HPO Enrichment Analyze

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HPO dataset

The Human Phenotype Ontology $(HPO)^1$ provides a standardized vocabulary of phenotypic abnormalities encountered in human disease. Each term in the HPO describes a phenotypic abnormality, such as Atrial septal defect.

¹Sebastian Köhler et al. "Expansion of the Human Phenotype Ontology (HPO) knowledge base and resources". In: *Nucleic acids research* 47.D1 (2018), pp. D1018–D1027.

Enrichment



40 m&m's in the bag

Red	=	13%
Yellow	=	14%
Orange	-	21%

20% Brown 12% Blue 21%

Fisher's exact test

	succeed	failed	Total
studying	i	k-i	k
non-studying	m-i		N-k
Total	m	N-m	N

The probability of hypergeometric distribution.

$$p(x=i) = \frac{\binom{m}{i} \binom{N-m}{k-i}}{\binom{N}{k}} \tag{1}$$

$$pvalue = \sum_{x=i}^{k} p(x)$$
 (2)

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Implementation

A Python package for HPO enrichment analyze.

An HPO GSEA example

SAGD³ gene samples, SAGD₀₀₀₅₅ (human hypothalamus tissue). https://nanguage.github.io/examples/hpo_enrich/example_sagd_00055.html

³Meng-Wei Shi et al. "SAGD: a comprehensive sex-associated gene database from transcriptomes". In: Nucleic acids research 47.D1 (2018), pp.> D835-D840.

Thank you!

Reference

Köhler, Sebastian, Leigh Carmody, Nicole Vasilevsky, Julius O B Jacobsen, Daniel Danis, Jean-Philippe Gourdine, Michael Gargano, Nomi L Harris, Nicolas Matentzoglu, Julie A McMurry, et al. "Expansion of the Human Phenotype Ontology (HPO) knowledge base and resources". In: Nucleic acids research 47.D1 (2018), pp. D1018–D1027.

Shi, Meng-Wei, Na-An Zhang, Chuan-Ping Shi, Chun-Jie Liu, Zhi-Hui Luo, Dan-Yang Wang, An-Yuan Guo, and Zhen-Xia Chen. "SAGD: a comprehensive sex-associated gene database from transcriptomes". In: *Nucleic acids research* 47.D1 (2018), pp. D835—D840.