



Why

We want to summarize the interaction between two binary traits.

Definition

The *contingency table* of a population $\{1, \dots, n\}$ with respect to binary traits $a, b : \{1, 2, \dots, n\} \rightarrow \{0, 1\}$ is the array $A \in \mathbf{N}^{2 \times 2}$ of natural numbers defined by

$$A = \begin{bmatrix} |a^{-1}(0) \cap b^{-1}(0)| & |a^{-1}(0) \cap b^{-1}(1)| \\ |a^{-1}(1) \cap b^{-1}(0)| & |a^{-1}(1) \cap b^{-1}(1)| \end{bmatrix}.$$

We interpret A_{11} as the number of individuals which have neither trait, A_{12} as the individuals which have trait b but not trait a , and so on.

Normalization

These four sets partition $\{1, 2, \dots, n\}$, so that if we divide the elements by n , we obtain four numbers which sum to 1, the 2 by 2 table with these entries is called the *normalized contingency table*.

Contingency arrays

In general, we have k binary traits, each of which an individual may or may not have. We encode these traits using k functions

$$a_1, \dots, a_k : \{1, 2, \dots, n\} \rightarrow \{0, 1\}.$$

The contingency array is k -dimensional array A , with

$$A_x = \cap_{j=1}^k a_j^{-1}(x_j),$$

where $x \in \{0, 1\}^k$.

