccccc} 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 2 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 1 & 0 & 1 \\ 0 & 0 & 0 & 1 & 1 & 0 & 1 & 1 \end{array} \right]$$

- We choose to use favourable CICYs for M, and a sum of line bundles $V = \oplus_{i=1}^{5} \mathcal{O}_X(\mathbf{k_i})$
  - Anderson, Gray, Lukas & Palti (2012)
- 5 Line bundles will lead to an SU(5) GUT in 4D
  - Breaks to standard model if you introduce Wilson line on the quotient manifold M/Γ
  - This is a special locus in the moduli space of SU(5) bundles

Line Bundle Sums

- For the algorithms we use, need to encode as a binary string
- Line bundle is classified by its first Chern class $c_1(\mathcal{O}_X(\mathbf{k})) = \sum_{\alpha=1}^{h_{11}} k^\alpha J_\alpha \in H^2(X, \mathbb{Z})$ ~ a vector of integers
- $V = \bigoplus_{i=1}^{5} \mathcal{O}_X(\mathbf{k_i})$ is described by a matrix of integers - fills lattice $\mathbb{Z}^{5h_{11}}$
  - Can drop to $\mathbb{Z}^{4h_{11}}$, from requirement that $c_1(V) = 0$
- Natural embedding of each element into (n+1) bits $k_i^\alpha \in \{-2^n + 1, \ldots, 2^n\}$
  - Need $4h_{11}(n+1)$ bits in total (we will use n=2 or n=3)
- Will also need a negative-semidefinite “fitness function” - next slide
  - Fitness = 0 corresponds to MSSM (+ Moduli Fields)

Fitness Function

Requirement	Expression	Fitness Contribution
E8 Embedding	$c_1(V) = \sum_{a=1}^{5} k_a \overset{!}{=} 0 \ .$	NA
Anomaly Cancelation	$c_{2,i}(V) = -\frac{1}{2} d_{ijk} \sum_{a=1}^{5} k_a^j k_a^k \overset{!}{\leq} c_{2,i}(TX) \ ,$	$f_{\text{anom}} = 10 \sum_{i=1}^{h} \frac{\min(c_{2,i}(V) - c_{2,i}(TX), 0)}{h k_{\text{max}}^2 \, \text{rk}(V)}$
Stability/Supersymmetry	$\mu(L_a) = d_{ijk} k_a^i t^j t^k \overset{!}{=} 0$ for $a = 1, \ldots, 5$	$f_{\text{slope}} = -\frac{n_{\text{pos}} + n_{\text{neg}}}{10} \ .$
Spectrum(When able)/Index	**10**-multiplets: $h^1(X,V) = 3\lvert\Gamma\rvert$ no $\overline{\mathbf{10}}$-multiplets: $h^2(X,V) = 0$ $\overline{\mathbf{5}}$-multiplets: $h^1(X, \wedge^2 V) = 3\lvert\Gamma\rvert + n_h, \ n_h > 0$ Higgs: $h^2(X, \wedge^2 V) = n_h$ $\chi(X,V) = \chi(X, \wedge^2 V) = 3\lvert\Gamma\rvert$	$f_{\text{spec}} = -1000 \frac{h^0(X,V) + h^3(X,V) + h^0(X,\wedge^2 V) + h^3(X,\wedge^2 V)}{h k_{max}^3 \, \text{rk}(V)^2} - 100 \frac{h^2(X,V)}{h k_{max}^3} + \frac{\theta(h^2(X,\wedge^2 V) - 1/2) - 1}{10} - 5 \frac{\max(h^2(X,\wedge^2 V)/\lvert\Gamma\rvert - 2, 0)}{h k_{max}^3 \, \text{rk}(V)} \ ,$ $f_{\text{ind}} = -100 \frac{\lvert \text{ind}(V) + 3\lvert\Gamma\rvert \rvert}{h k_{\text{max}}^3 \, \text{rk}(V)} \ .$
Equivariance	…	…

Results-GA

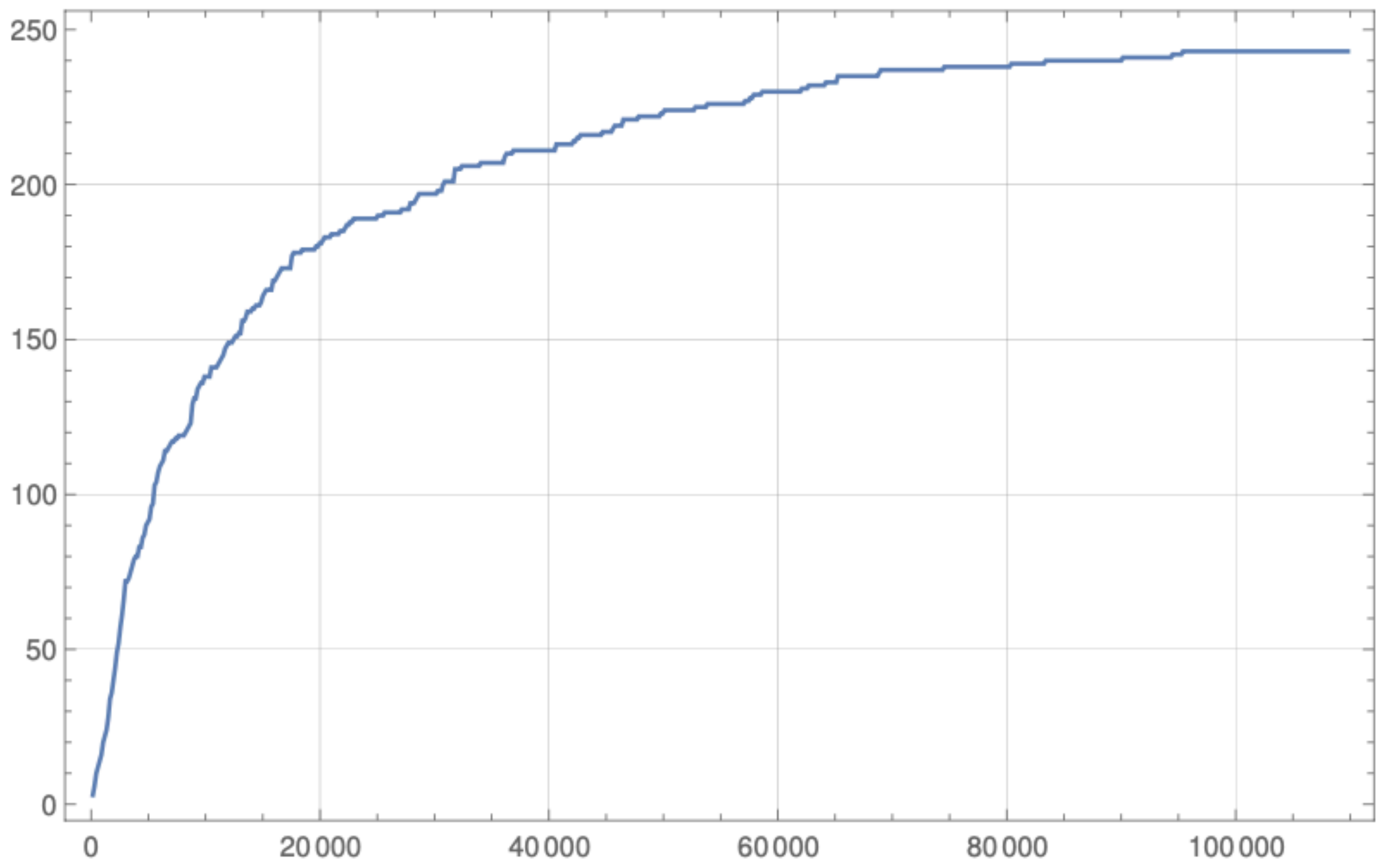
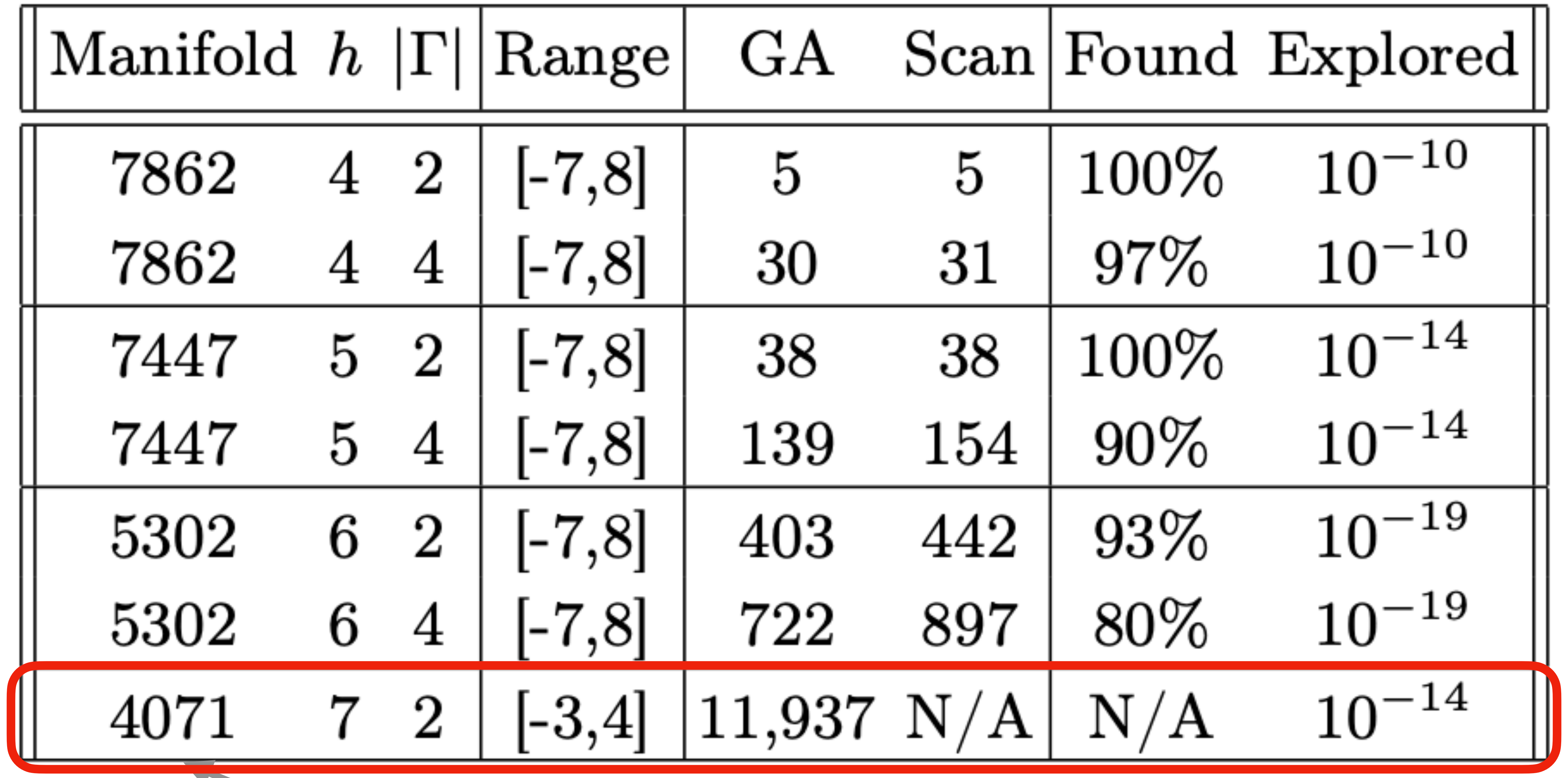


Figure 1. Saturation plot for the GA search on X_{7447} with $|\Gamma| = 4$ and $h^{1,1}(X_{7447}) = 5$. The horizontal axis represents the number of genetic episodes, in each episode a number of 90,000 states being visited. The vertical axis corresponds to the number of inequivalent models found in the search satisfying the necessary criterion (C3) for poly-stability. The computational time for a genetic episode is $O(10)$ seconds on a standard machine.

Very efficient compared to direct scans, and finds almost all states



Manifold	h	$\|\Gamma\|$	Range	GA	Scan	Found	Explored
7862	4	2	[-7,8]	5	5	100%	10^{-10}
7862	4	4	[-7,8]	30	31	97%	10^{-10}
7447	5	2	[-7,8]	38	38	100%	10^{-14}
7447	5	4	[-7,8]	139	154	90%	10^{-14}
5302	6	2	[-7,8]	403	442	93%	10^{-19}
5302	6	4	[-7,8]	722	897	80%	10^{-19}
4071	7	2	[-3,4]	11,937	N/A	N/A	10^{-14}

Can consider higher Picard number than was possible with direct scans

Results-GQAA vs GA

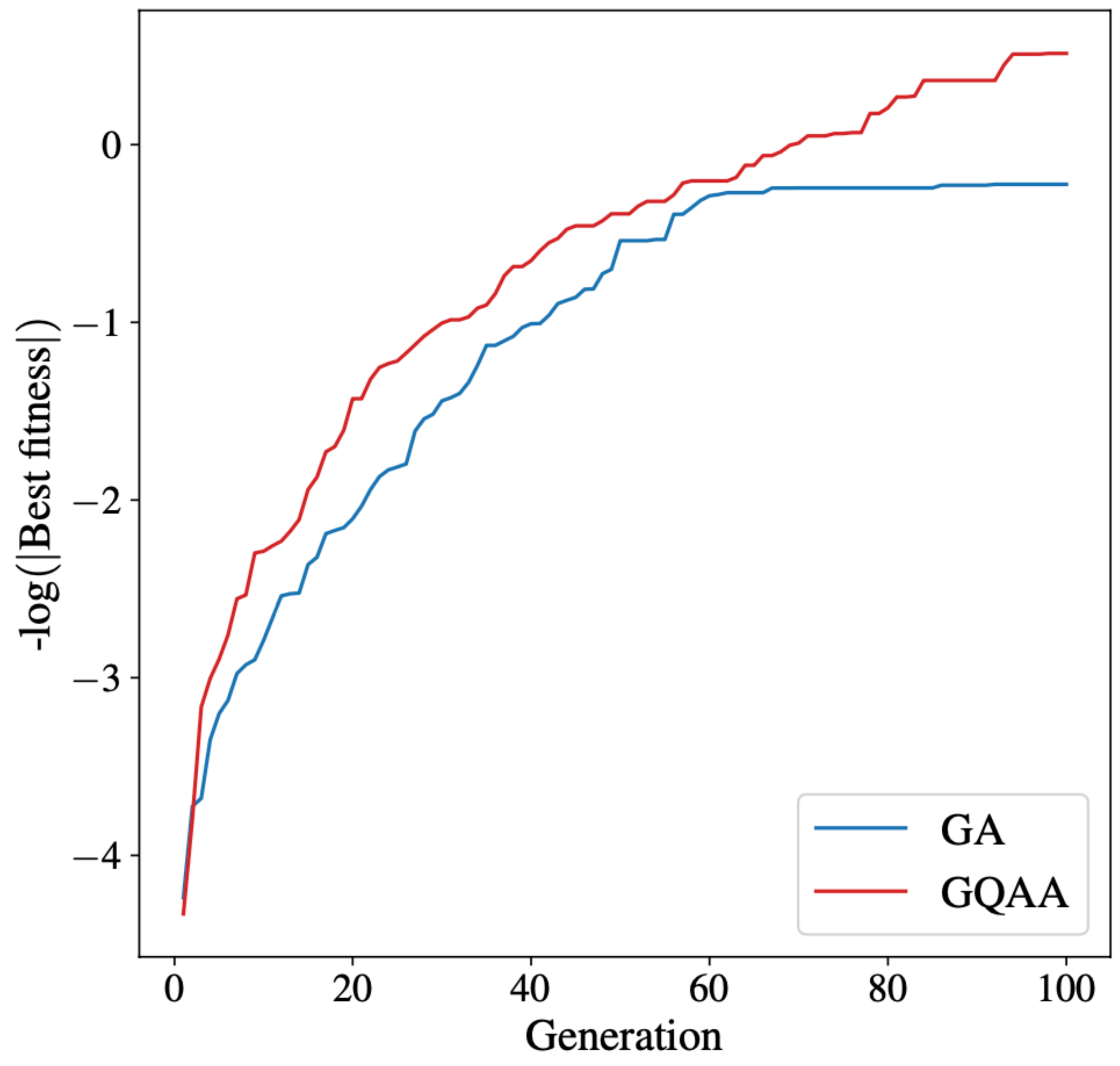


Figure 3. Fitness of the fittest individual for both GA and GQAA for the first 100 generations on X_{7447} with $|\Gamma| = 4$. The optimal value of the GA mutation rate is 0.5% and the range for the integers k_a^i is chosen to be $[-4, 3]$. N_{pop} was set to 50 for both GA and GQAA. The fitness was averaged over 20 runs. All the other parameters related to the GQAA part are specified in Table II.

GQAA saturates faster for a single genetic run

Will have full saturation in ~1/2 the number of genetic runs.

However, it currently takes more real time. Time is spent moving between classical computer and annealer

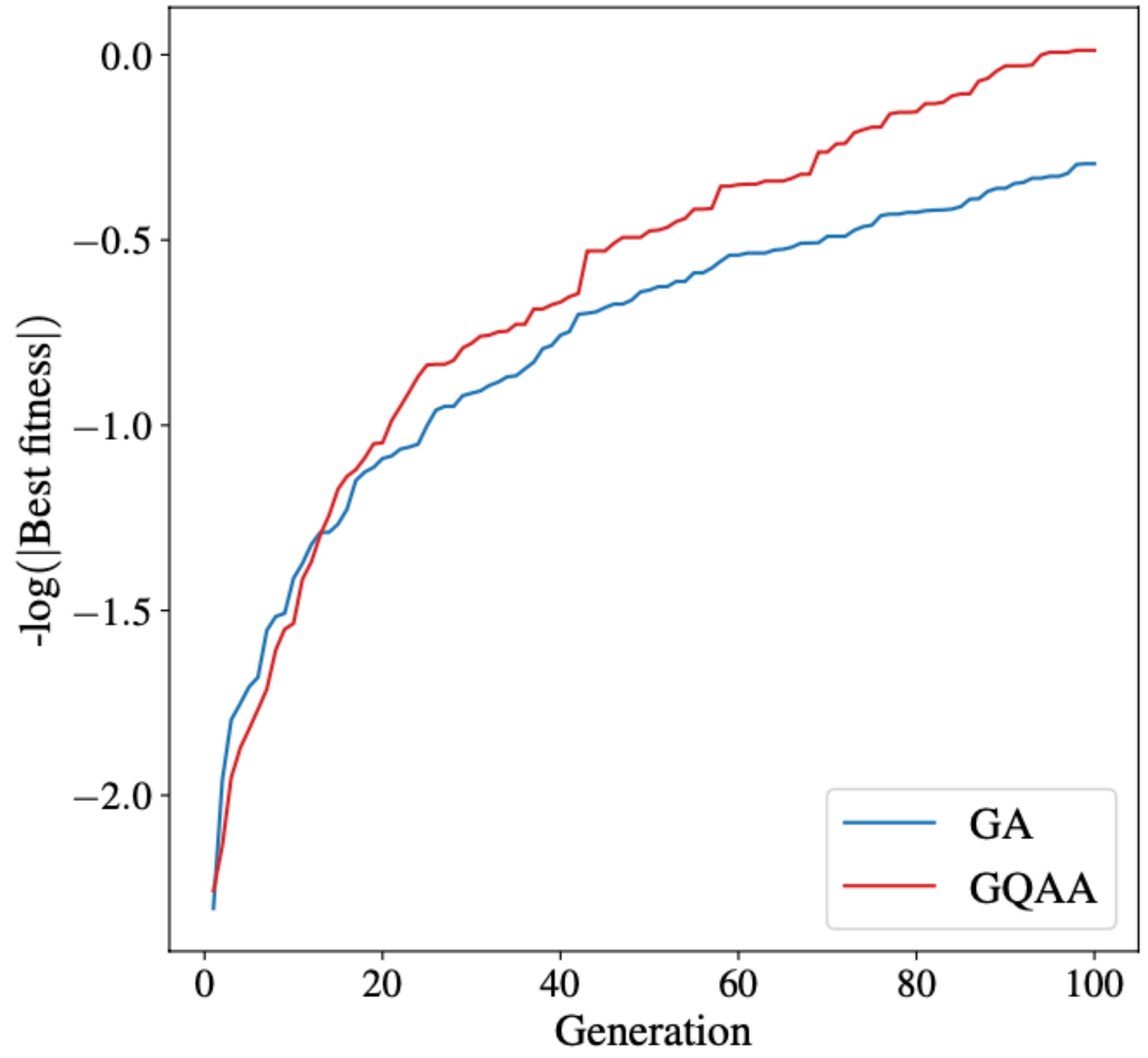


Figure 4. Fitness of the fittest individual for both GA and GQAA for the first 100 generations on X_{5302} with $|\Gamma| = 2$. The optimal value of the GA mutation rate is 1% and the line bundle integers are chosen in the range $k_a^i \in [-7, 8]$. N_{pop} was set to 35 for both GA and GQAA. The fitness was averaged over 20 runs. All the other parameters related to the GQAA part are specified in Table II.

Conclusion and Outlook

- GA is able to search the space if line bundle sums for interesting models
  - Up to $\sim 10^{19}$ more efficient than a systematic scan in some cases
  - We have been able to explore higher Picard number than has been possible with direct scans
- Evidence suggests that the method will improve with quantum annealing, but currently slowed down moving between classical computer and quantum annealer
- Even in these huge landscapes, it's possible to identify the points of physical interest efficiently
  - This method can be applied to other string constructions
  - Even adding further constraints e.g. Yukawa Couplings