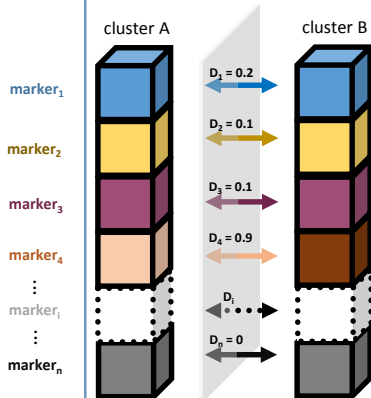


1. Computation of marker similarities



2. Count of marker similarity successes

$$D_{th} = 0.3$$

$$D_1 < D_{th} \rightarrow$$

success

1

$$D_2 < D_{th} \rightarrow$$

success

1

$$D_3 < D_{th} \rightarrow$$

success

3

$$D_4 > D_{th} \rightarrow$$

fail

2

$$D_i \text{ vs } D_{th} \rightarrow$$

...

...

$$D_n < D_{th} \rightarrow$$

success

1

similarity trial (fail or success)	marker weights
success	1
success	1
success	3
fail	2
...	...
success	1

3. Aggregation of marker similarities using an exact binomial test

Firstly, the weighted number of success x and the weighted number of trials w are calculated using these two formulas:

$$x = \sum_{i=1}^n \text{trial}_i \times \text{weight}_i \quad w = \sum_{i=1}^n \text{weight}_i$$

where

trial_i is equal to 0 iff the trial fail for marker_i or else is equal to 1 iff the trial success for marker_i. Those marker trials will then correspond to success or fail in a Bernoulli experiment.

Secondly, using x and w , an exact right-tailed binomial test is performed between the null hypothesis defined by the probability of success P (provided by the user) and the observed number of success x in the w number of trials. A low p-value can then be interpreted as a high proportion of marker successes corresponding to similar cell clusters.

Moreover, an aggregated similarity measure is computed using the following formula:

$$D = \sum_{i=1}^n D_i \times \text{weight}_i$$

where

D_i correspond to the similarity measure for marker_i.