

Here we derive the theoretical value distribution for a gene in uniformly-sampled probability vectors, and compare it with empirical results:

Since the entries of p add up to 1, we can compute $P(p_i = k)$ by evaluating its equivalent $P\left(\sum_{j \neq i} p_j = 1 - k\right)$. Let S_1 be the solution space spanned by the condition

$$\sum_{j \neq i} p_j = 1 - k$$

or equivalently,

$$\|p_{-i}\|_1 = 1 - k, \quad p_{-i} = \{p_0, \dots, p_{i-1}, p_{i+1}, \dots, p_n\}$$

In this formulation, we see that S_1 forms the surface of a taxicab (L_1) sphere. From [1], we know that the volume of S_1 is proportional to the radius raised by the degree of freedom. Since p_i is an independent variable, the degree of freedom is one less $|p| - 1$, yielding

$$V_n(S_1) \propto (1 - k)^{|p|-2} \quad (1)$$

Since the probability density is uniform across all vector solutions, we know that the probability mass of S_1 is directly proportional to its volume defined in Equation (1),

$$P(p_i = k) = \lambda(1 - k)^{|p|-2}$$

where λ is a normalizing constant,

$$\begin{aligned} \int_0^1 \lambda(1 - k)^{|p|-2} dk &= 1 \\ \lambda \left[\frac{1}{|p| - 1} (1 - k) \right]_1^0 &= 1 \\ \lambda &= |p| - 1 \end{aligned}$$

$$P(p_i = k) = (|p| - 1)(1 - k)^{|p|-2} \quad (2)$$

Equation (2) thus gives us the theoretical distribution of a gene in uniformly-sampled probability vectors.

REFERENCES

- [1] K. P. Thompson, "The nature of length, area, and volume in taxicab geometry," *arXiv preprint arXiv:1101.2922*, 2011.