Gene_interaction

A convenient way to see the general rule is via "inclusion-exclusion" on the lower-order terms. Concretely, label your fitness (or response) for a subset of genes $S \subseteq \{1, \ldots, n\}$ by f_S. Then define the interaction ϵ_S for that subset by recursively subtracting off all interactions belonging to strict sub-subsets of S. In symbols,

$$\epsilon_S = f_S - \sum_{\emptyset \neq T \subset S} \epsilon_T$$

Here are the small cases to see the pattern:

- Singles: $\epsilon_{\{i\}} = f_{\{i\}}$.
- Pairs: $\epsilon_{\{i,j\}} = f_{\{i,j\}} - \epsilon_{\{i\}} - \epsilon_{\{j\}} = f_{ij} - f_i - f_j$.
- Triples:

$$\epsilon_{\{i,j,k\}} = f_{ijk} - \left(\epsilon_{\{i\}} + \epsilon_{\{j\}} + \epsilon_{\{k\}}\right) - \left(\epsilon_{\{i,j\}} + \epsilon_{\{i,k\}} + \epsilon_{\{j,k\}}\right)$$

and so forth. Equivalently, one may write this as an inclusion-exclusion formula

$$\epsilon_S = \sum_{T \subseteq S} (-1)^{|S|-|T|} f_T$$

provided you set $f_\emptyset = 0$. Either expression generalizes the notion that, to isolate a genuine k-way interaction, you must "peel off" all interactions from sub-collections off the same genes.

2025.01.27 - Derivation of Tau

The derivation for τ_{ijk}, the triple interaction term, follows from the recursive definition of interactions. Let's walk through the steps systematically.

We start with the general recursive formula:

$$\tau_{ijk} = f_{ijk} - \sum_{S \subset \{i,j,k\}, |S|=2} \tau_S - \sum_{T \subset \{i,j,k\}, |T|=1} f_T$$

Here's the breakdown step by step:

1. Subtract contributions from single elements (f_i, f_j, f_k):

The single fitness terms contribute:

$$\sum_{T \subset \{i,j,k\}, |T|=1} f_T = f_i + f_j + f_k$$

These are the individual effects of the single genes i, j, k. 2. Subtract contributions from pairs $\left(\tau_{ij}, \tau_{ik}, \tau_{jk}\right)$:

The pairwise interaction terms contribute:

$$\sum_{S \subset \{i,j,k\}, |S|=2} \tau_S = \tau_{ij} + \tau_{ik} + \tau_{jk}$$

Each of these pairwise terms has already been recursively defined as:

$$\tau_{ij} = f_{ij} - f_i - f_j$$
$$\tau_{ik} = f_{ik} - f_i - f_k$$
$$\tau_{jk} = f_{jk} - f_j - f_k$$

3. Combine terms:

The triple interaction term τ_{ijk} is then:

$$\tau_{ijk} = f_{ijk} - \left(f_{ij} - f_i - f_j\right) - \left(f_{ik} - f_i - f_k\right) - \left(f_{jk} - f_j - f_k\right) - f_i - f_j - f_k$$

Simplify step by step:

- Combine the single terms f_i, f_j, f_k :

$$\tau_{ijk} = f_{ijk} - f_{ij} - f_{ik} - f_{jk} + f_i + f_j + f_k$$

Final Form:

$$\tau_{ijk} = f_{ijk} - f_{ij} - f_{ik} - f_{jk} + f_i + f_j + f_k$$

This is the full expanded form of the triple interaction term τ_{ijk}. It subtracts all pairwise and single contributions to isolate the unique interaction between i, j, k.

2025.02.02 - Gene Interaction Not Regressive Form

Digenic Interaction:

$$\epsilon_{ij} = f_{ij} - f_i f_j, \quad \text{where } f_i \text{ is fitness,}$$

$$\epsilon_{ij} = \mathcal{F}(f_i, f_j, f_{ij}).$$

Trigenic Interaction:

$$\tau_{ijk} = f_{ijk} - f_i f_j f_k - \varepsilon_{ij} f_k - \varepsilon_{ik} f_j - \varepsilon_{jk} f_i.$$

Full Recursive Definition (subtracting out effects of digenic interactions):

$$\begin{aligned}
\tau_{ijk} = {} & f_{ijk} - f_i f_j f_k \\
& - \left(f_{ij} - f_i f_j\right) f_k \\
& - \left(f_{ik} - f_i f_k\right) f_j \\
& - \left(f_{jk} - f_j f_k\right) f_i, \\
\tau_{ijk} = {} & \mathcal{F}\left(f_i, f_j, f_k, f_{ij}, f_{ik}, f_{jk}, f_{ijk}\right).
\end{aligned}$$

Fitness

$$f_i = \mathcal{F}(g_i, g_{wt})$$

Digenic Interaction:

$$\epsilon_{ij} = \mathcal{F}(f_i, f_j, f_{ij})$$

Trigenic Interaction:

$$\tau_{ijk} = \mathcal{F}\left(f_i, f_j, f_k, f_{ij}, f_{ik}, f_{jk}, f_{ijk}\right)$$