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統計的パターンマイニング Significant Pattern Mining

大阪大学 産業科学研究所
さきがけ研究者
杉山 磨人 Mahito Sugiyama

Outline

- (Discriminative) Pattern mining
- Statistical hypothesis testing of patterns
- Multiple hypothesis testing in pattern mining
- Testable patterns
- Permutation testing in pattern mining
- Conclusion

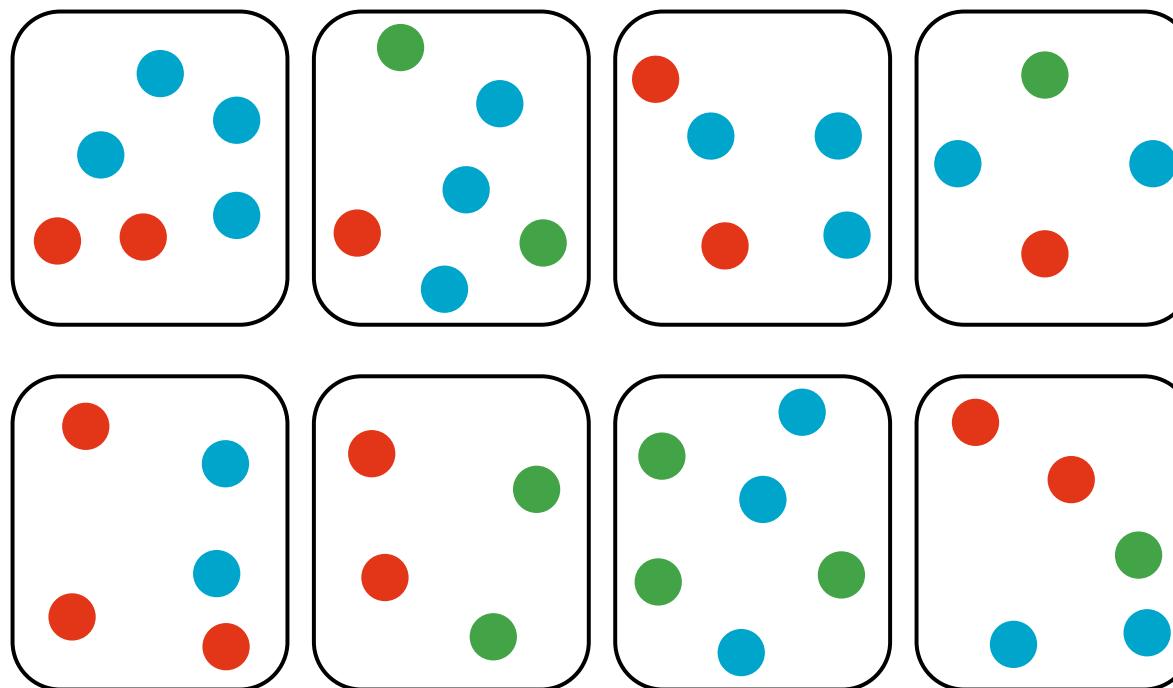
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Itemset Mining

- Find interesting **combinatorial patterns** from massive data

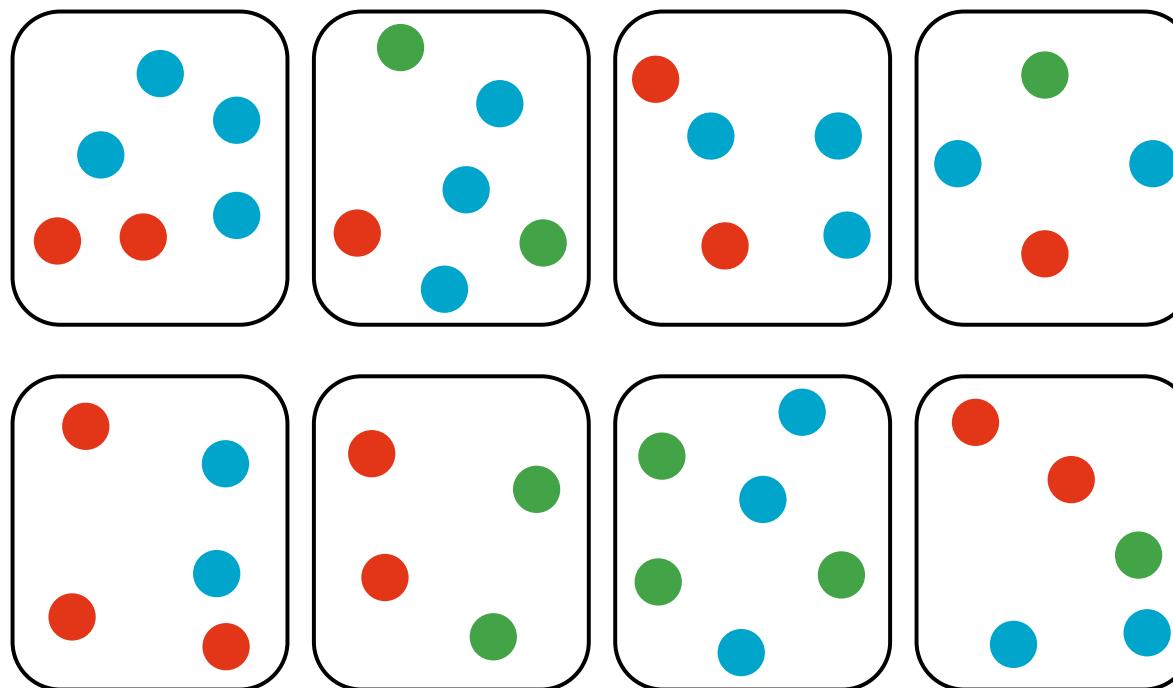
Database



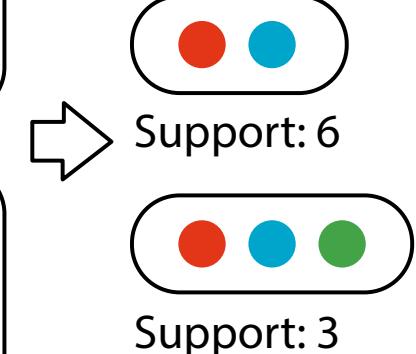
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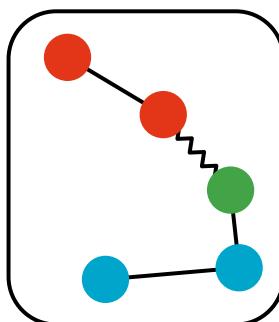
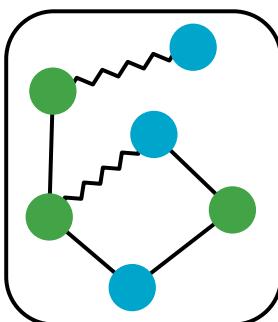
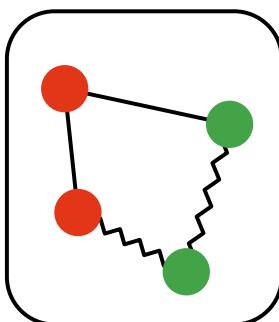
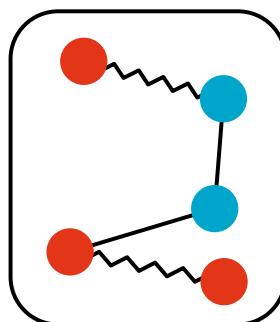
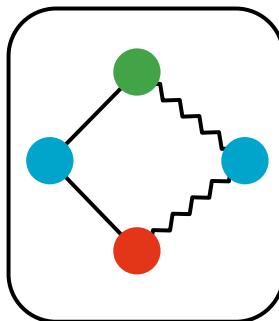
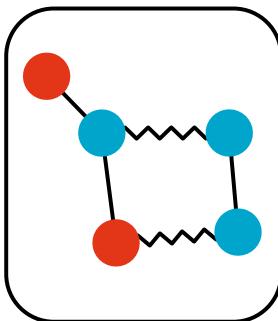
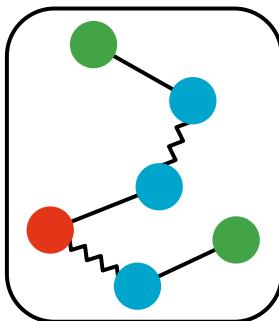
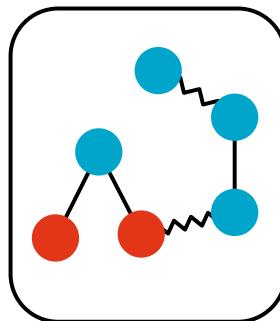
Itemset
(combination
of colors)



Subgraph Mining

- Find interesting **combinatorial patterns** from massive data

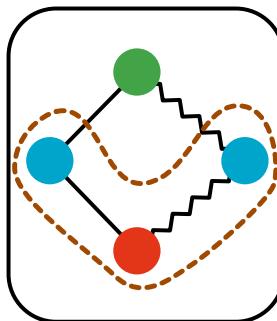
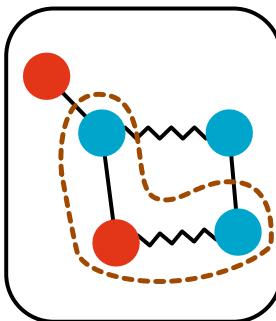
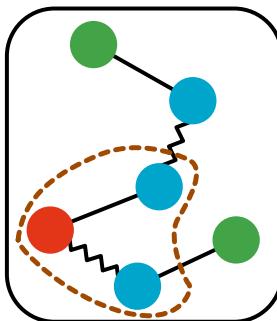
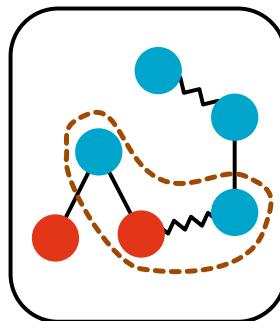
Database



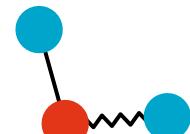
Subgraph Mining

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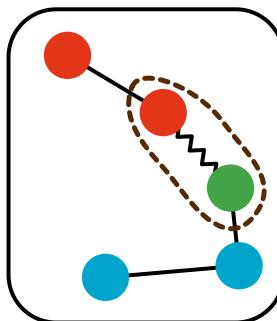
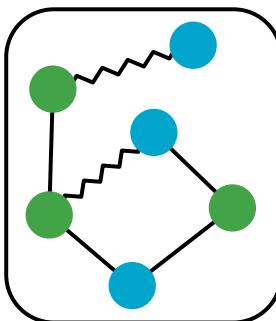
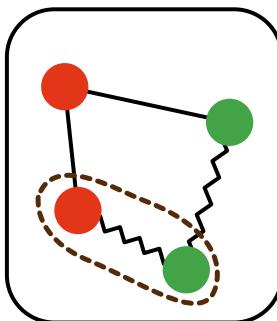
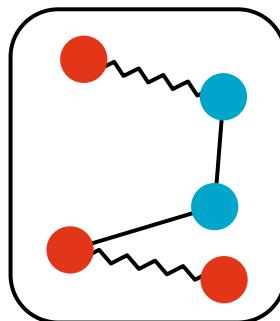
Database



Subgraph



Support: 4



Support: 2

Apriori on Itemset Lattice

Transaction
database

ID 1:  

ID 2:   

ID 3:  

ID 4:   

ID 5:  

ID 6:  

ID 7:  

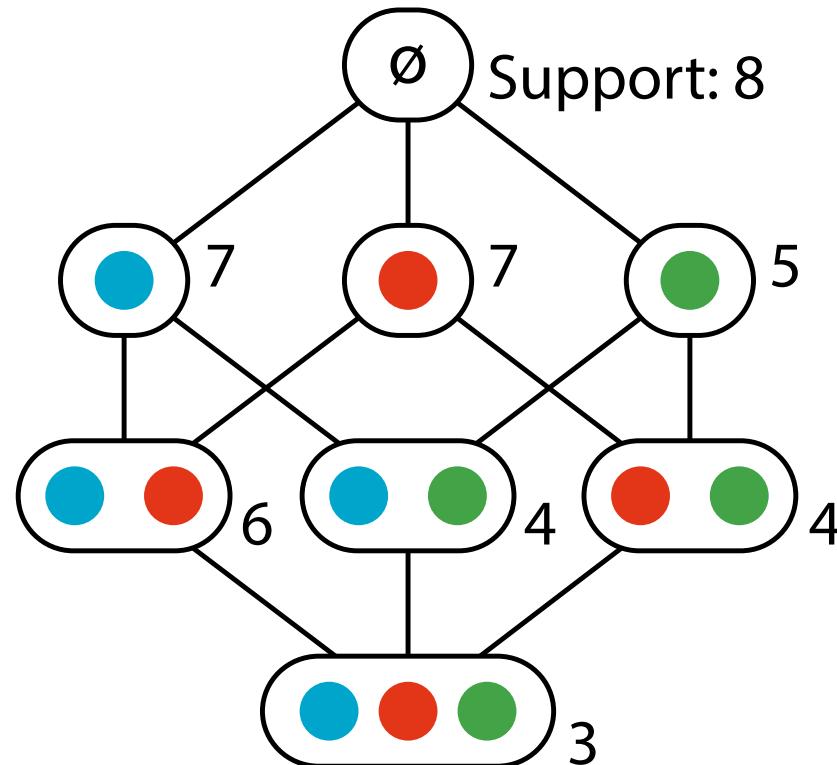
ID 8:   

Apriori on Itemset Lattice

Transaction
database

ID 1:	●	●	
ID 2:	●	●	●
ID 3:	●	●	
ID 4:	●	●	●
ID 5:	●	●	
ID 6:	●	●	
ID 7:	●	●	
ID 8:	●	●	●

Itemset lattice



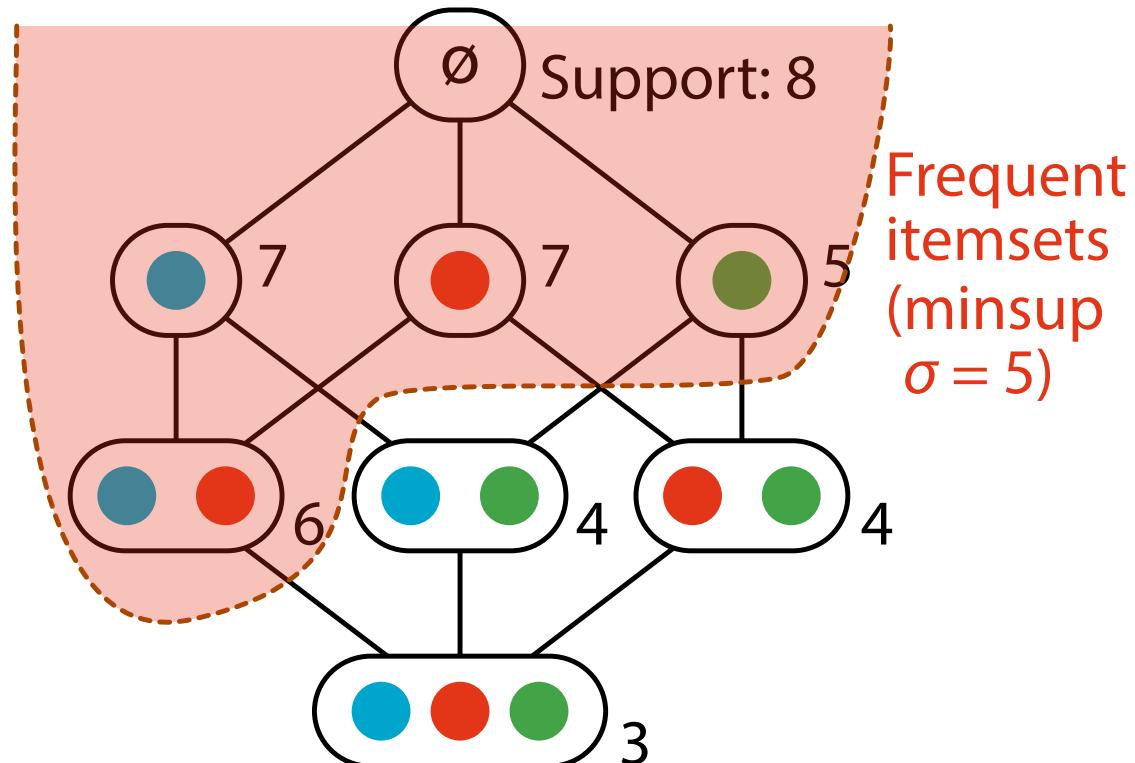
Apriori principle:
Support is monotonically decreasing

Apriori on Itemset Lattice

Transaction database

ID 1:	●	●	
ID 2:	●	●	●
ID 3:	●	●	
ID 4:	●	●	●
ID 5:	●	●	
ID 6:	●	●	
ID 7:	●	●	
ID 8:	●	●	●

Itemset lattice

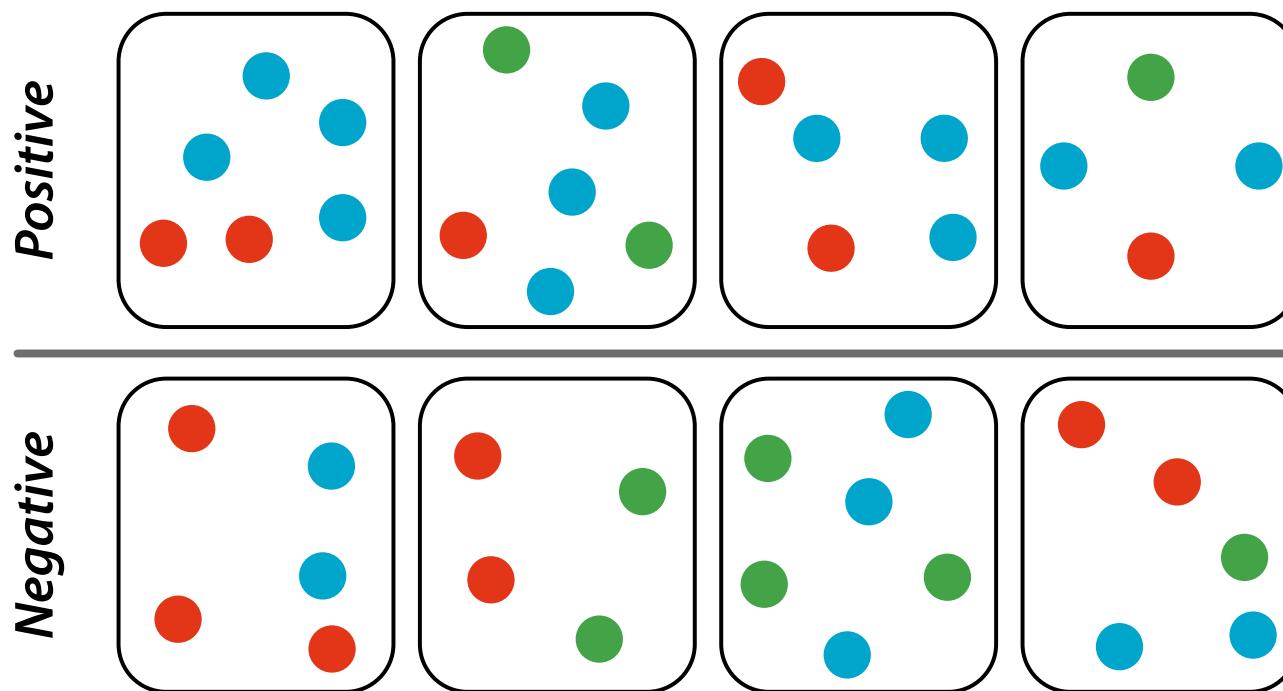


Apriori principle:
Support is monotonically decreasing

Discriminative Itemset Mining

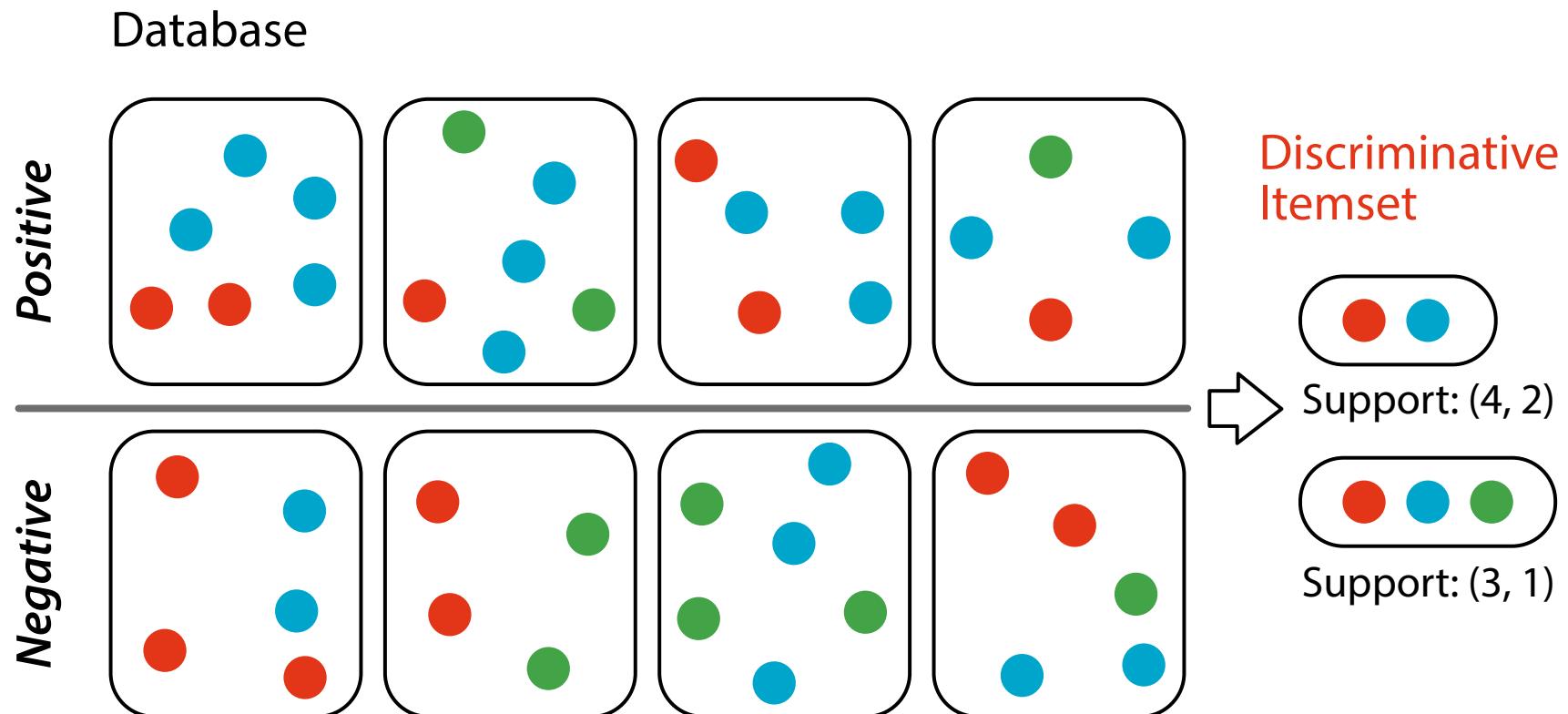
- Find **discriminative patterns** from **supervised data**
 - e.g. Genome-wide association studies in Bioinformatics

Database



Discriminative Itemset Mining

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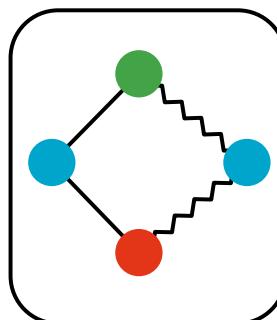
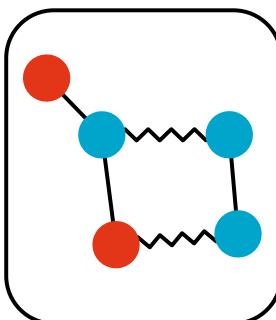
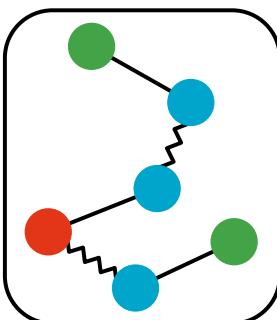
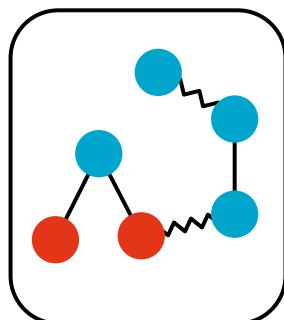


Discriminative Subgraph Mining

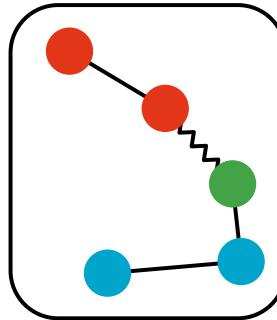
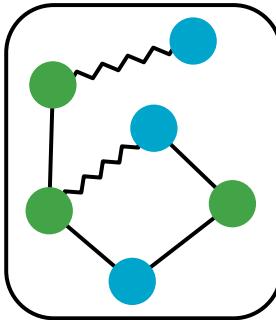
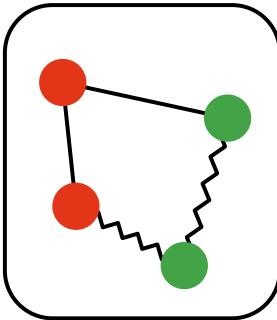
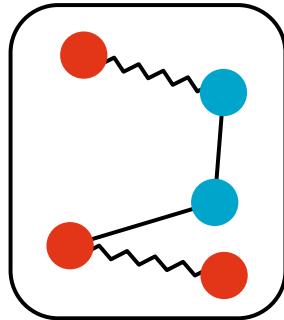
- Find **discriminative patterns** from **supervised data**
 - e.g. Drug discovery

Database

Positive

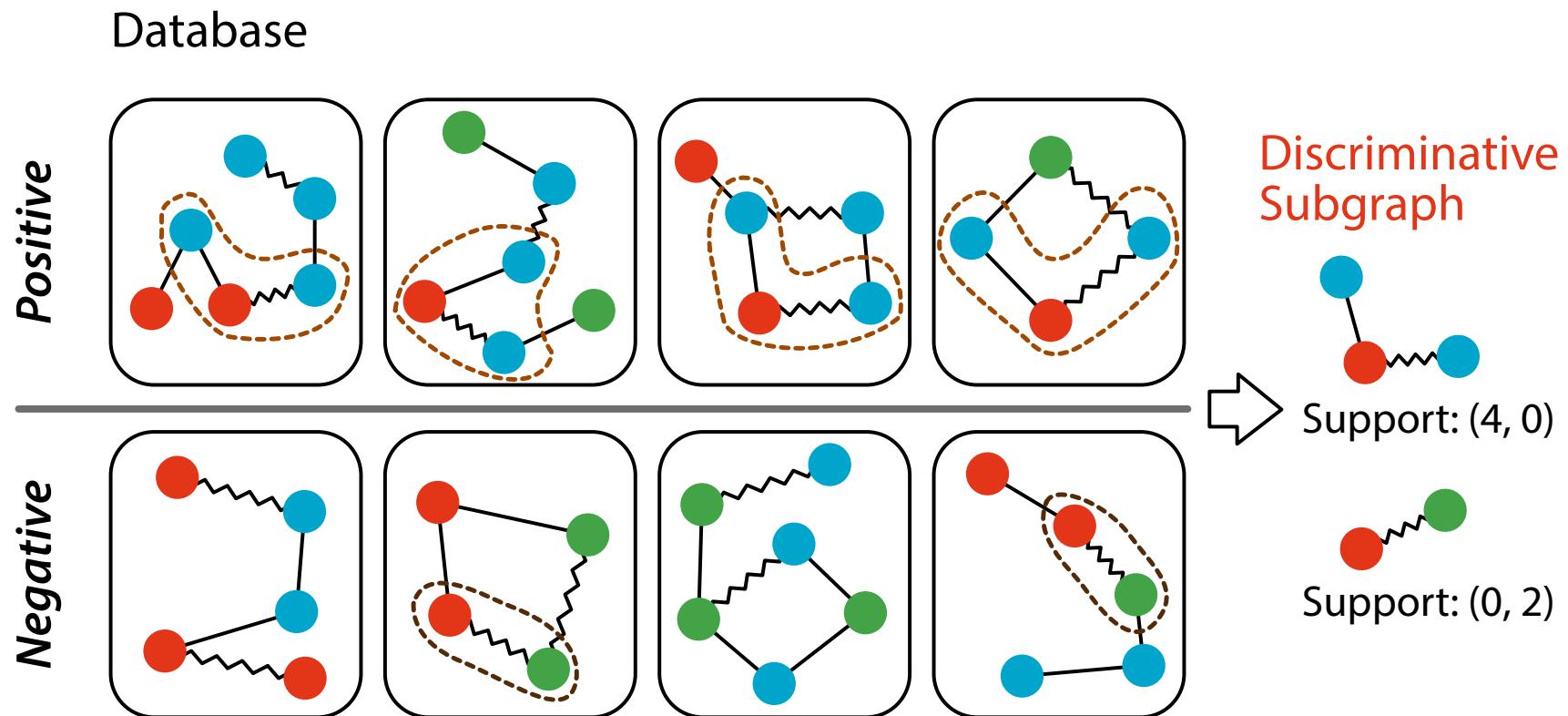


Negative



Discriminative Subgraph Mining

- Find **discriminative patterns** from **supervised data**
 - e.g. Drug discovery



Agenda

- In discriminative pattern mining:
 1. How to measure the **discriminability** of patterns?
 2. How to enumerate all discriminative patterns?

Agenda

- In discriminative pattern mining:
 1. How to measure the **discriminability** of patterns?
 2. How to enumerate all discriminative patterns?
- Answer to 1:
 - Compute the **p-value** via **statistical hypothesis testing**
 - Discriminative pattern \iff (Statistically) Significant pattern
- Answer to 2:
 - Integrate evaluation of discriminability and enumeration of patterns

Outline

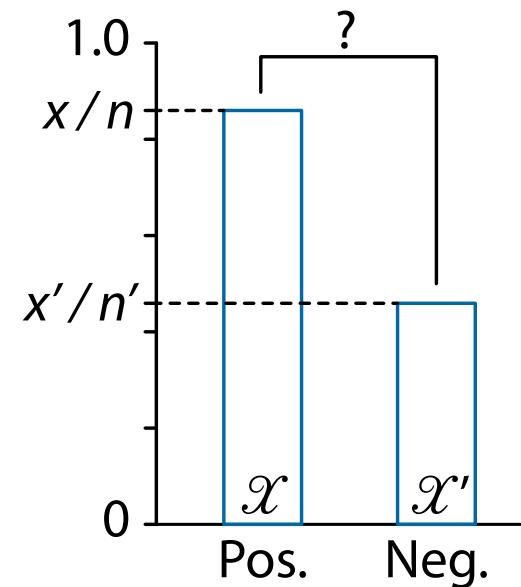
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Computing p -value of Pattern

- Given positive and negative sets of transactions $\mathcal{X}, \mathcal{X}'$
 - $|\mathcal{X}| = n, |\mathcal{X}'| = n' (n \leq n')$
- The *p-value* of each pattern H is determined by the *Fisher's exact test*
 - $x = |\{X \in \mathcal{X} \mid H \subseteq X\}|$

	Occ.	Non-occ.	Total
\mathcal{X} (Pos.)	x	$n - x$	n
\mathcal{X}' (Neg.)	x'	$n' - x'$	n'
Total	$x + x' = \sigma$	$(n - x) + (n' - x')$	$n + n'$

Support

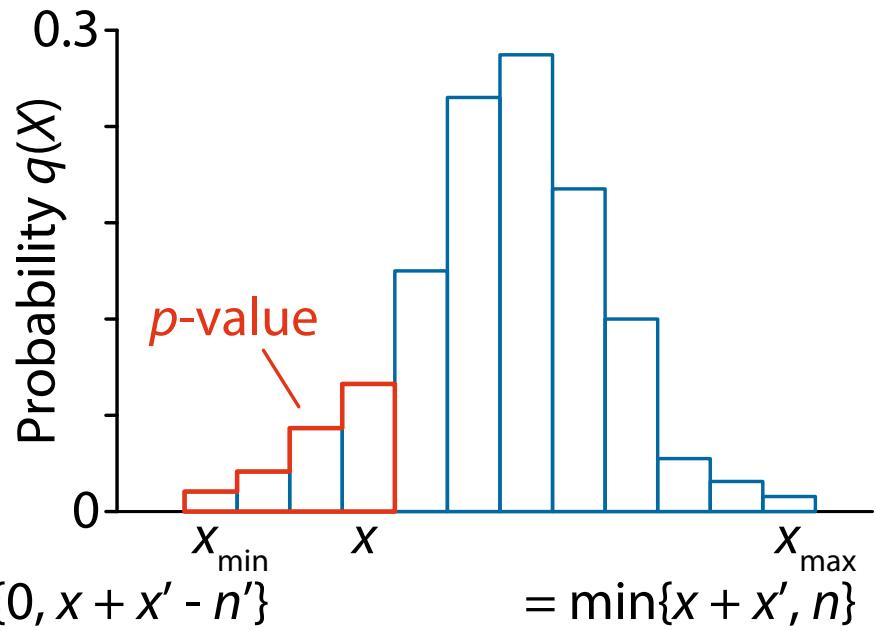


Fisher's Exact Test

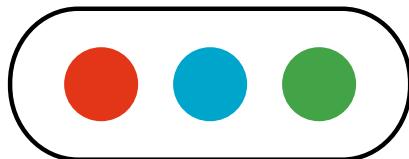
- The probability $q(x)$ of obtaining x and x' is given by the hypergeometric distribution:

$$q(x) = \binom{n}{x} \binom{n'}{x'} / \binom{n+n'}{x+x'}$$

	Occ.	Non-occ.	Total
\mathcal{X} (Pos.)	x	$n - x$	n
\mathcal{X}' (Neg.)	x'	$n' - x'$	n'
Total	$x + x' = \sigma$	$(n - x) + (n' - x')$	$n + n'$



Hypothesis Test for Each Pattern



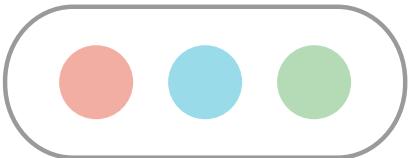
Alternative hypothesis
is true Null hypothesis
is true

Declared significant ($p\text{-value} < \alpha$)	True Positive	False Positive (Type I Error)
Declared non-significant	False Negative (Type II Error)	True Negative

Null hypothesis: The occurrence of the pattern is **independent** from classes

Alternative hypothesis: The occurrence of the pattern is **associated with** classes

Hypothesis Test for Each Pattern



Alternative hypothesis
is true Null hypothesis
is true

Declared
significant
($p\text{-value} < \alpha$)

True Positive

False Positive
(Type I Error)

Declared
non-signif.

False Negative

True Negative

Binary desicion (significant or not) via
the user specified threshold α

Null hypothesis:

The occurrence of the pattern is
independent from classes

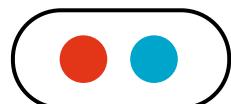
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Multiple Testing

Pattern:



	Occ.	Non-occ.	Total
Positive	4	0	4
Negative	2	2	4
Total	6	2	8

Fisher's exact test: $p\text{-value} = 0.429$

Multiple Testing

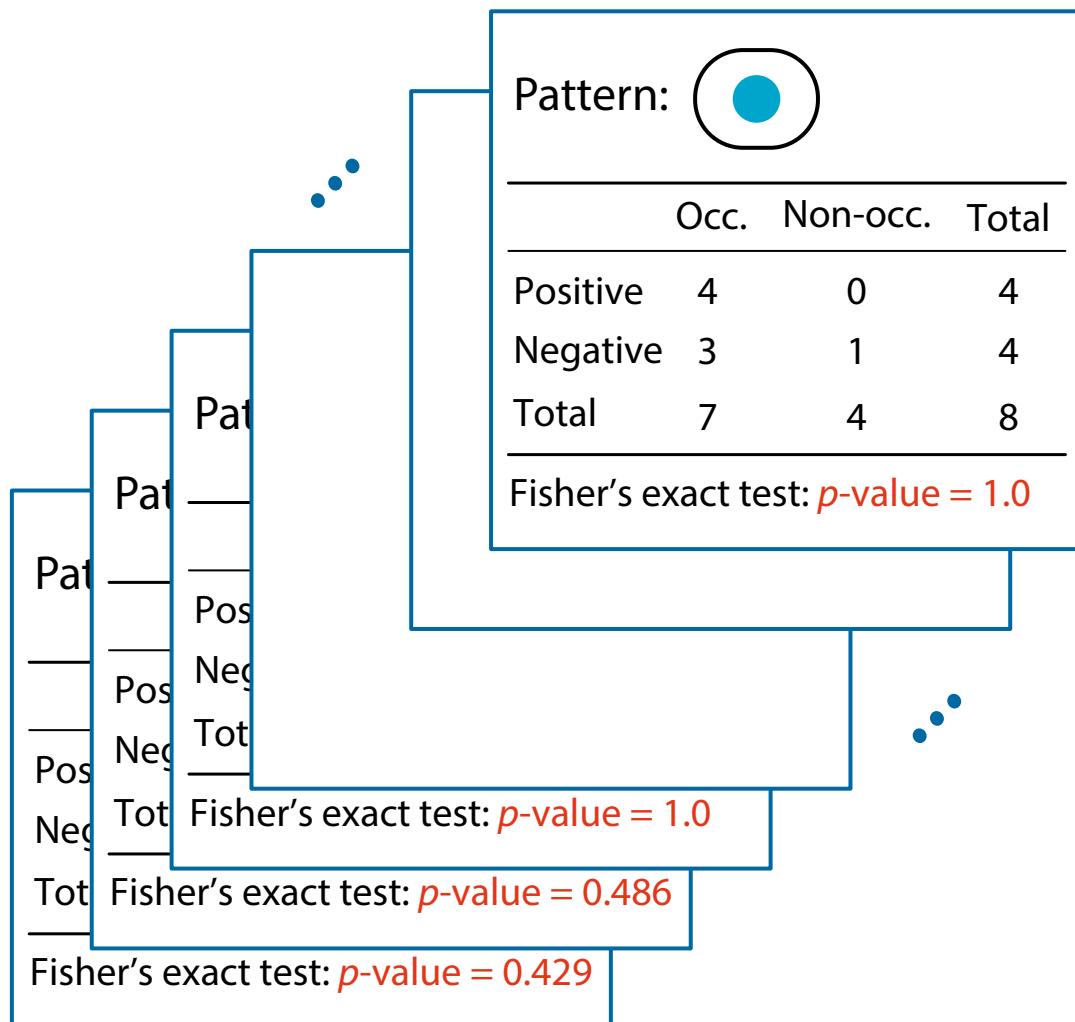
Pattern:				
		Occ.	Non-occ.	Total
Pat	Positive	3	1	4
Pos	Negative	1	3	4
Neg	Total	4	4	8
Tot	Fisher's exact test: <i>p</i> -value = 0.486			

Fisher's exact test: *p*-value = 0.429

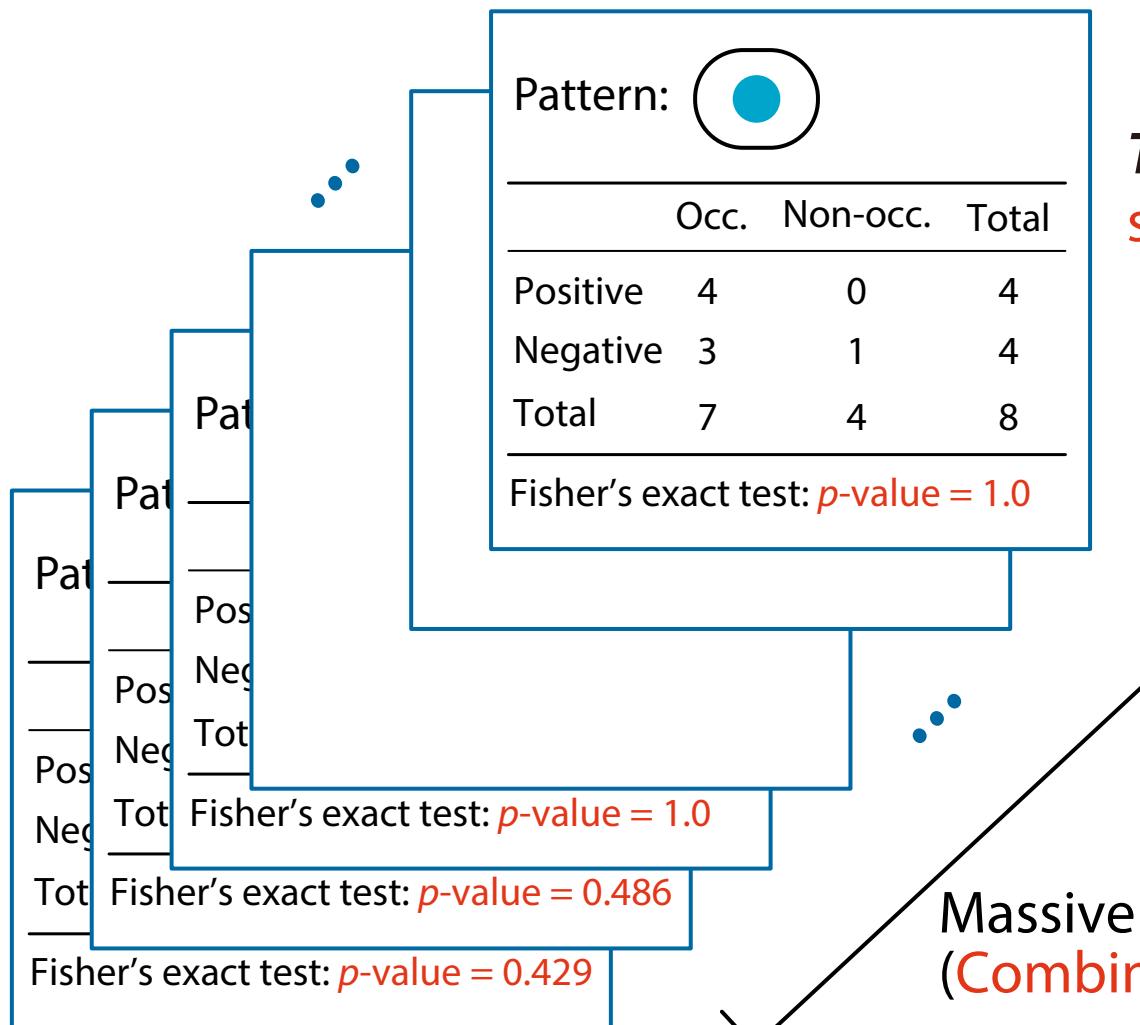
Multiple Testing

		Pattern: 		
		Occ.	Non-occ.	Total
Pat				
Pat	Positive	2	2	4
Pos	Negative	2	2	4
Pos	Total	4	4	8
Neg		Fisher's exact test: <i>p</i> -value = 1.0		
Tot		Fisher's exact test: <i>p</i> -value = 0.486		
		Fisher's exact test: <i>p</i> -value = 0.429		

Multiple Testing



Multiple Testing



Task: Enumerate all significant patterns

Massive number of patterns
(Combinatorial explosion!)

Multiple Testing Correction

- In each test, [probability of having a false positive] $\leq \alpha$
- If we repeat m tests, αm patterns can be false positives
 - Too many if m is large!
 - Example in itemset mining:
 - For 100000 items, #patterns = 2^{100000}
 - Set significance level $\alpha = 0.01$
 - Number of false positives: $0.01 \cdot 2^{100000} = 10^{30101}$

Multiple Testing Correction

- In each test, [probability of having a false positive] $\leq \alpha$
- If we repeat m tests, *αm patterns can be false positives*
 - Too many if m is large!
 - Example in itemset mining:
 - For 100000 items, #patterns = 2^{100000}
 - Set significance level $\alpha = 0.01$
 - Number of false positives: $0.01 \cdot 2^{100000} = 10^{30101}$
- FWER (family-wise error rate): *Probability of having more than one false positives among all patterns*
 - One of the standard criteria in multiple testing
 - $\text{FWER} = 1 - (1 - \alpha)^m$ if patterns are independent

Controlling the FWER

- $\text{FWER} = \Pr(\text{FP} > o)$
 - FP: Number of false positives
- To achieve $\text{FWER} = a$, change the significance level for each pattern from a to δ ($\delta \leq a$)
 - δ : corrected significance level

Controlling the FWER

- $\text{FWER} = \Pr(\text{FP} > 0)$
 - FP: Number of false positives
- To achieve $\text{FWER} = \alpha$, change the significance level for each pattern from α to δ ($\delta \leq \alpha$)
 - δ : corrected significance level
- **Objective:** Optimize (maximize) δ
$$\delta^* = \underset{\delta}{\operatorname{argmax}} \text{FWER}(\delta) \quad \text{s.t. } \text{FWER}(\delta) \leq \alpha$$
 - $\text{FWER}(\delta)$: FWER at corrected significance level δ
 - Cannot be evaluated in closed form (simple but not easy!)
 - Bonferroni correction is popular: $\delta_{\text{Bon}}^* = \alpha/m$

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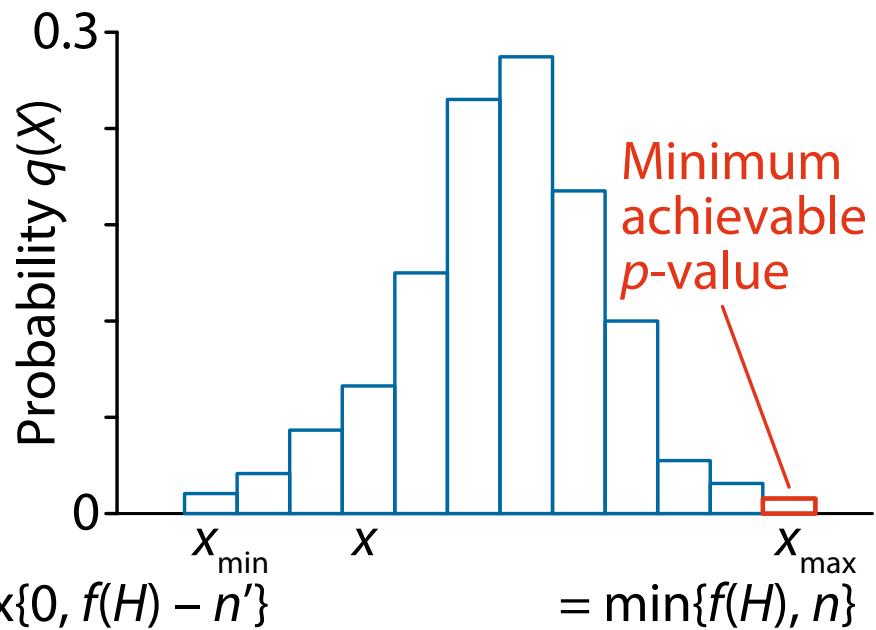
Minimum Achievable p -value $\Psi(\sigma)$

- Consider the **minimum achievable p -value $\Psi(\sigma)$** of a pattern H for its **support** $\sigma = |\{X \in \mathcal{X} \cup \mathcal{X}' \mid H \subseteq X\}|$
 - $\Psi(\sigma) = \min\{p(x) \mid x_{\min} \leq x \leq x_{\max}\}$
 - $x_{\min} = \max\{0, \sigma - n'\}$, $x_{\max} = \min\{\sigma, n\}$

	Occ.	Non-occ.	Total
\mathcal{X} (Pos.)	x	$n - x$	n
\mathcal{X}' (Neg.)	x'	$n' - x'$	n'
Total	$x + x' = \sigma$	$(n - x) + (n' - x')$	$n + n'$

Support

$$= \max\{0, f(H) - n'\}$$



Computing $\Psi(\sigma)$

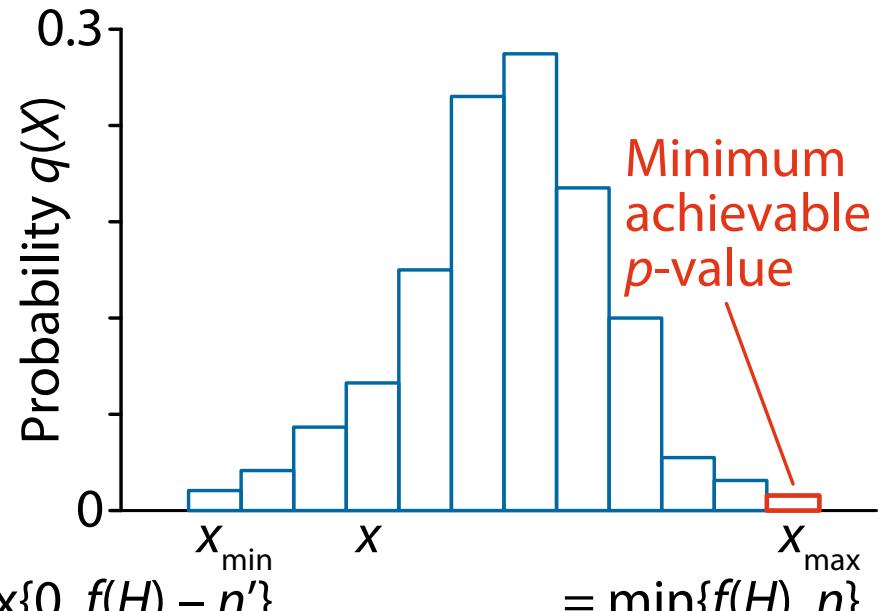
- Consider the **minimum achievable p -value** $\Psi(\sigma)$ of a pattern H for its support $\sigma = |\{X \in \mathcal{X} \cup \mathcal{X}' \mid H \subseteq X\}|$

$$\Psi(\sigma) = \binom{n}{\sigma} / \binom{n+n'}{\sigma}$$

	Occ.	Non-occ.	Total
\mathcal{X} (Pos.)	σ	$n - \sigma$	n
\mathcal{X}' (Neg.)	0	n'	n'
Total	σ	$(n - \sigma) + n'$	$n + n'$

Most biased case ($\sigma < n$)

$$= \max\{0, f(H) - n'\}$$



Testability

- Consider the **minimum achievable p -value** $\Psi(\sigma)$ of a pattern H for its **support** $\sigma = |\{X \in \mathcal{X} \cup \mathcal{X}' \mid H \subseteq X\}|$

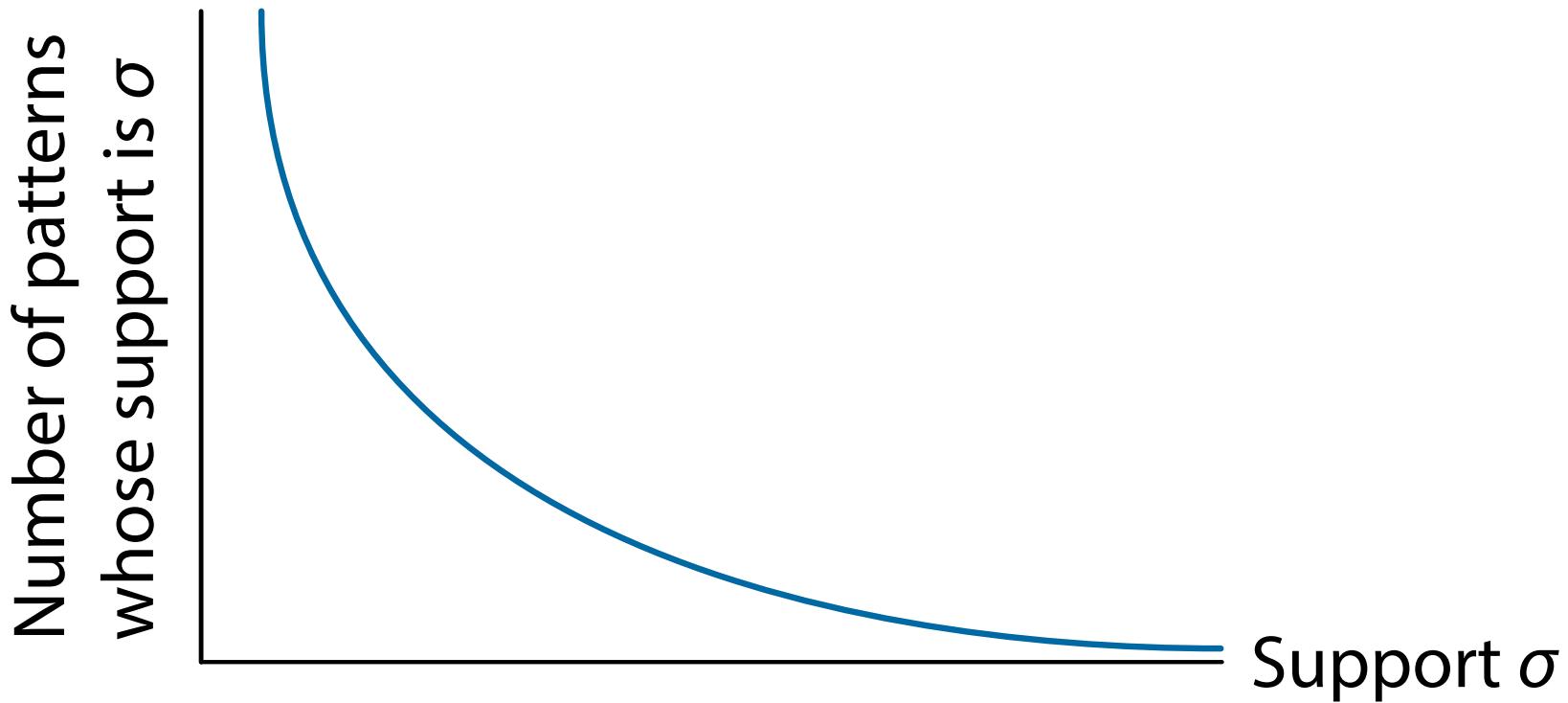
$$\Psi(\sigma) = \binom{n}{\sigma} / \binom{n + n'}{\sigma}$$

- Tarone (1990) pointed out (and Terada et al. (2013) revisited):

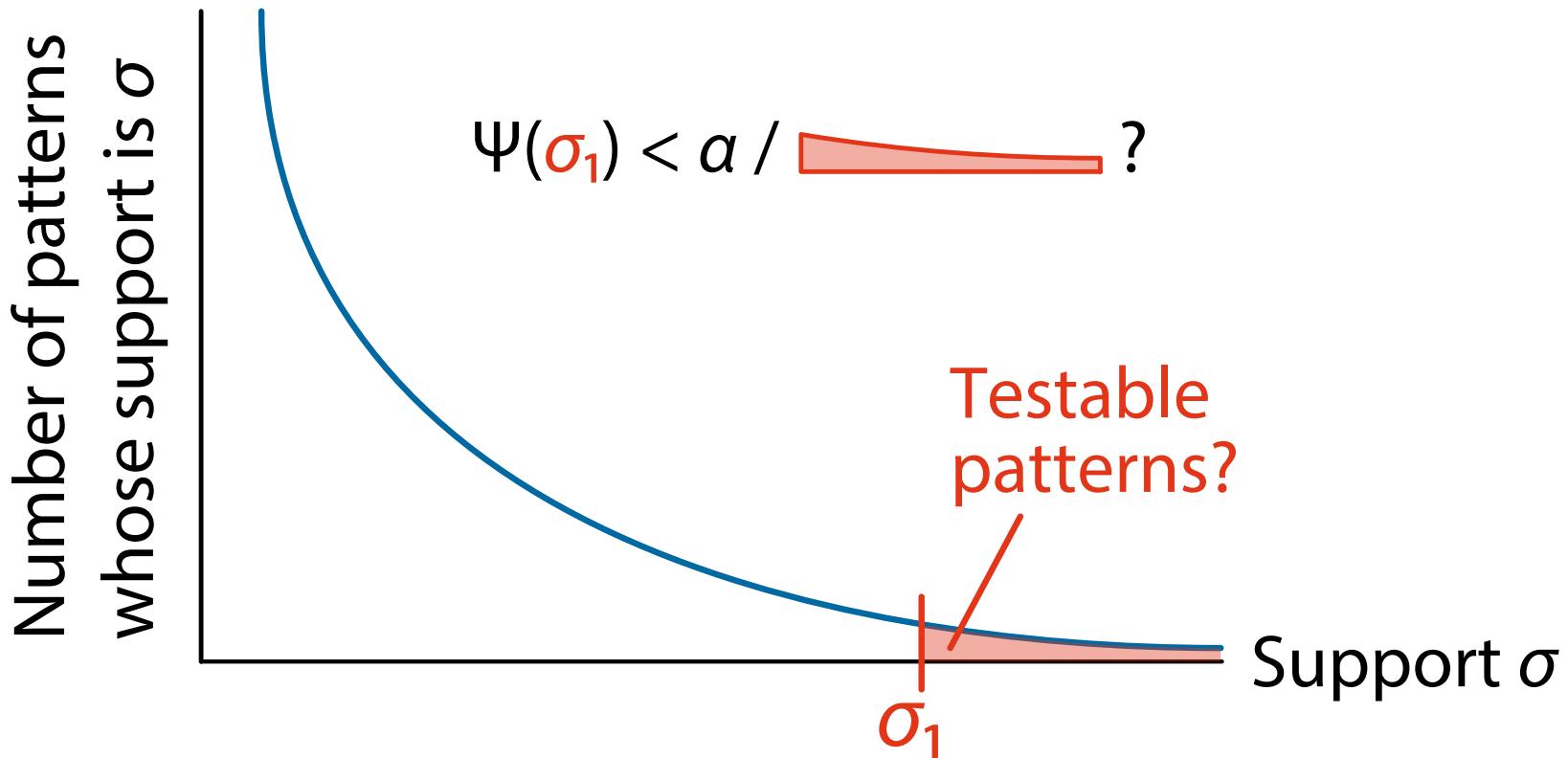
*For a pattern H , if $\Psi(\sigma)$ is larger than the significance threshold, this is **untestable** and we can ignore it*

- Significance threshold = $a / [\# \text{ testable patterns}]$

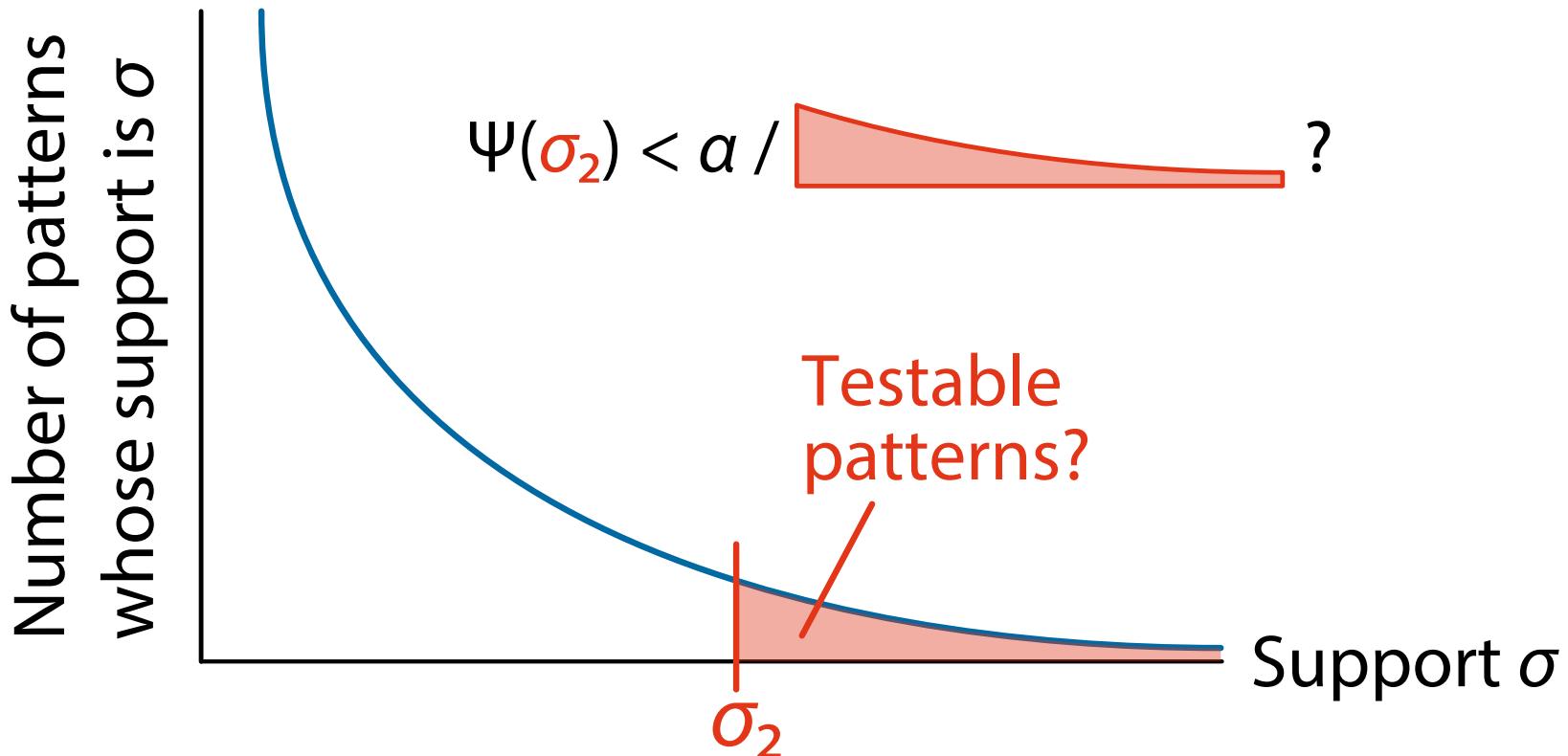
Finding Testable Patterns



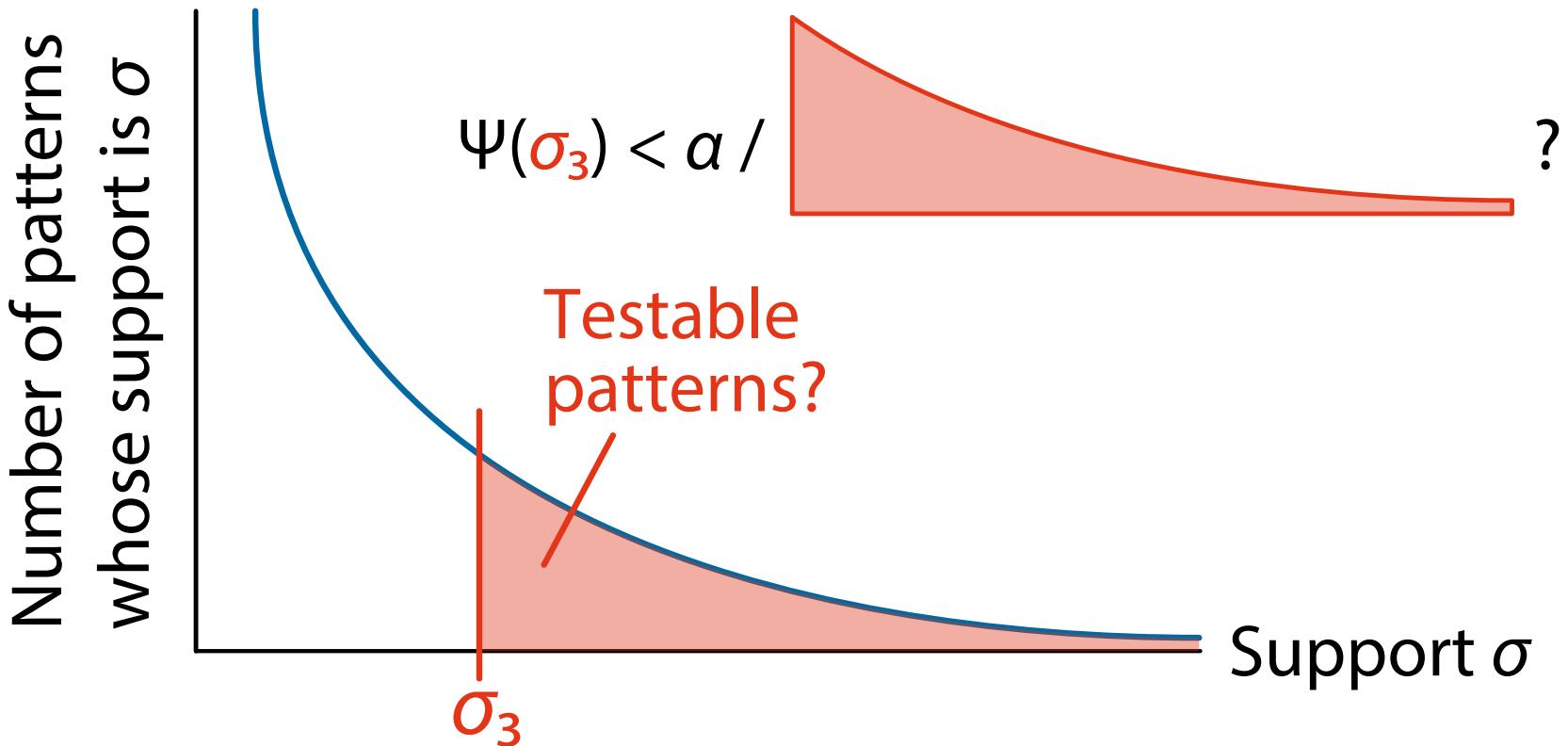
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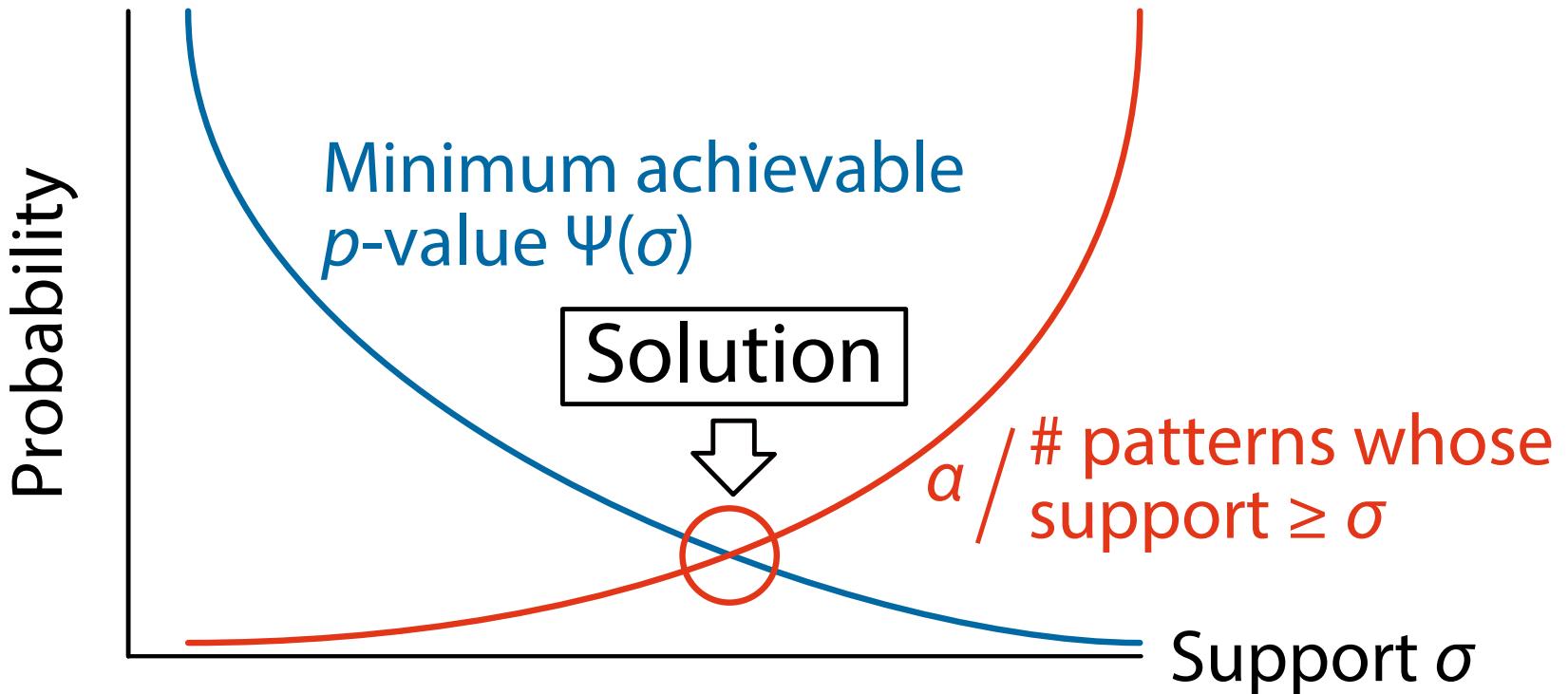
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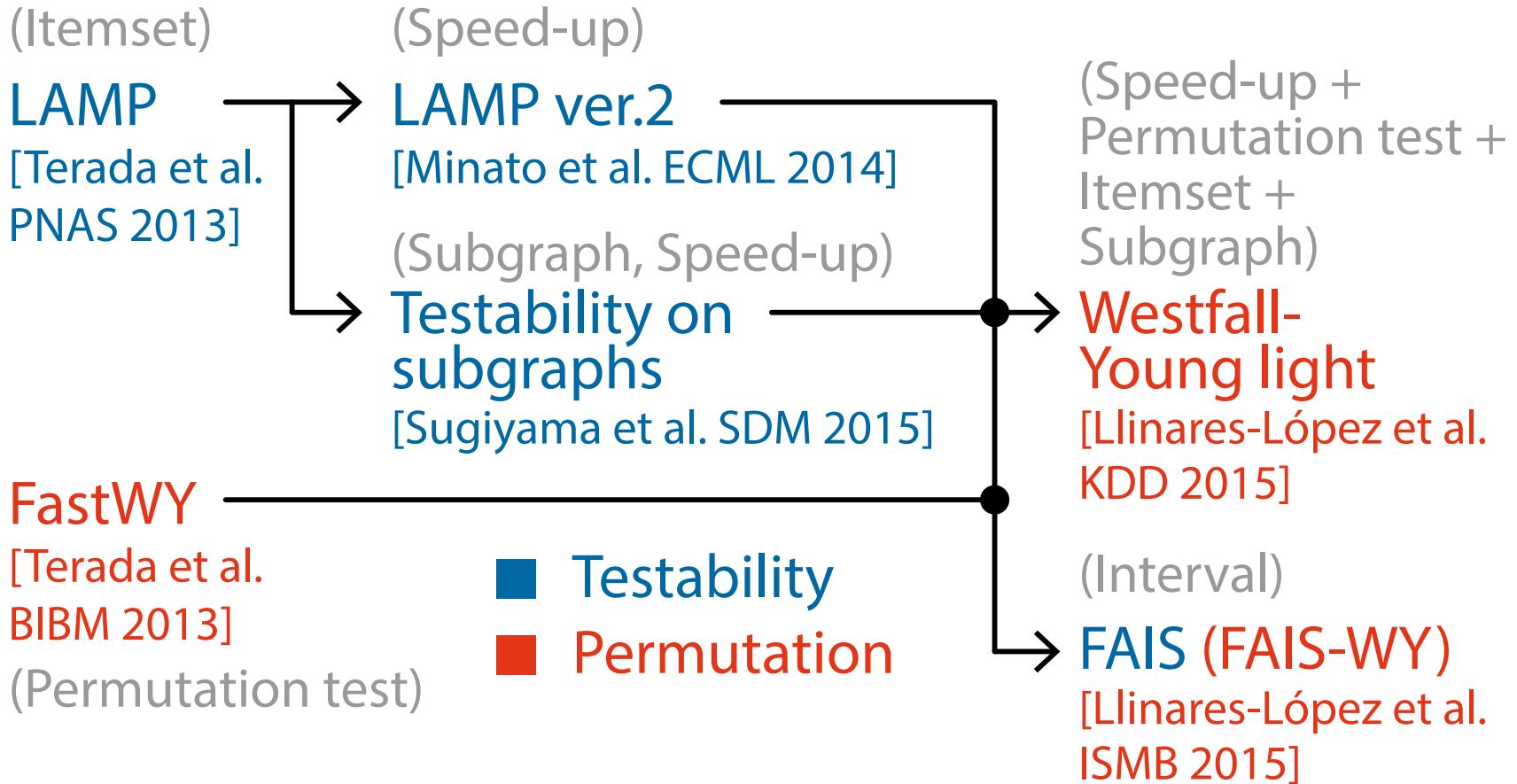
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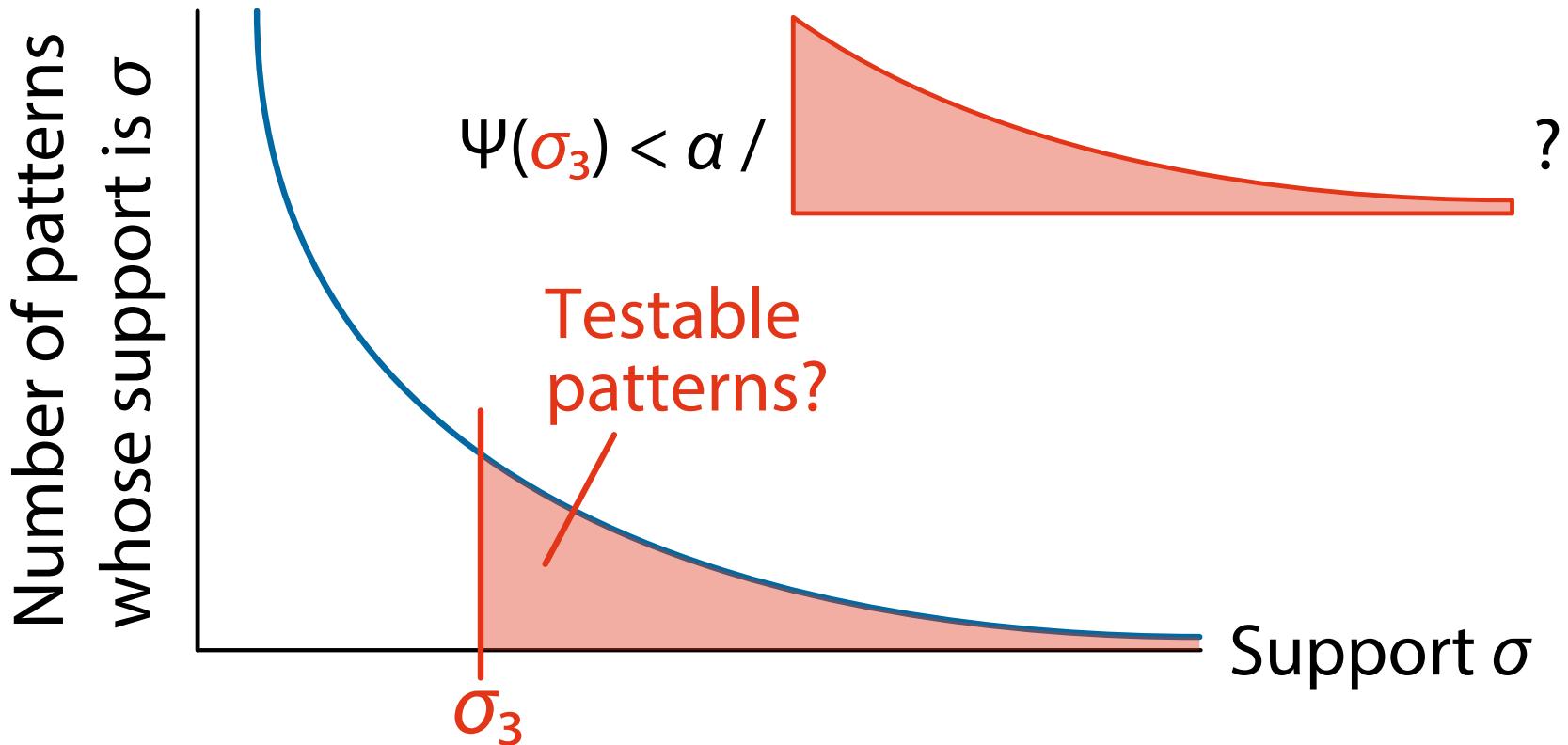
Finding Testable Patterns



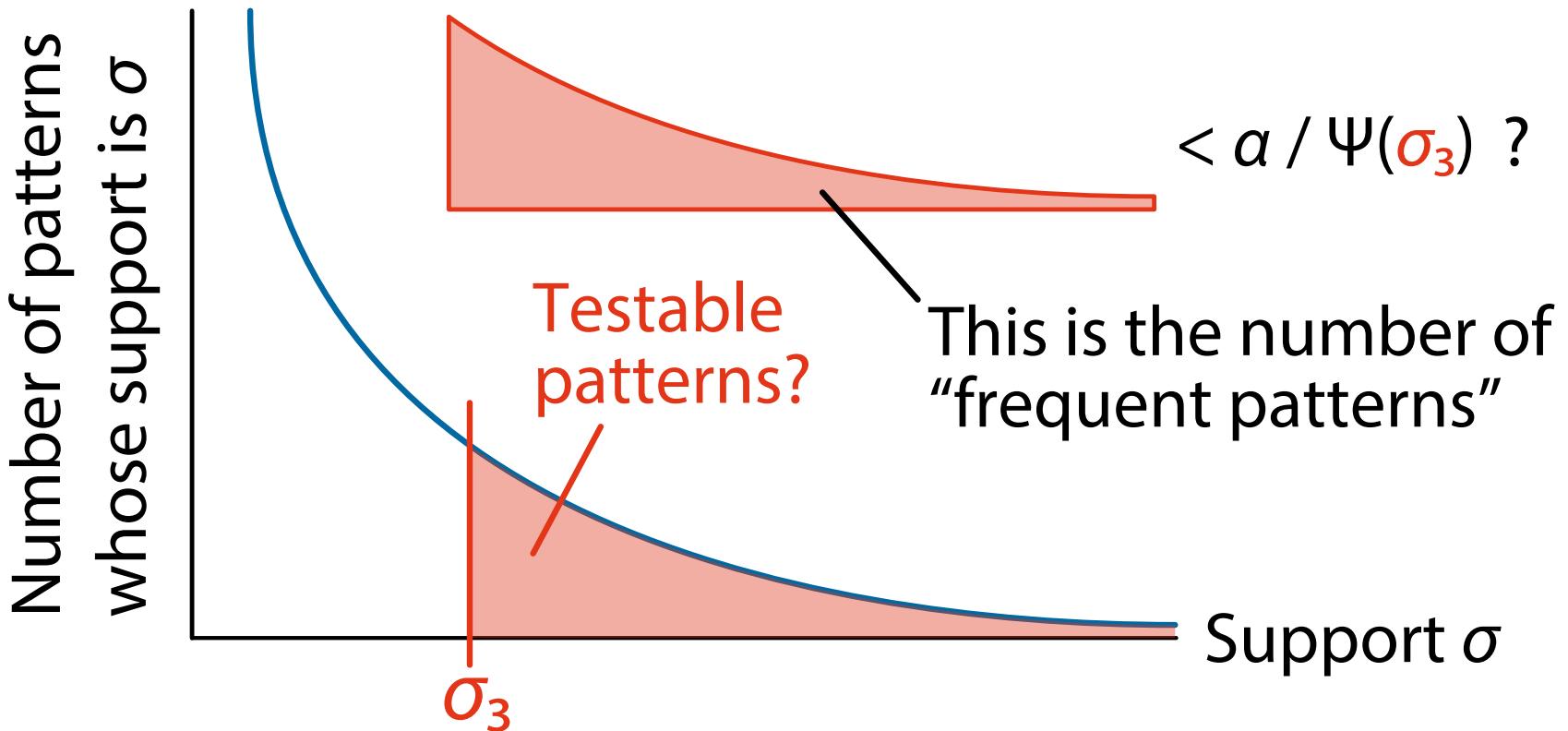
State-of-the-art



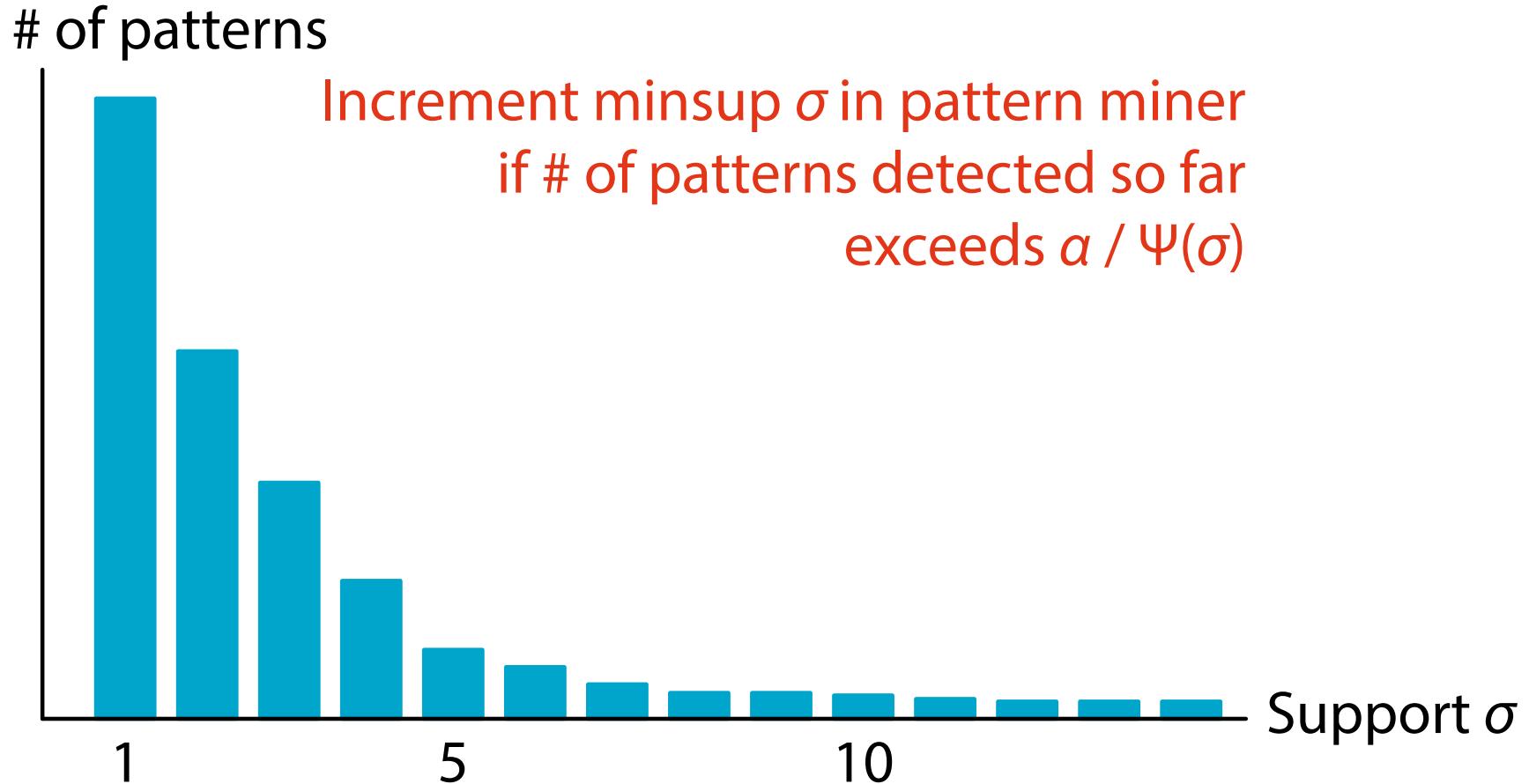
How to Find Testable Patterns?



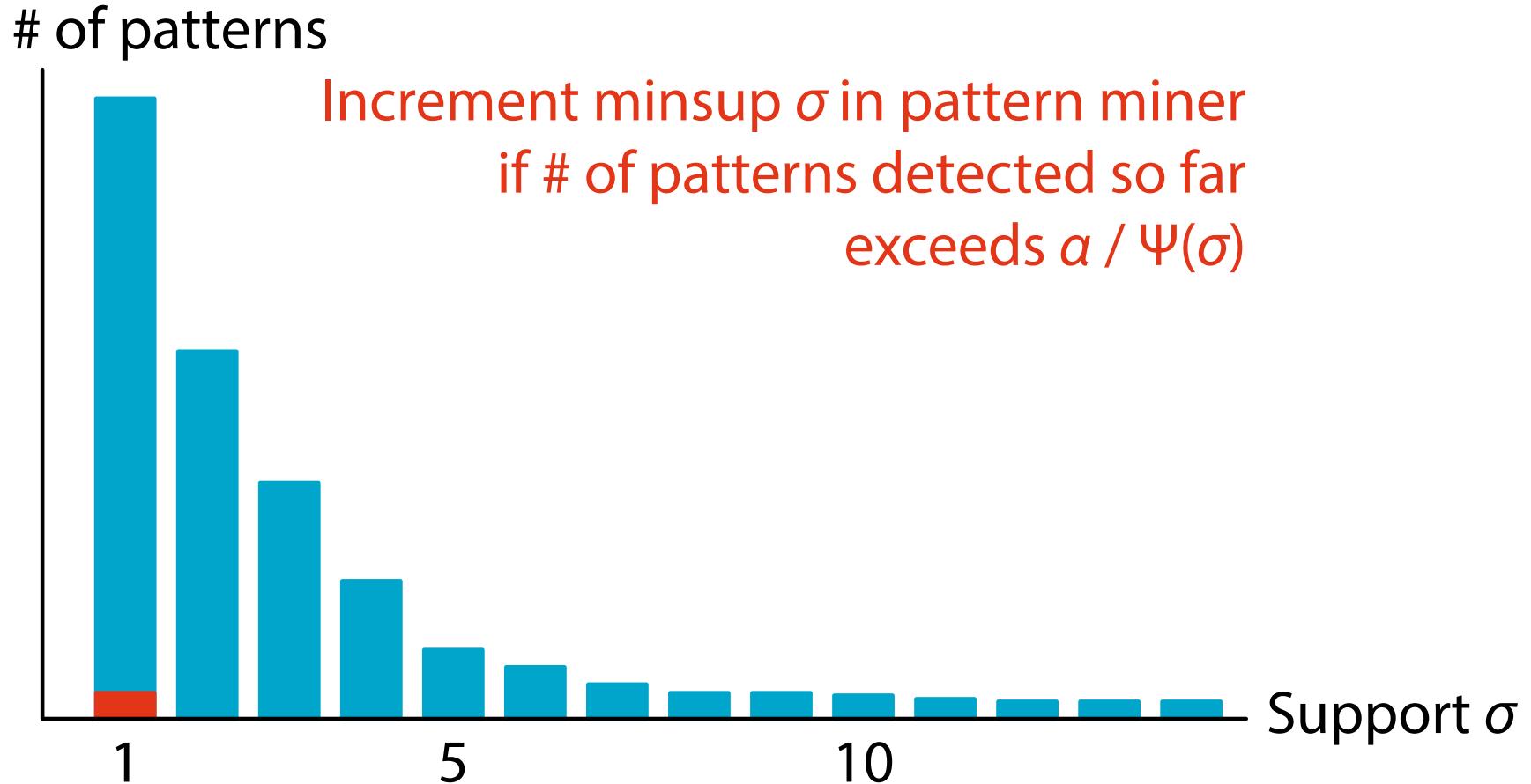
How to Find Testable Patterns?



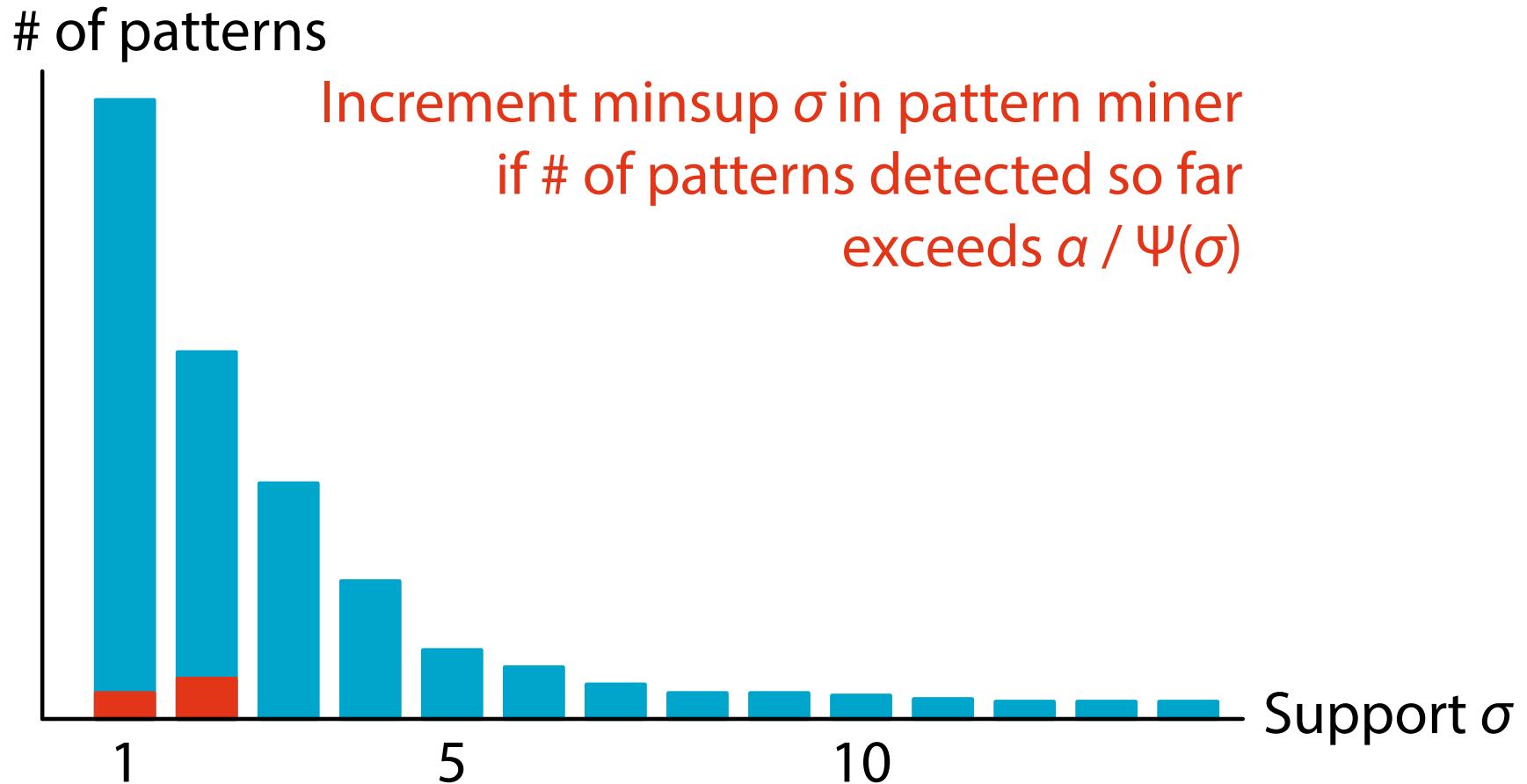
LAMP ver.2 [Minato et al. ECML PKDD 2014]



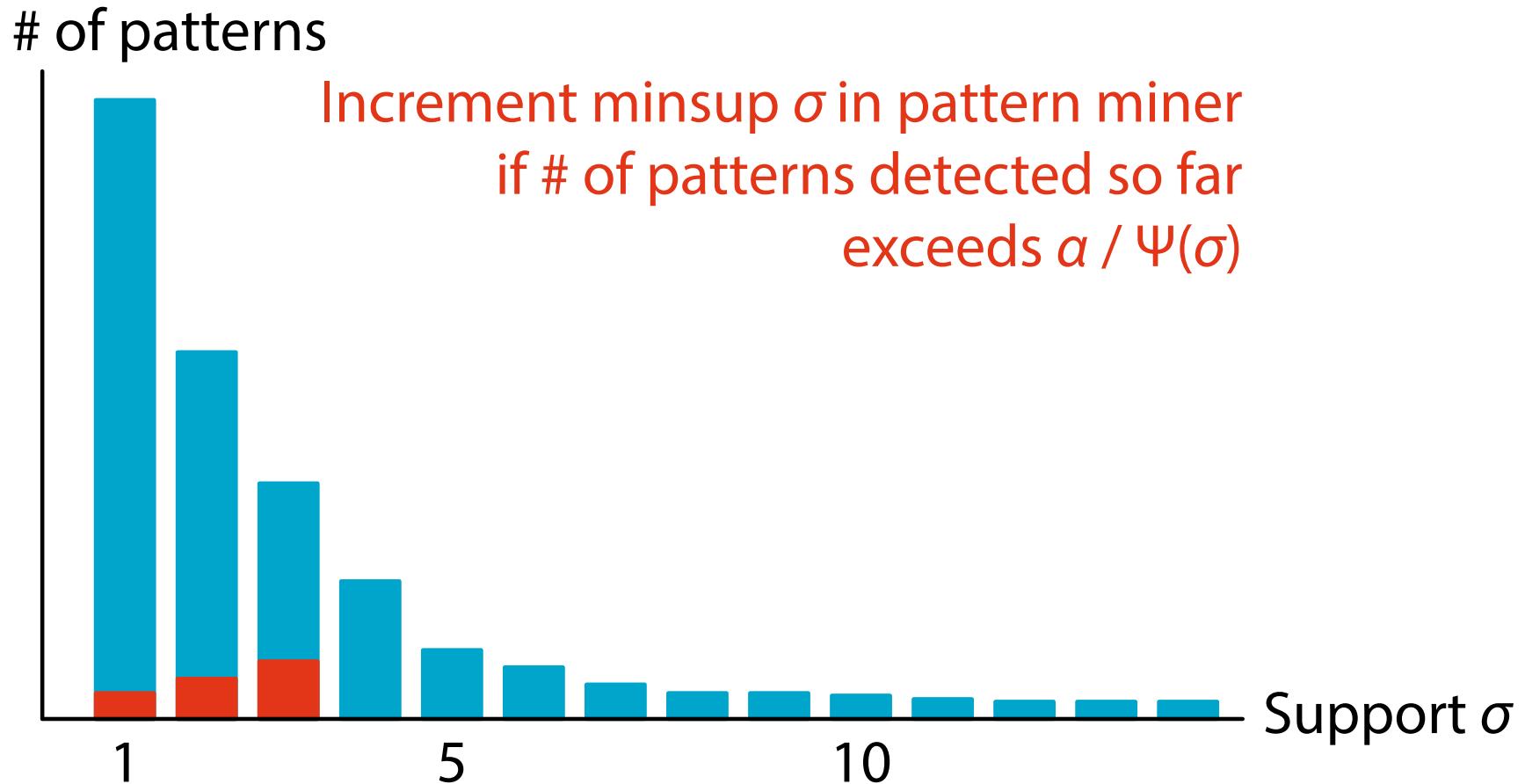
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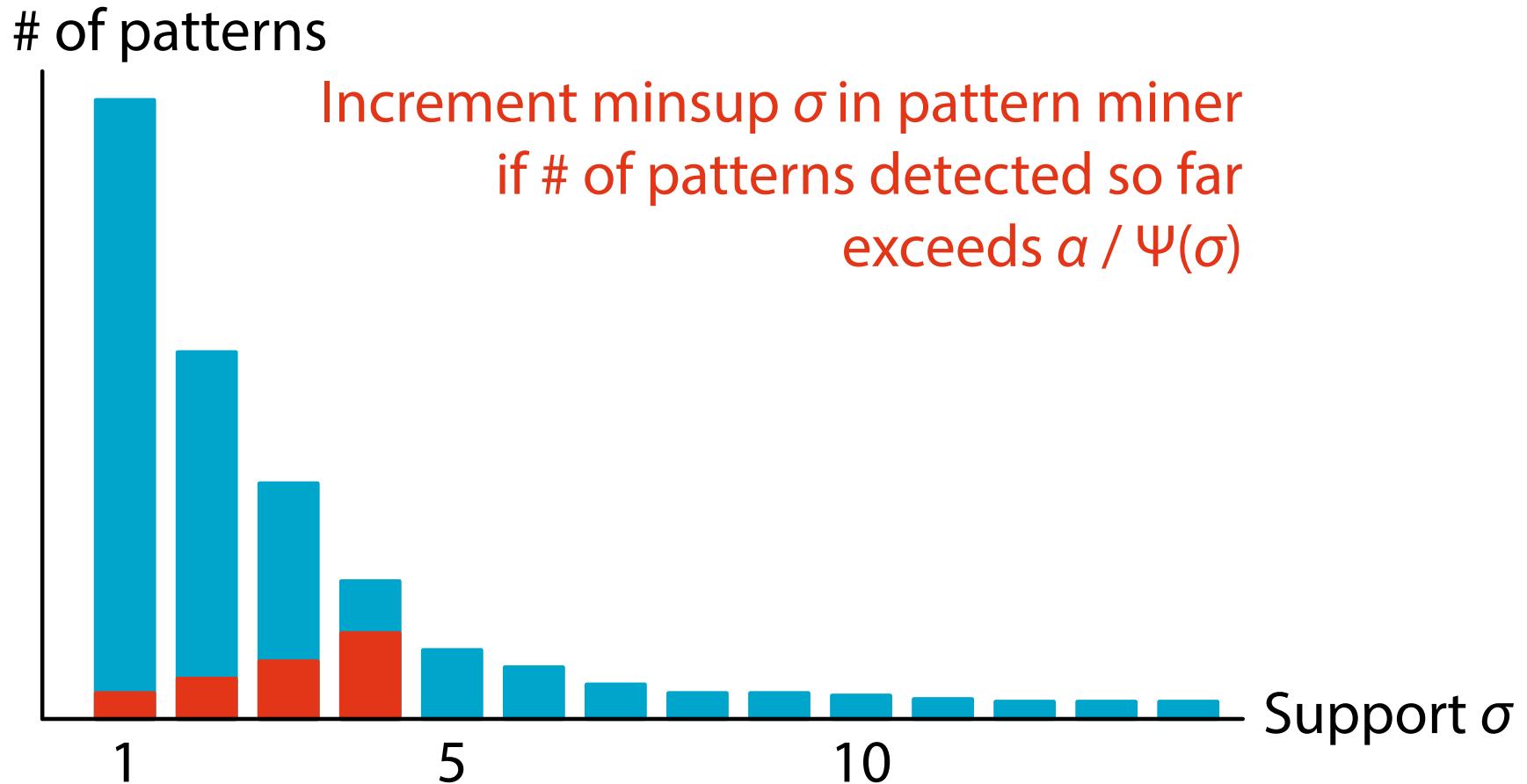
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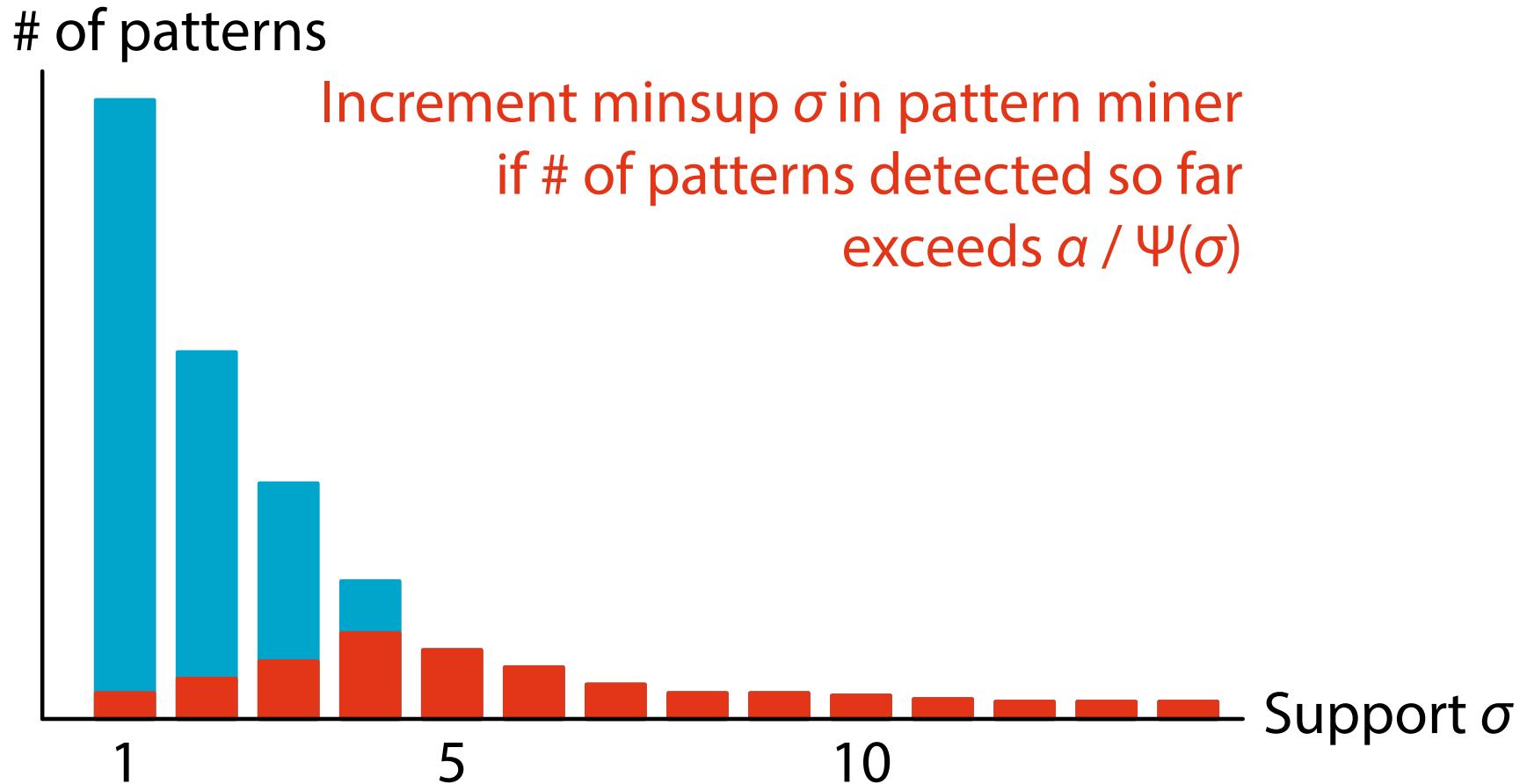
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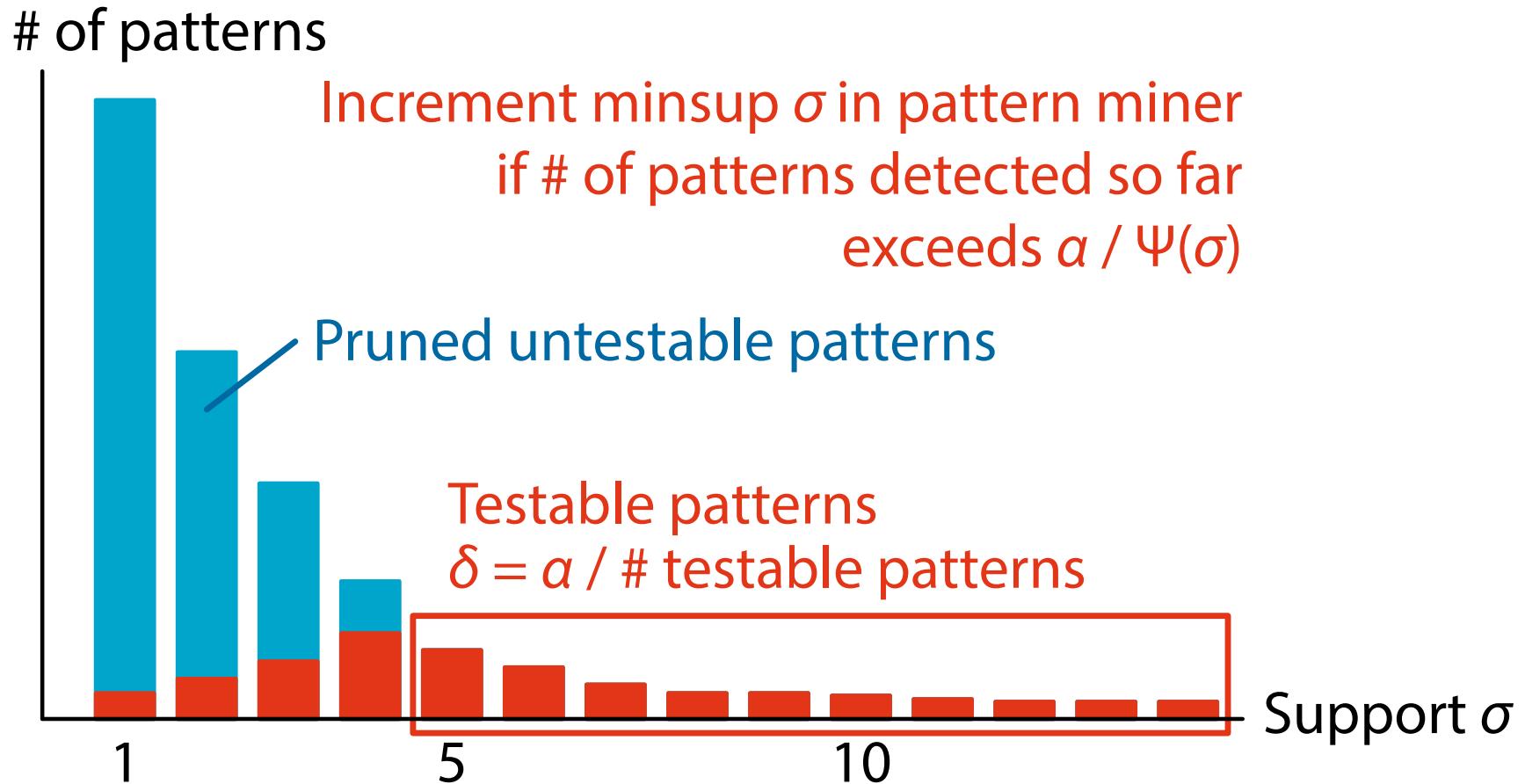
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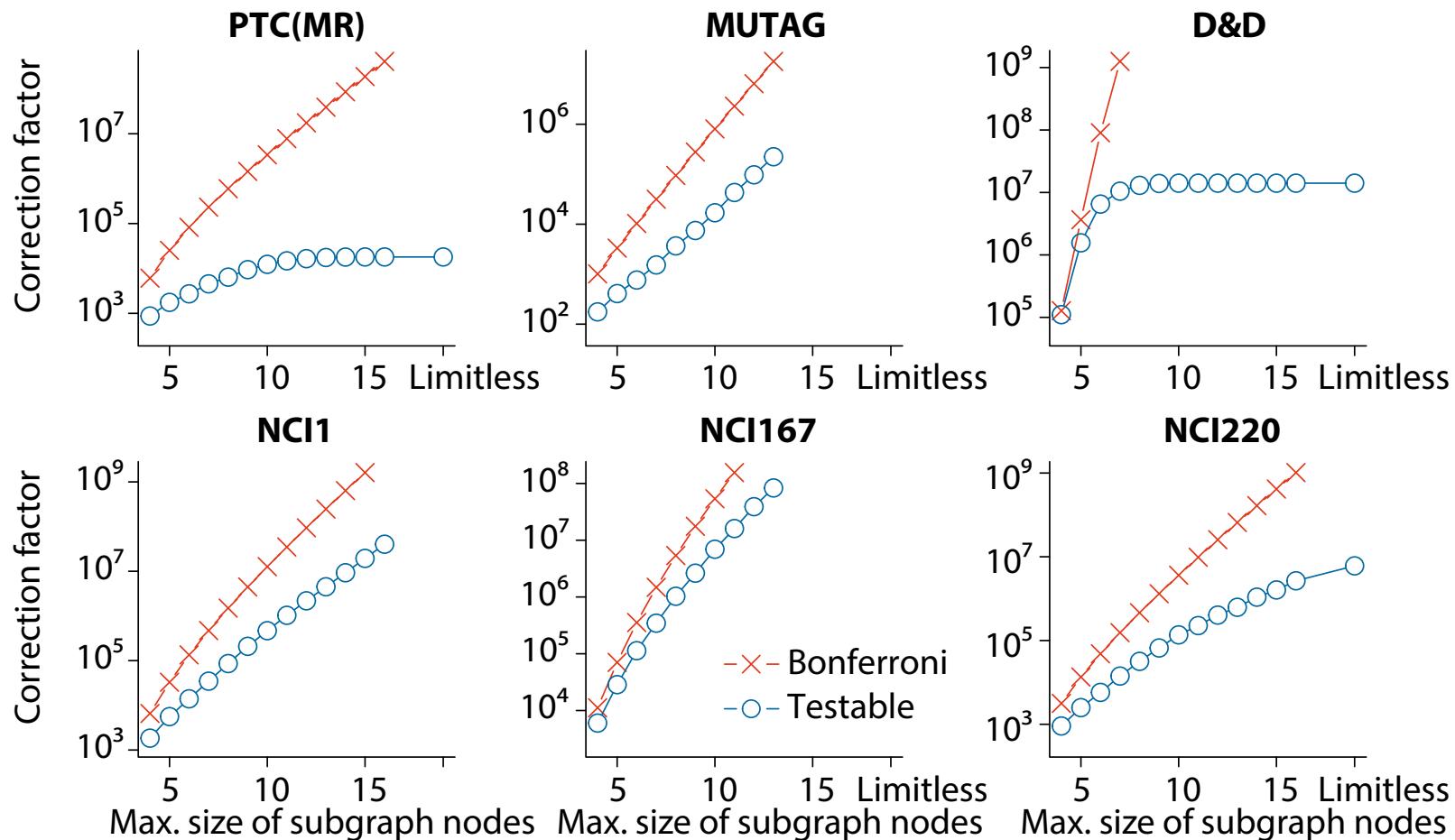
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LAMP ver.2 [Minato et al. ECML PKDD 2014]



Testable Patterns in Subgraph Mining

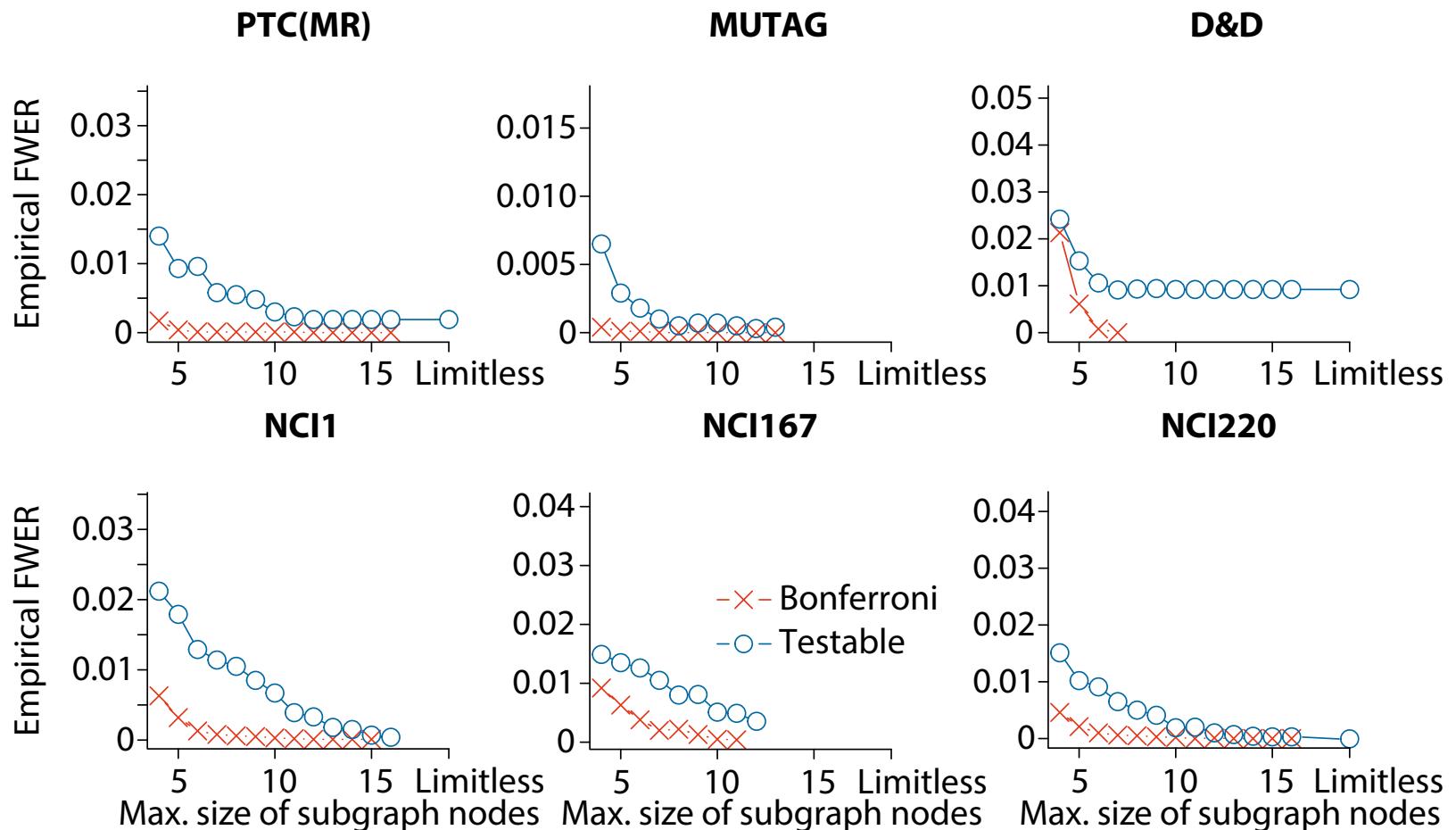


from [Sugiyama et al. SDM2015]

Outline

- (Discriminative) Pattern mining
- Statistical hypothesis testing of patterns
- Multiple hypothesis testing in pattern mining
- Testable patterns
- Permutation testing in pattern mining
- Conclusion

FWER Is Still Too Low!

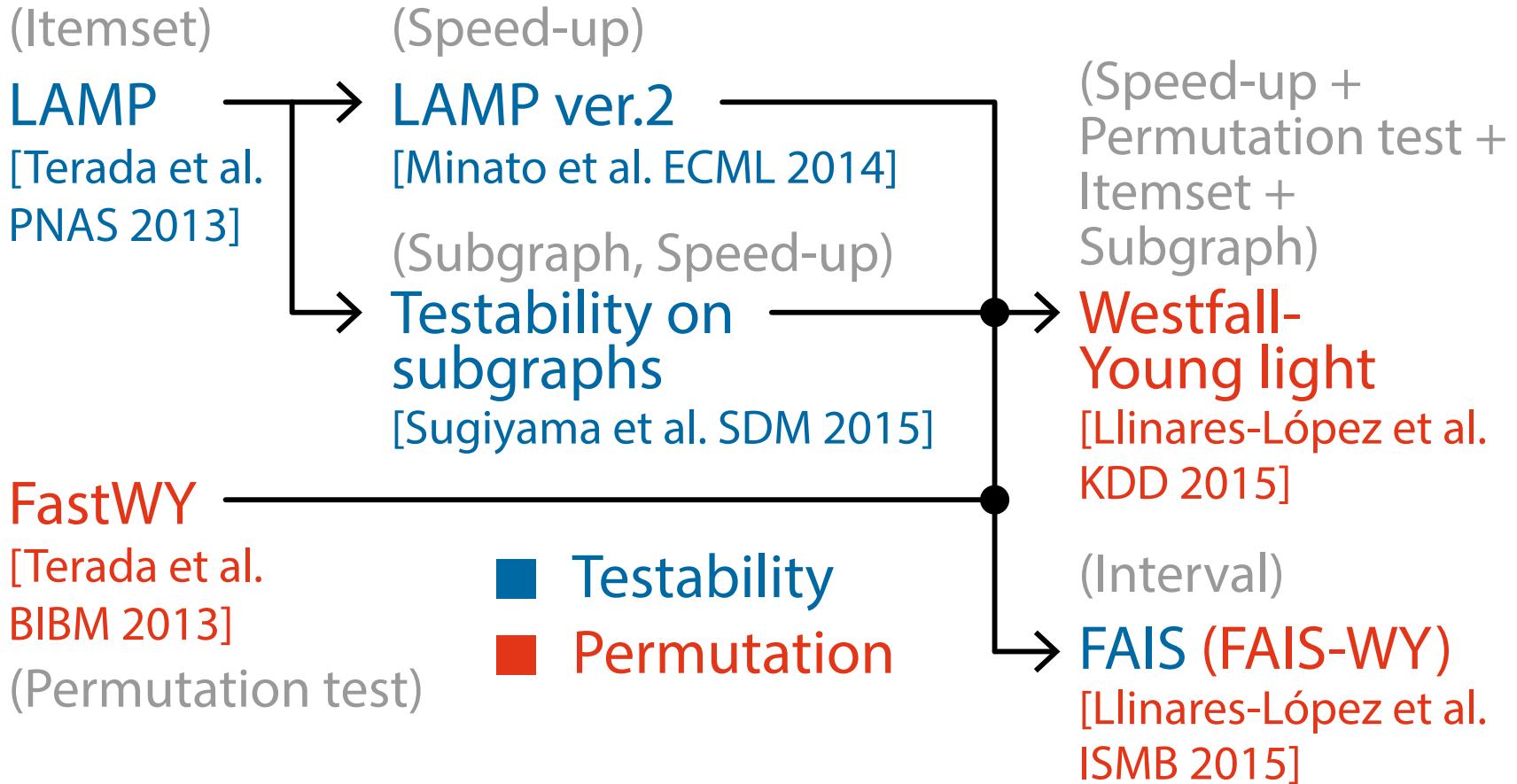


from [Sugiyama et al. SDM2015]

Take Dependencies into Account

- **Problem:** Dependencies between patterns are not considered
- **Solution:** Permutation test
 - Repeat random permutation of class labels ($10^3 \sim 10^4$ times)
 - Get the null distribution of p -values
 - The optimal correction factor can be obtained

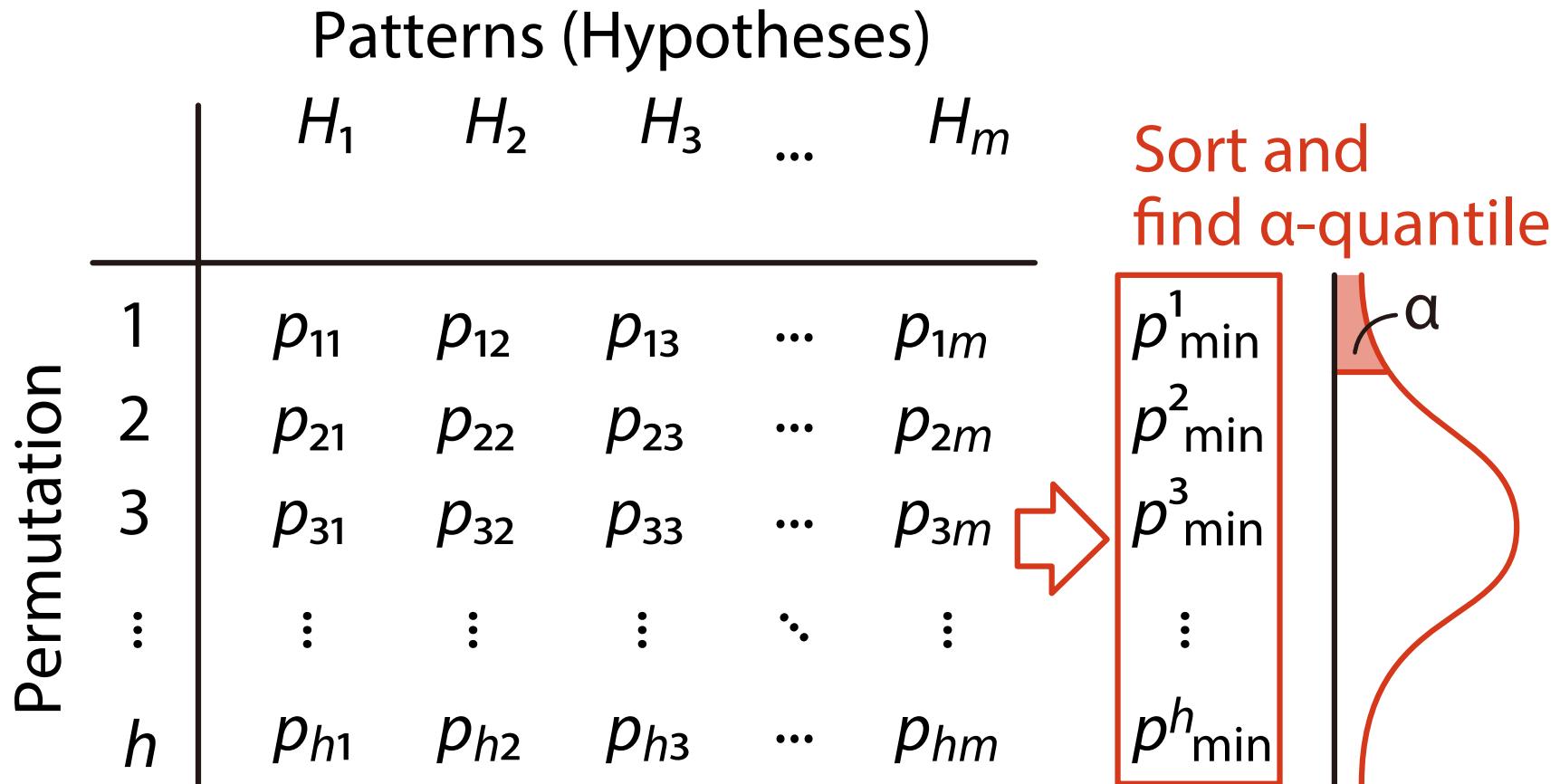
State-of-the-art



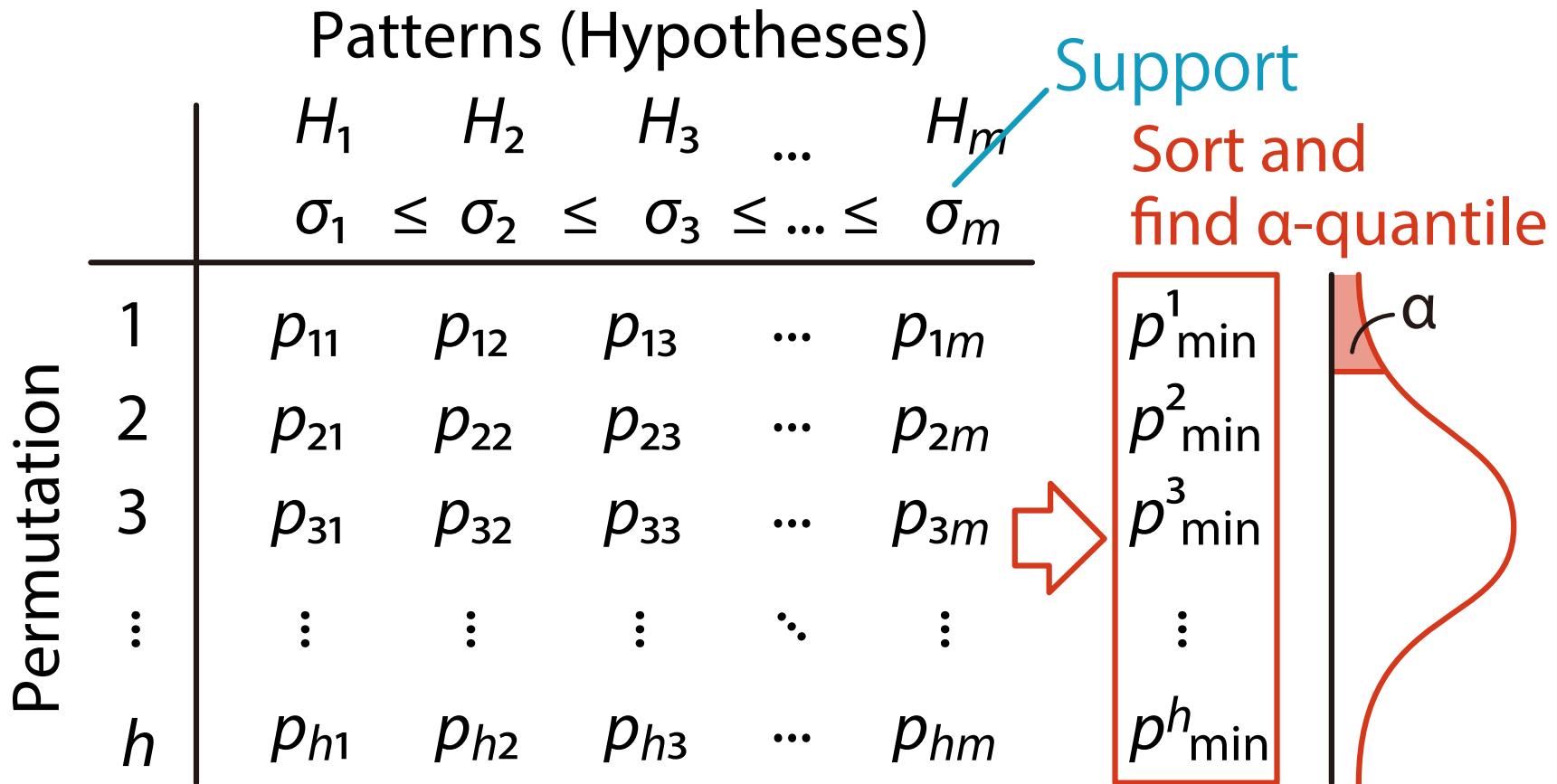
Westfall-Young Permutation

1. Randomly permute class labels
2. Compute p -values for all patterns using the permuted class labels
3. Find the minimum p -value p_{\min} among them
 - $\text{FP} > 0 \iff p_{\min} < \delta$
 - FP: Number of false positives
4. Repeat steps 1 to 3 h times and obtain $p_{\min}^1, p_{\min}^2, \dots, p_{\min}^h$
 - $\text{FWER}(\delta) \approx |\{i : p_{\min}^i \leq \delta\}| / h$
5. δ^* is the α -quantile of $p_{\min}^1, p_{\min}^2, \dots, p_{\min}^h$

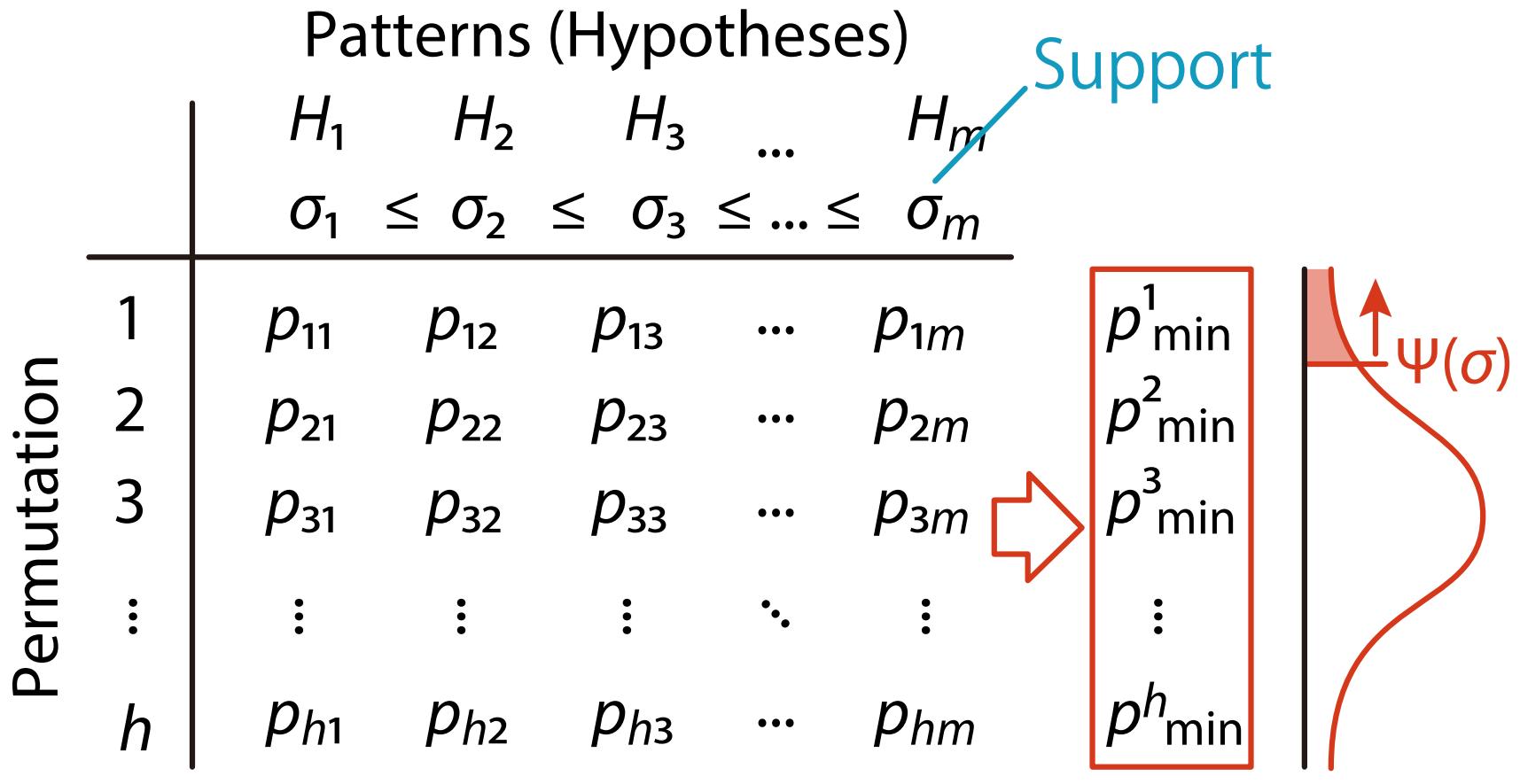
Westfall-Young Permutation



Using Support for Estimating FWER

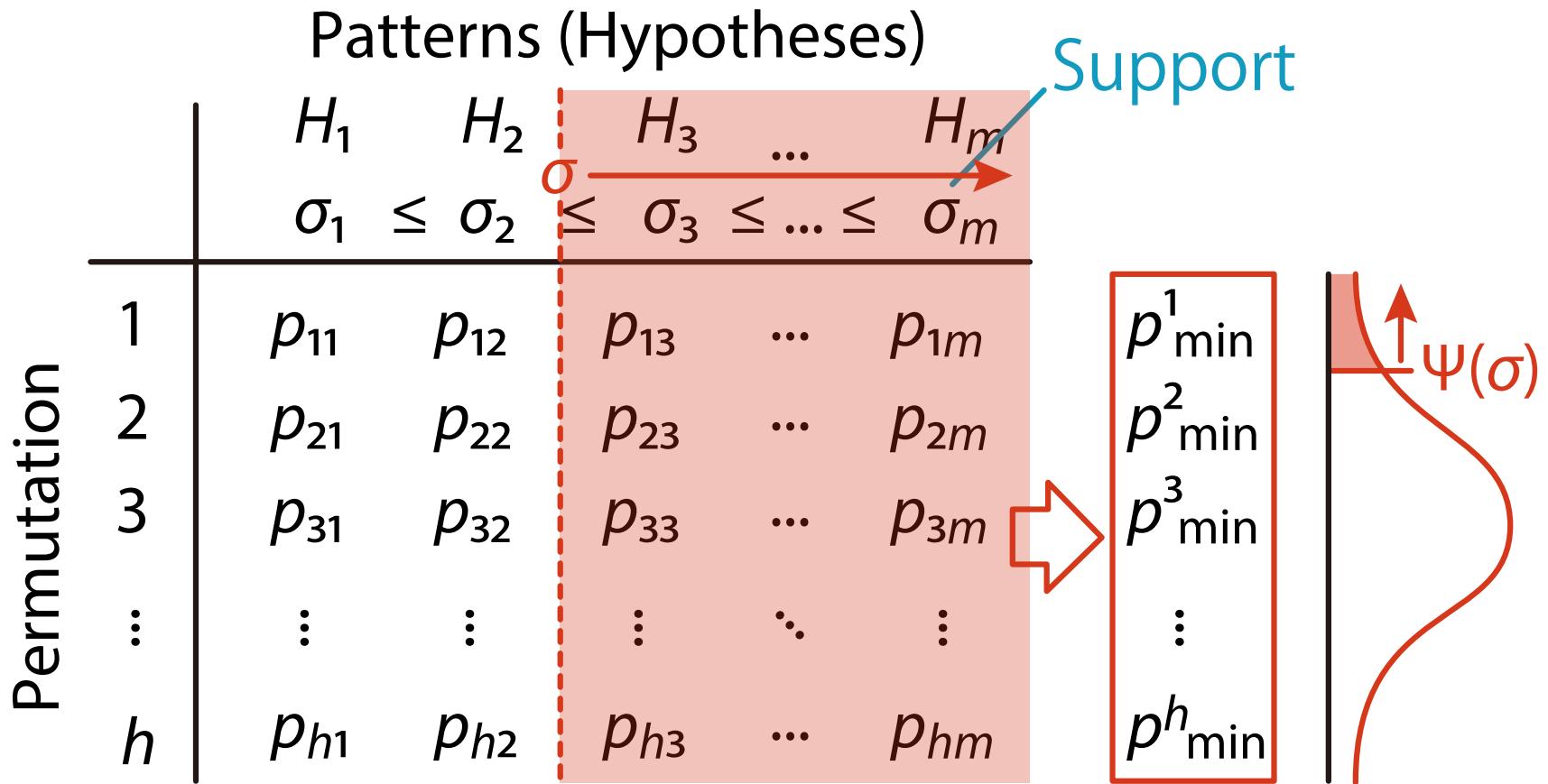


Estimating FWER



$$\text{Estimator of FWER} = |\{i : p_{\min}^i \leq \Psi(\sigma)\}| / h$$

Estimating FWER



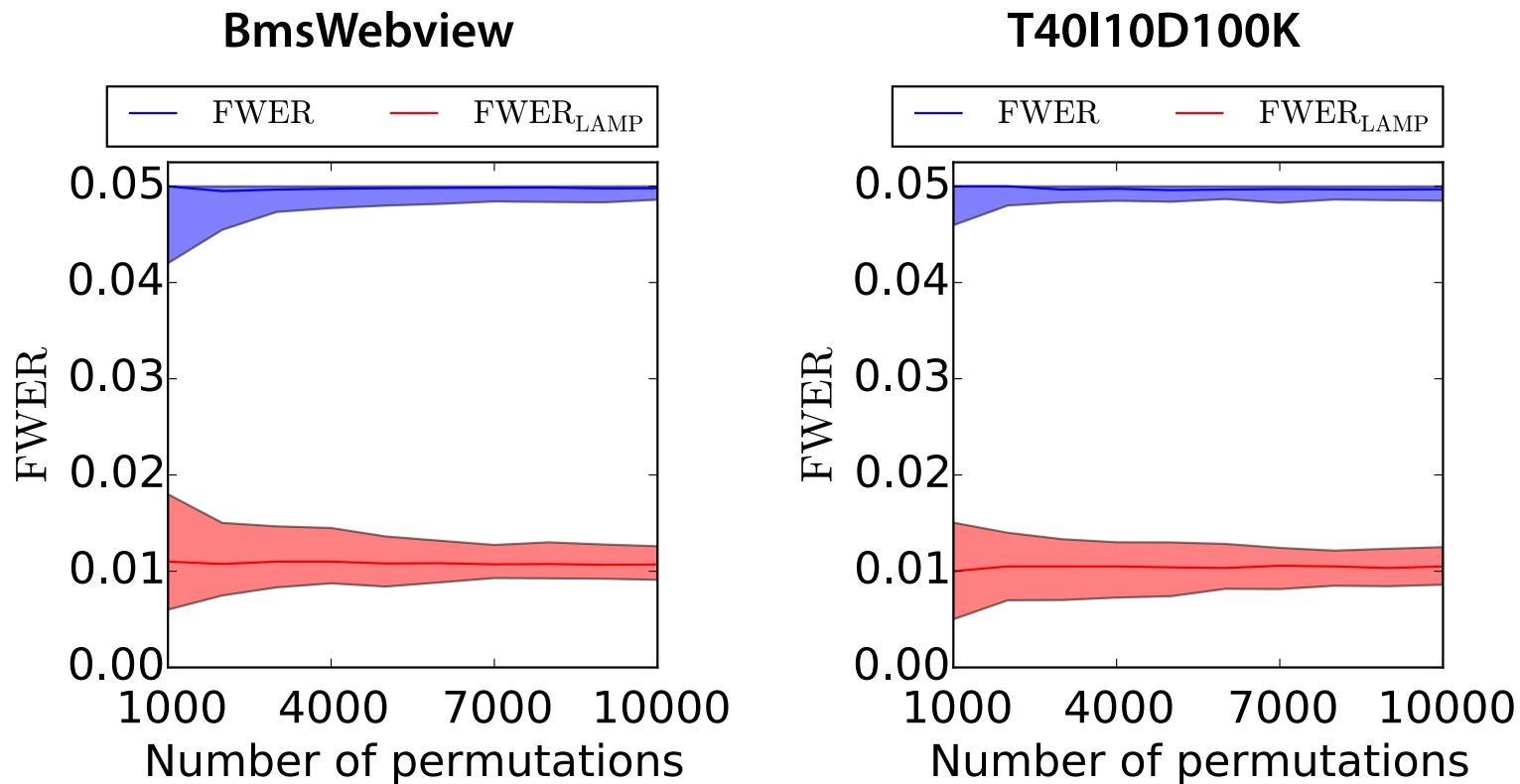
$$\text{Estimator of FWER} = |\{i : p_{\min}^i \leq \Psi(\sigma)\}| / h$$

“Westfall-Young light”

[Llinares-López et al. KDD’15]

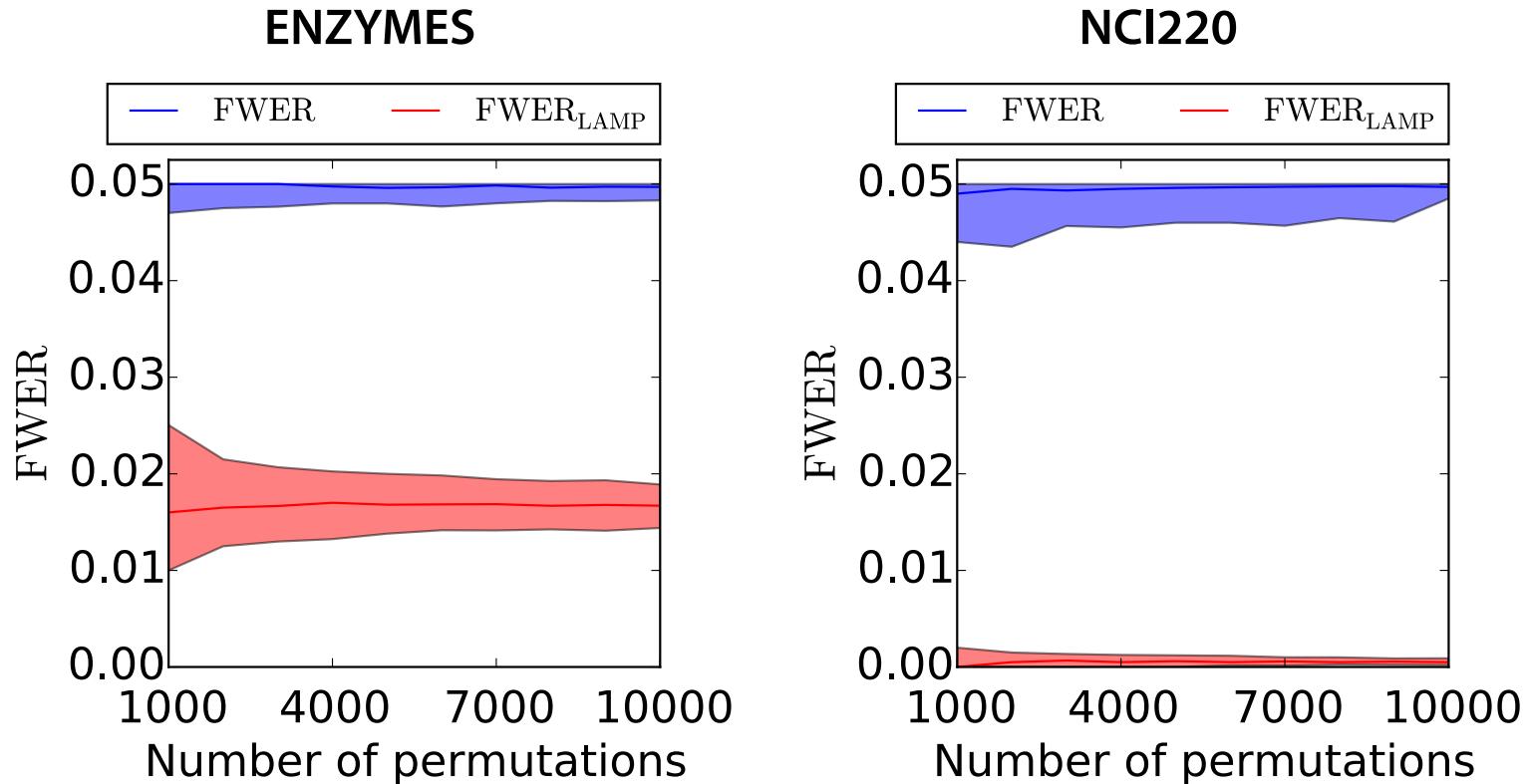
- Precompute h permuted labels; $\sigma \leftarrow 1$; $p_{\min}^i \leftarrow 1$
- Westfall-Young light does the following whenever a miner (like LCM) finds a new frequent pattern H :
 - **for** $i \leftarrow 1$ **to** h **do**:
 - $p^i \leftarrow$ the p -value of H for i th permutation
 - $p_{\min}^i \leftarrow \min\{p_{\min}^i, p^i\}$
 - $\text{FWER} \leftarrow |\{i : p_{\min}^i \leq \Psi(\sigma)\}| / h$
 - **while** $\text{FWER} > \alpha$ **do**:
 - $\sigma \leftarrow \sigma + 1$ // σ is the **minimum support**
 - $\text{FWER} \leftarrow |\{i : p_{\min}^i \leq \Psi(\sigma)\}| / h$
 - Go children of H

FWER in Itemset Mining



from [Llinares-López et al. KDD2015]

FWER in Subgraph Mining



from [Llinares-López et al. KDD2015]

Outline

- (Discriminative) Pattern mining
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Conclusion

- The area of **significant pattern mining** is emerging
 - Find **statistically significant combinatorial patterns** while controlling false positive rate
- Pattern mining, a classical yet central topic in data mining, can be enriched by introducing statistical assessment
 - Can be applied in scientific fields such as biology

Appendix

Papers about Testability

- Tarone, R.E.:
A modified Bonferroni method for discrete data
Biometrics (1990)
- [LAMP] Terada, A., Okada-Hatakeyama, M., Tsuda, K., Sese, J.:
Statistical significance of combinatorial regulations,
Proc. Natl. Acad. Sci. USA (2013).
- [LAMP ver.2] Minato, S., Uno, T., Tsuda, K., Terada, A., Sese, J.:
**Fast Statistical Assessment for Combinatorial Hypotheses
Based on Frequent Itemset Mining**
ECML PKDD 2014
- Sugiyama, M., Llinares-López, F., Kasenburg, N., Borgwardt, K.:
Significant Subgraph Mining with Multiple Testing Correction,
SIAM SDM 2015

Papers about Permutation Testing

- Westfall, P. H. and Young, S. S.
Resampling-based multiple testing: Examples and methods for *p*-value adjustment
John Wiley & Sons (1993)
- [FastWY] Terada, A. and Tsuda, K. and Sese, J.:
Fast Westfall-Young permutation procedure for combinatorial regulation discovery, IEEE BIBM 2013
- [Westfall-Young light] Llinares-López, F., Sugiyama, M., Papaxanthos, L., Borgwardt, K.:
Fast and Memory-Efficient Significant Pattern Mining via Permutation Testing, ACM SIGKDD 2015
- [FAIS-WY] Llinares-López, F., et al.:
Genome-Wide Detection of Intervals of Genetic Heterogeneity Associated with Complex Traits, ISMB 2015

Frequent Itemset Miners

- [Apriori] Agrawal, R. and Imielinski, T. and Swami, A.:
Mining association rules between sets of items in large databases,
ACM SIGMOD 1993
- [FP-Growth] Han, J. and Pei, J. and Yin, Y.:
Mining frequent patterns without candidate generation,
ACM SIGMOD 2000
- [LCM] Uno, T. and Asai, T. and Uchida, Y. and Arimura, H.:
An efficient algorithm for enumerating closed patterns in transaction databases,
DS 2004
(won FIMI'04 competition)

Frequent Subgraph Miners

- [AGM] Inokuchi, A. and Washio, T. and Motoda, H.:
An Apriori-Based Algorithm for Mining Frequent Substructures from Graph Data, PKDD 2000
- [gSpan] Yan, X. and Han, J.:
gSpan: Graph-based substructure pattern mining, ICDM 2002
- [GASTON] Nijssen, S. and Kok, J. N.:
A Quickstart in Frequent Structure Mining Can Make a Difference, KDD 2004
- (comparison) Wörlein, M. and Meinl, T. and Fischer, I. and Philippsen, M.
A Quantitative Comparison of the Subgraph Miners MoFa, gSpan, FFSM, and Gaston, PKDD 2005
 - We used GASTON as it is the fastest