



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



