Optimally combining BSM searches using graph theory

Presentation by Jamie Yellen

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This work forms part of the TACO project

(Testing Analyses' COrrelations)

"Strength in numbers: optimal and scalable combination of LHC new-physics searches"

https://arxiv.org/abs/2209.00025

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- Introduction to TACO
- Brief introduction to the overlap matrix
- Weighted Hereditary Depth First Search
  - Development
  - Implementation
- Results
  - pMSSM-19 Reinterpretation

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"In this work we determine the parameter space accessed by the topologies which populate the different signal regions contained in a sample of 18 CMS and ATLAS Analyses"

ATLAS-SUSY-2015-06:SR2jl
ATLAS-SUSY-2015-06:SR2jm
ATLAS-SUSY-2015-06:SR2jt
ATLAS-SUSY-2015-06:SR4jt
ATLAS-SUSY-2015-06:SR5j
ATLAS-SUSY-2015-06:SR6jm
ATLAS-SUSY-2015-06:SR6jt
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The Overlap Matrix
(A whole talk in itself)

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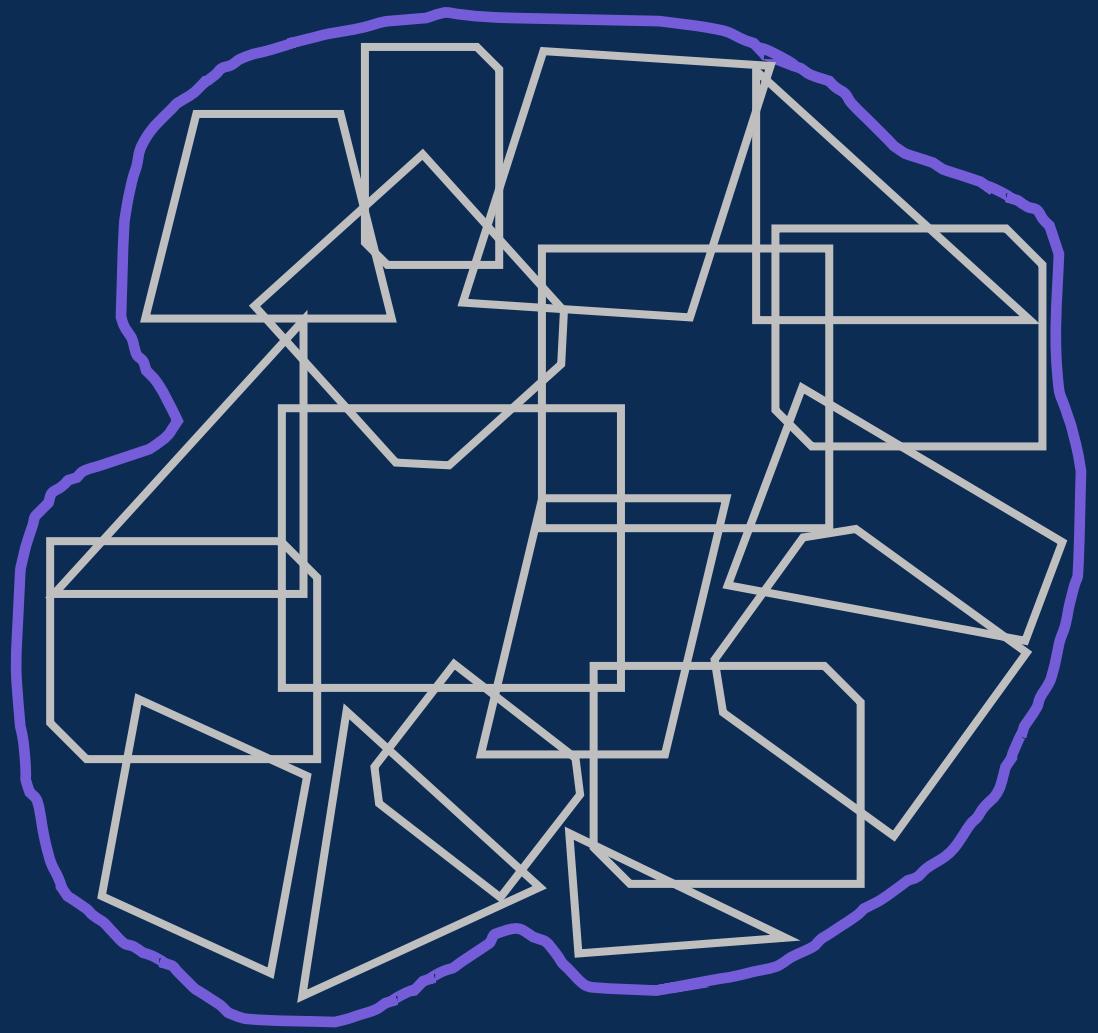

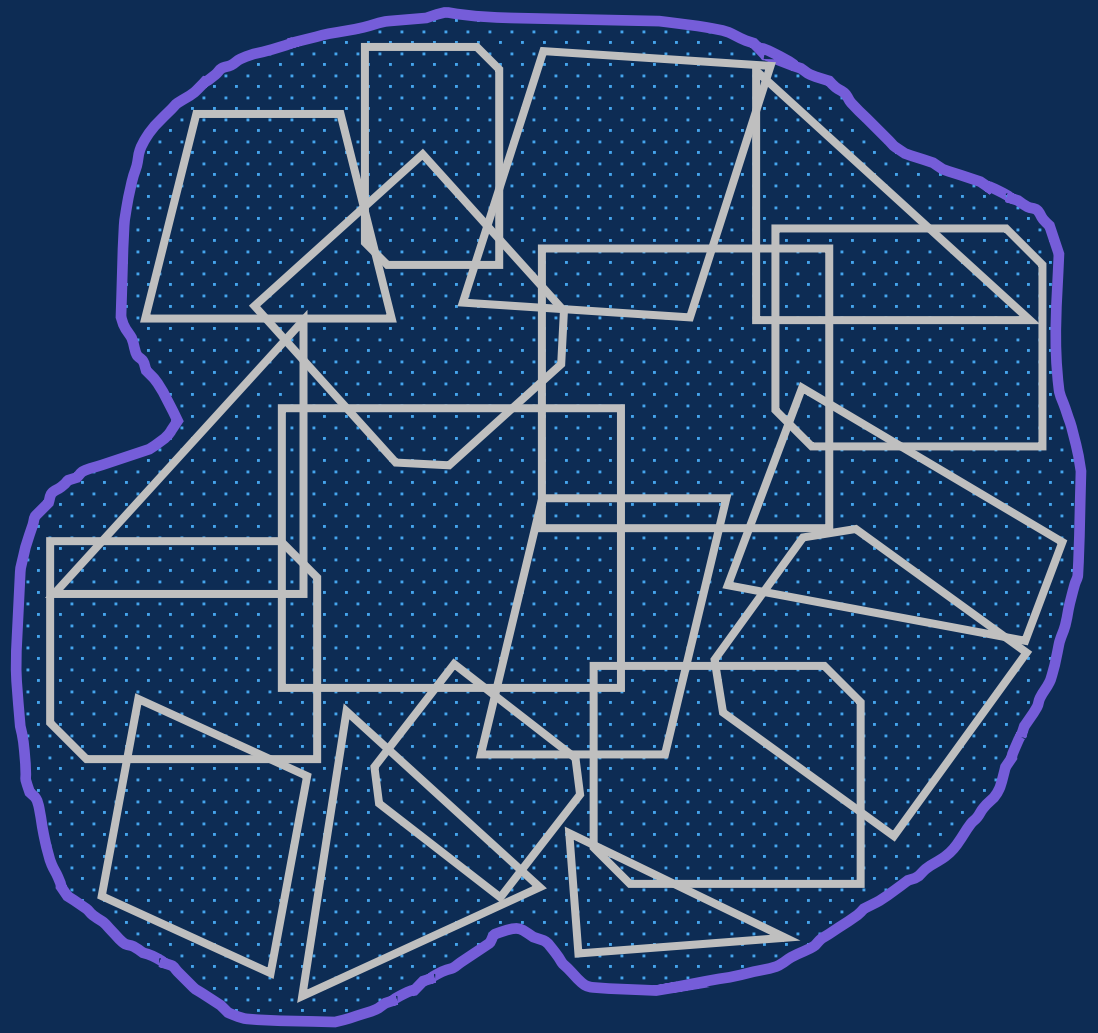

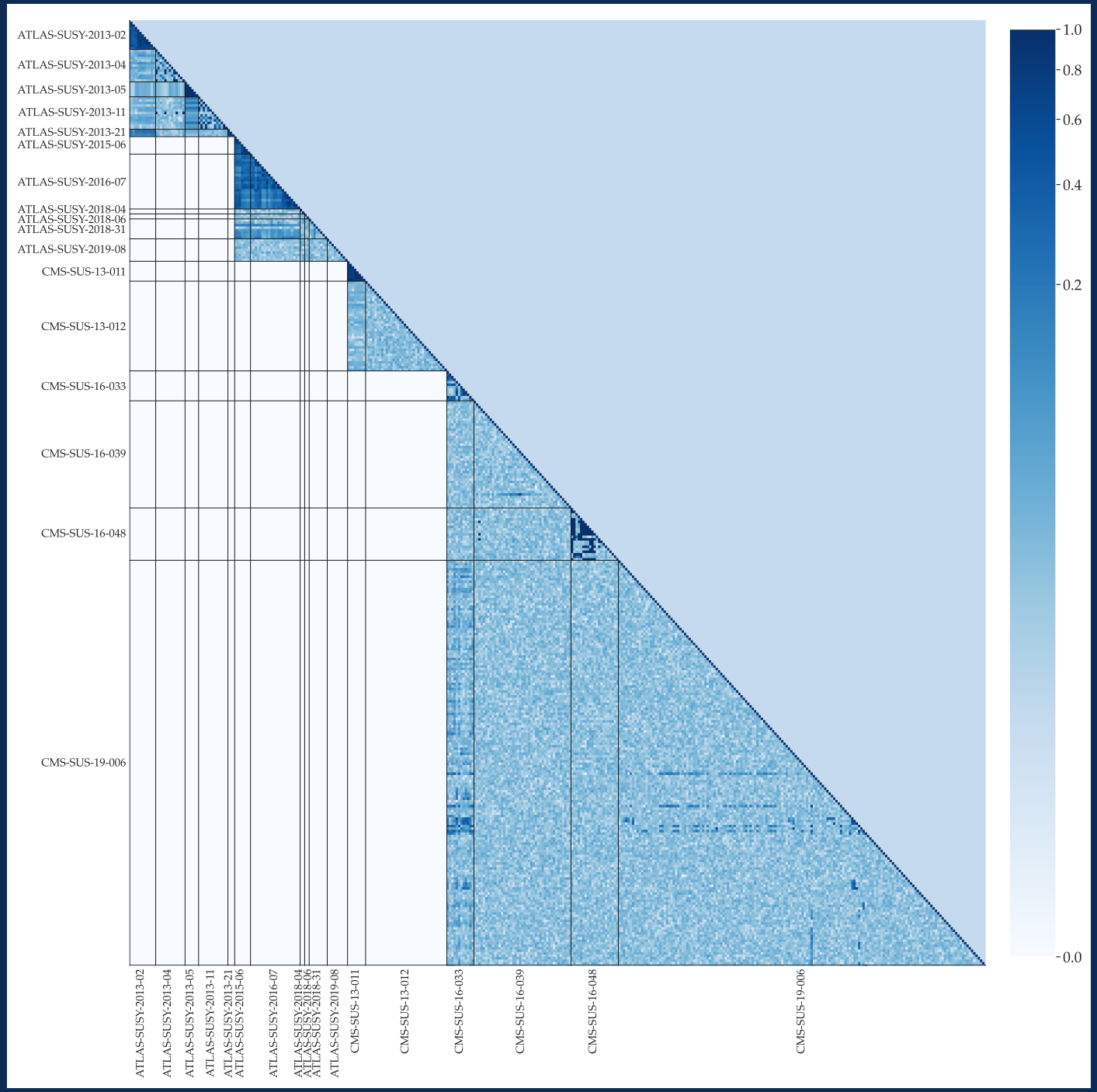
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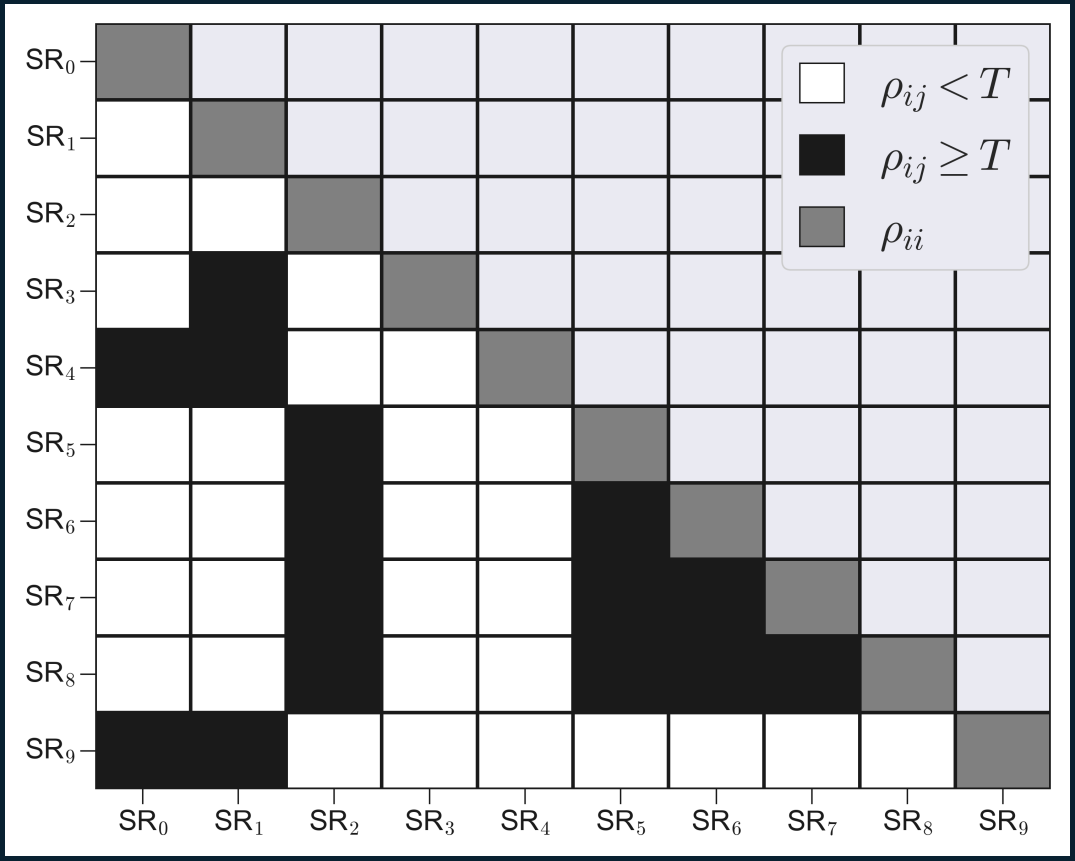
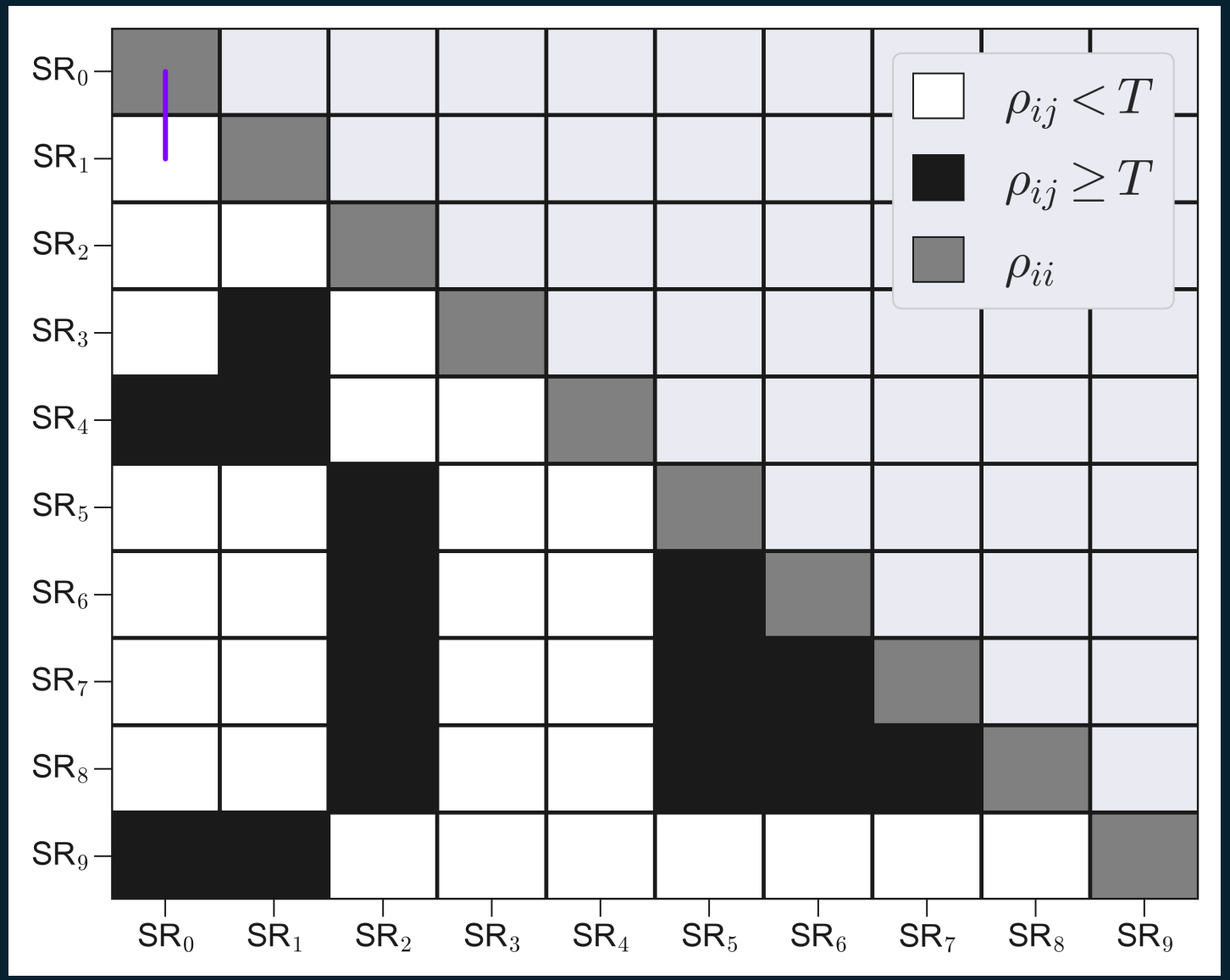
0.0

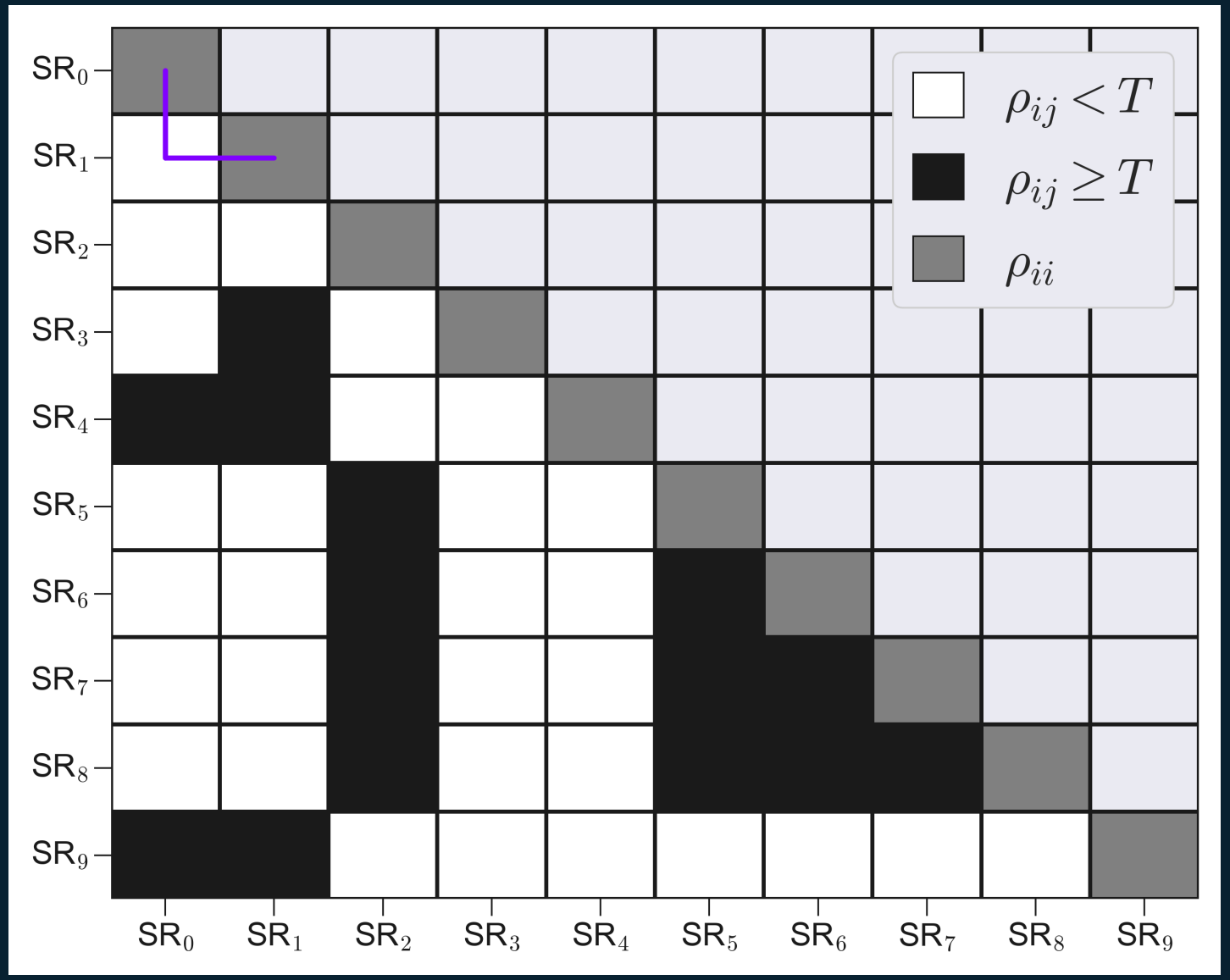


Exclusivity Matrix

Boolean “mask” of overlap matrix where true is defined as having an overlap below threshold T.

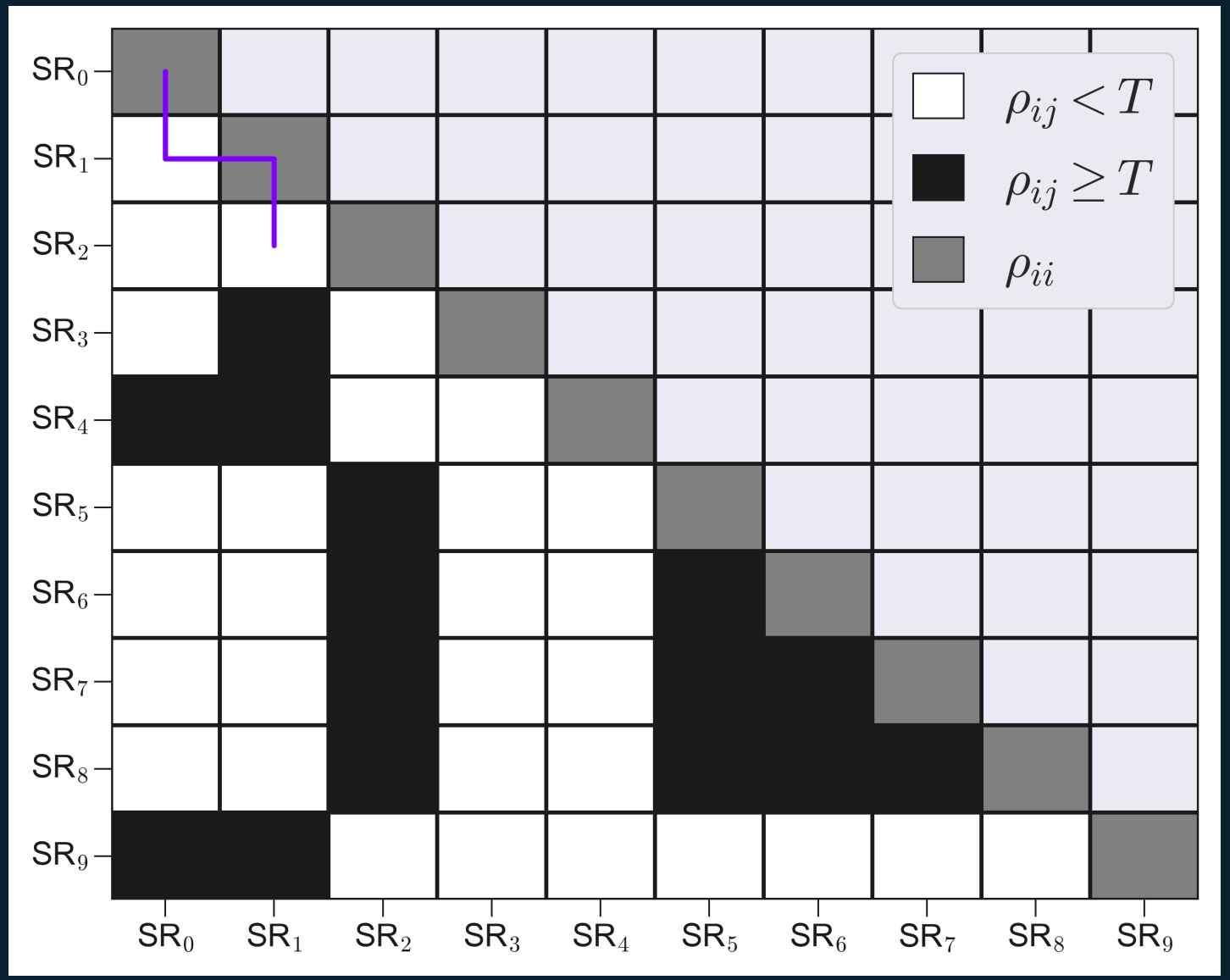


$\overbrace{\quad}^{\mathrm{SR}_0}$



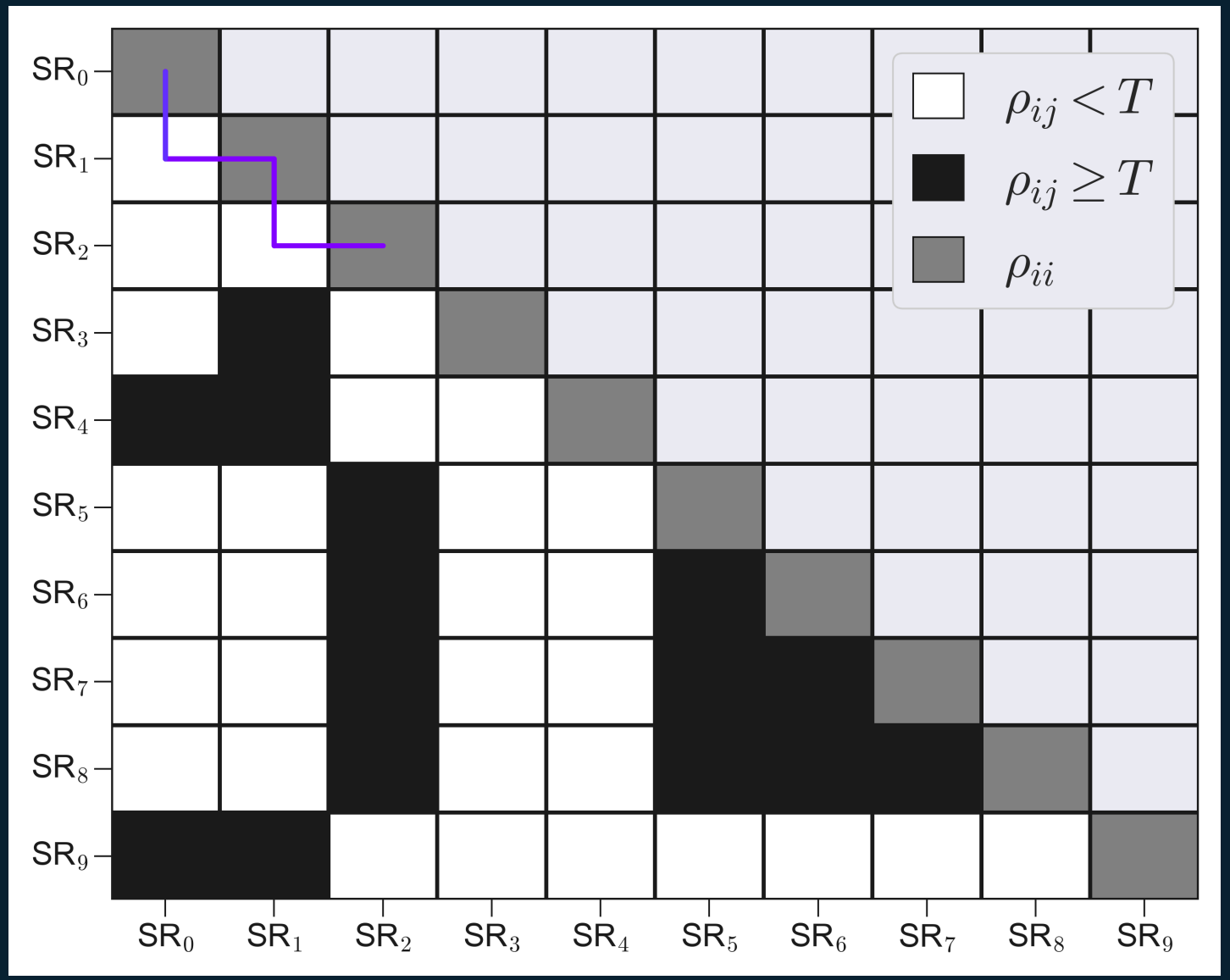
$\overbrace{\text{SR}_0}$

$\underbrace{\text{SR}_1}$

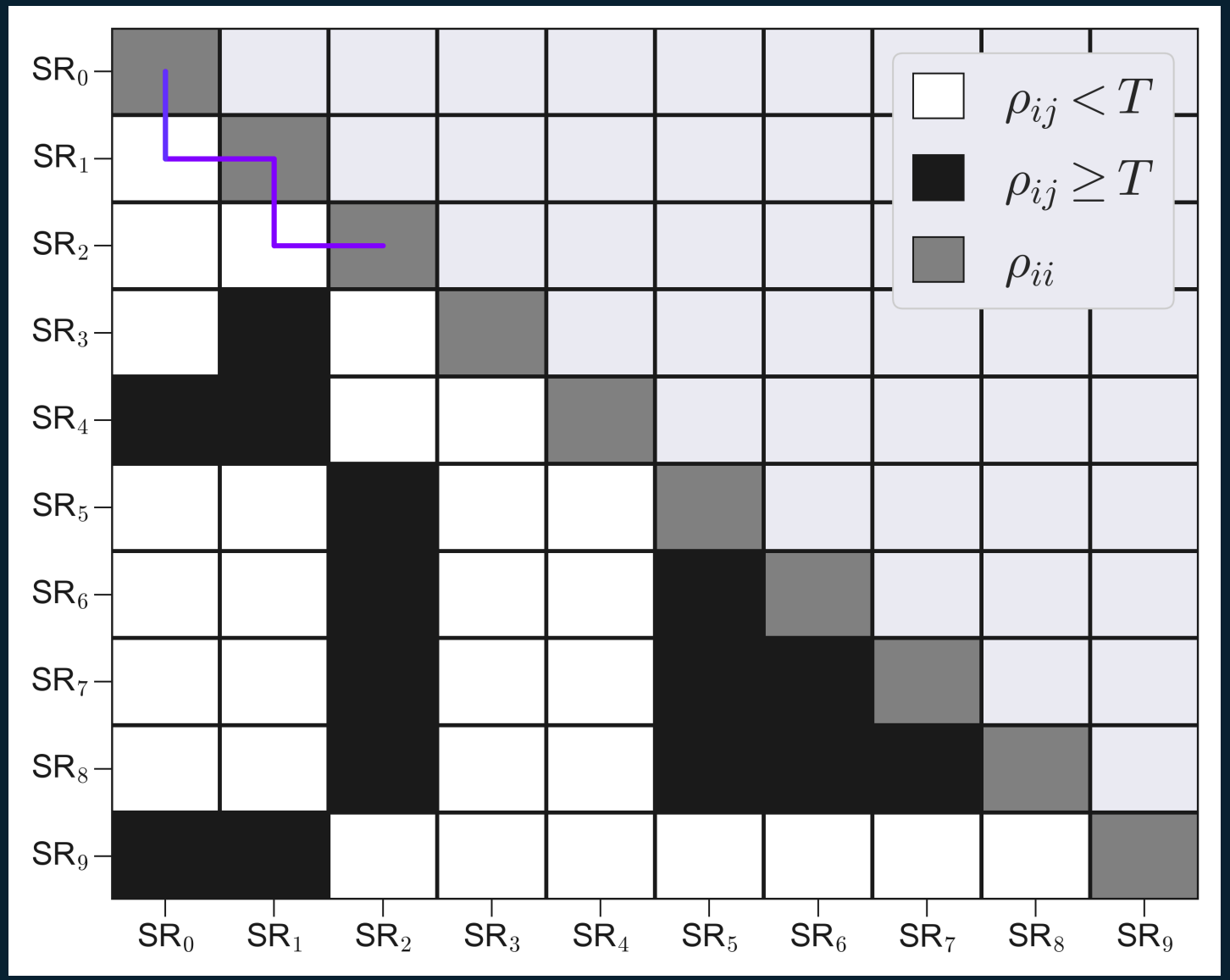


$\overbrace{\text{SR}_0}$

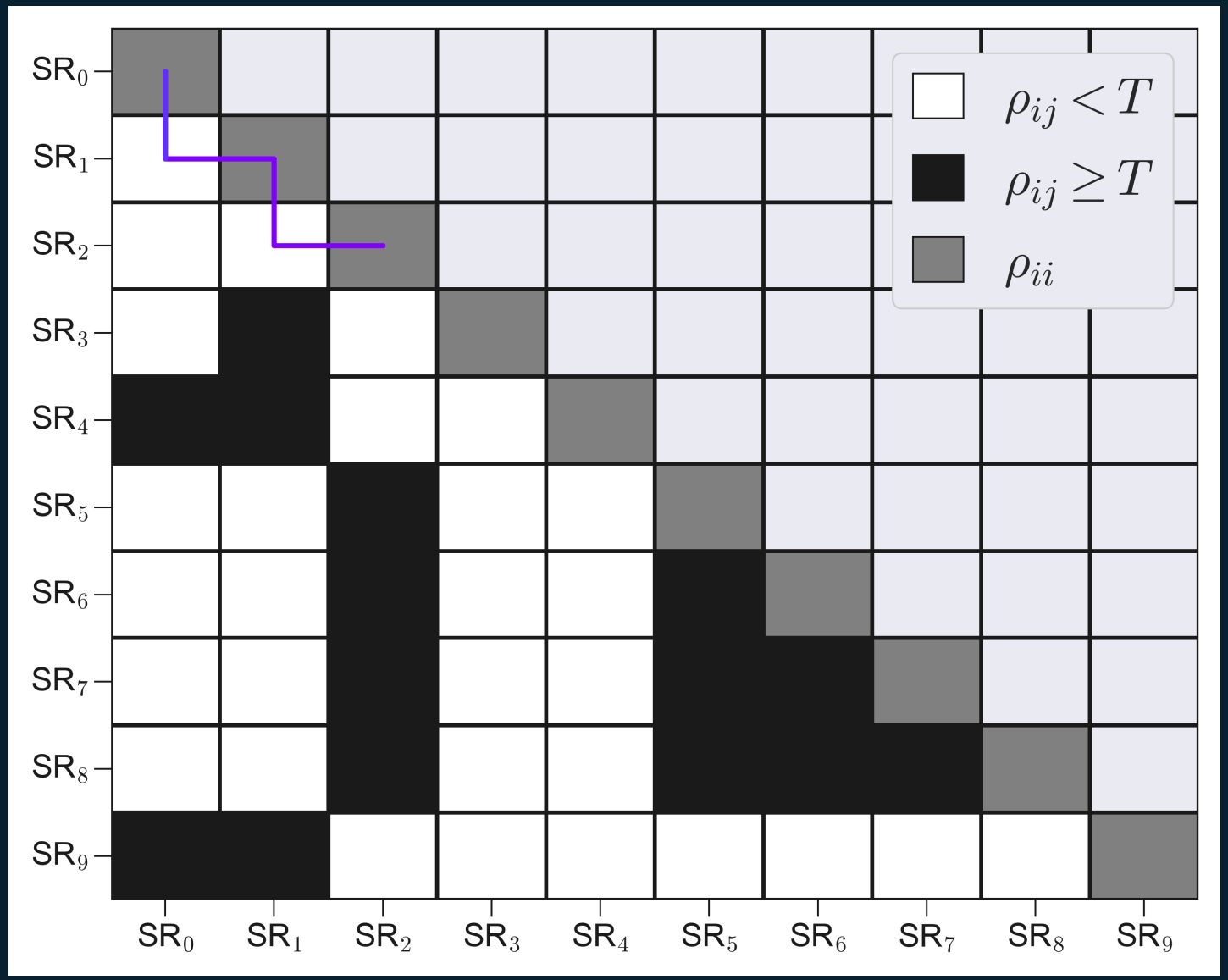
$\underbrace{\text{SR}_1}$

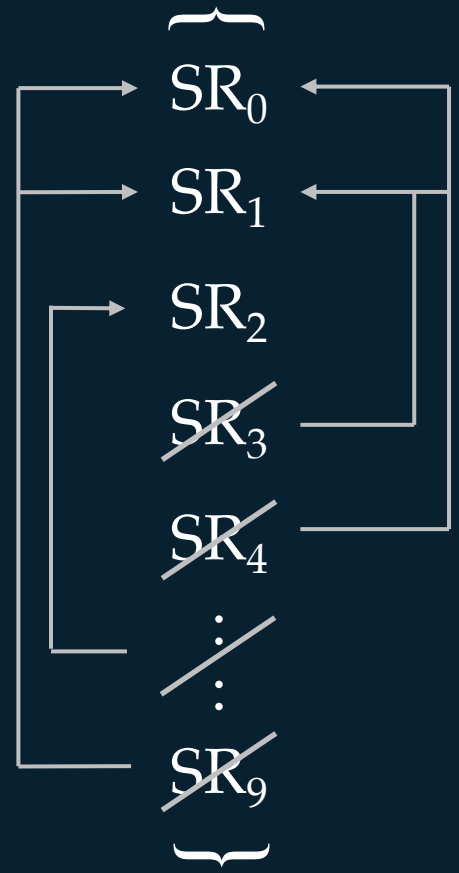


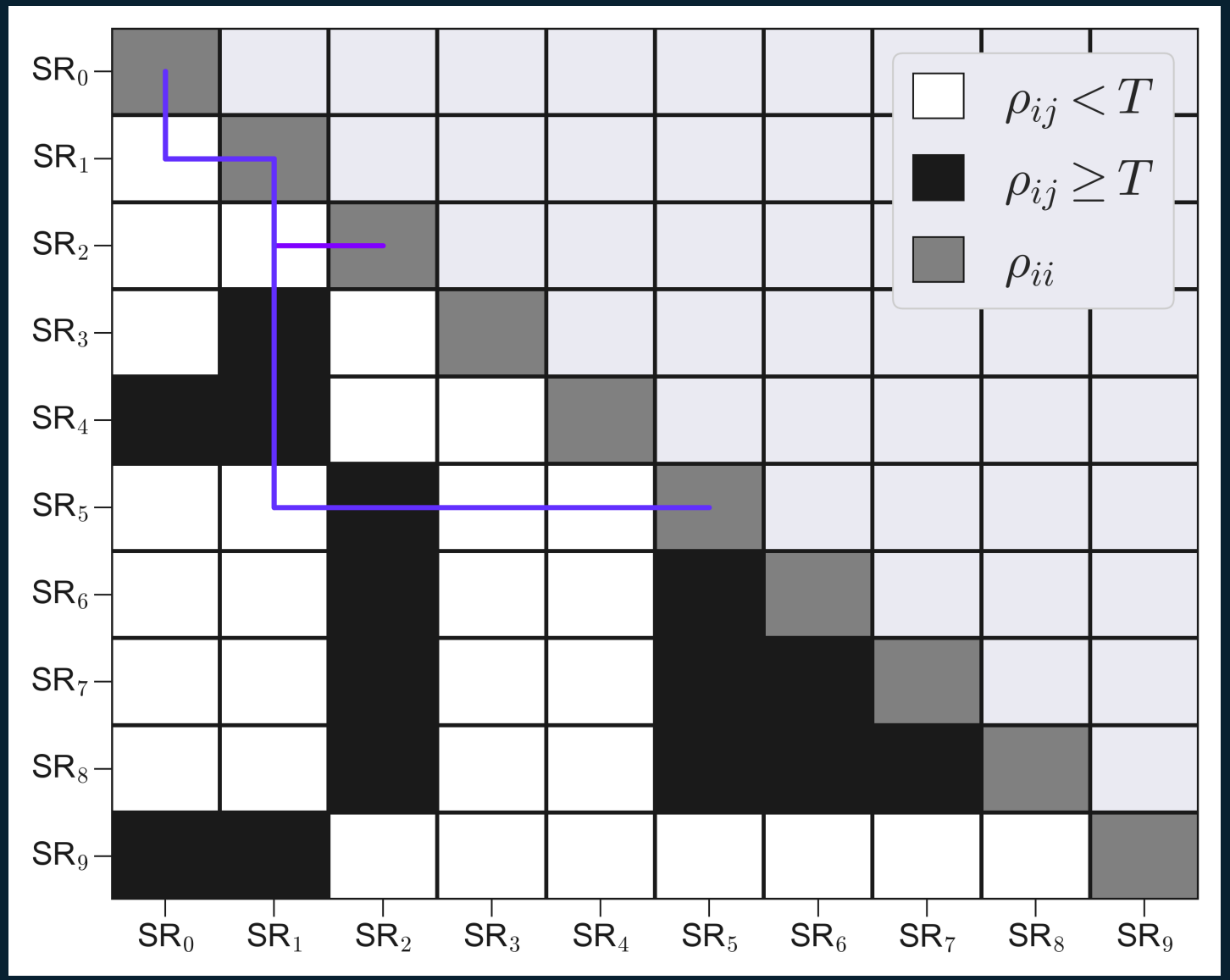
$\overbrace{\text{SR}_0}$
SR_1
$\underbrace{\text{SR}_2}$



$\overbrace{\quad}$
SR_0
SR_1
SR_2
~~SR_3~~
~~SR_4~~
$\vdots$
~~SR_9~~
$\underbrace{\quad}$


SR0
SR1
SR2
SR3
SR4
SR5
SR6
SR7
SR8
SR9
$\rho_{ij} < T$
$\rho_{ij} \geq T$
ρ_{ii}

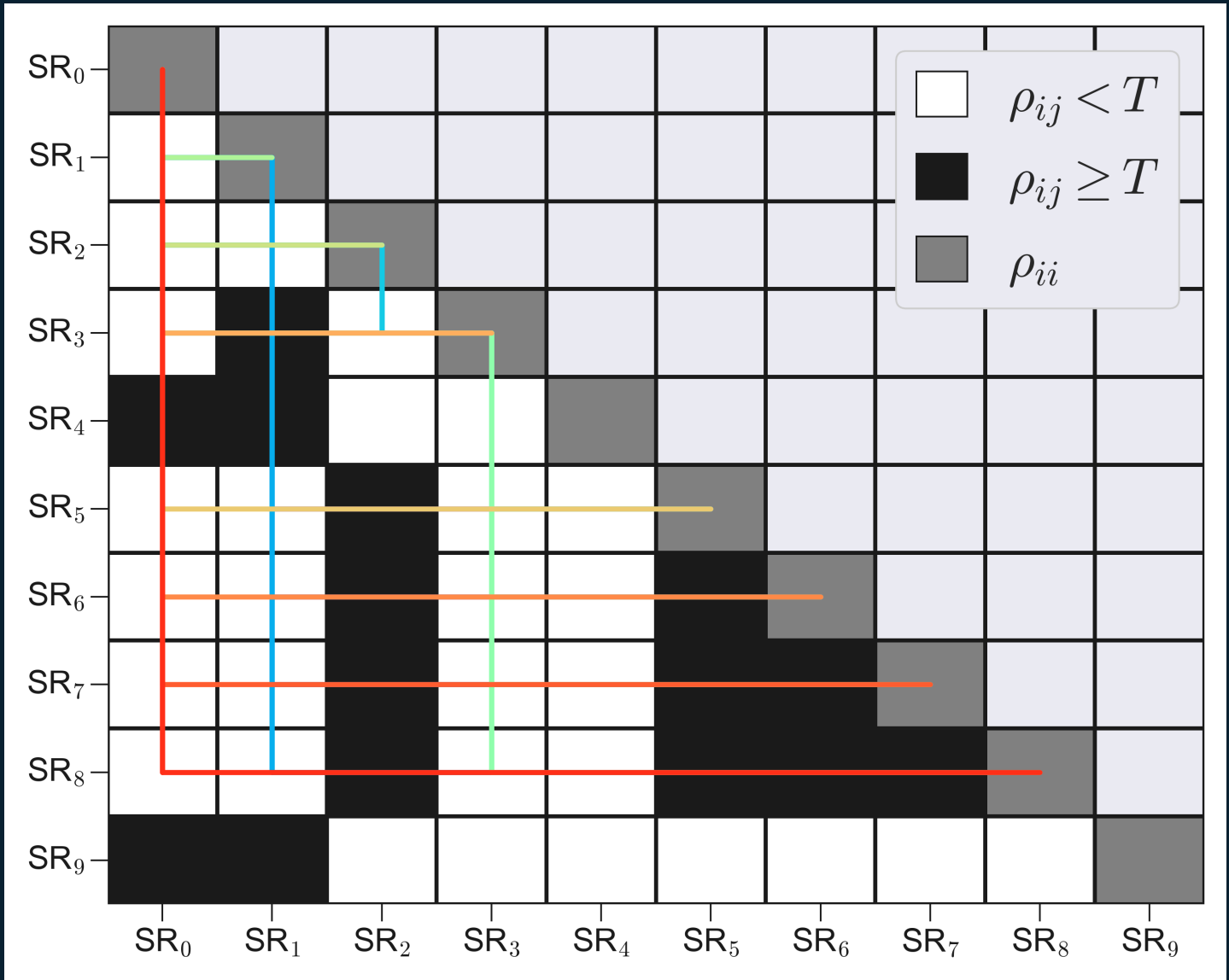

SR0
SR1
SR2
SR3
SR4
SR9



$\overbrace{\text{SR}_0}$ $\overbrace{\text{SR}_0}$

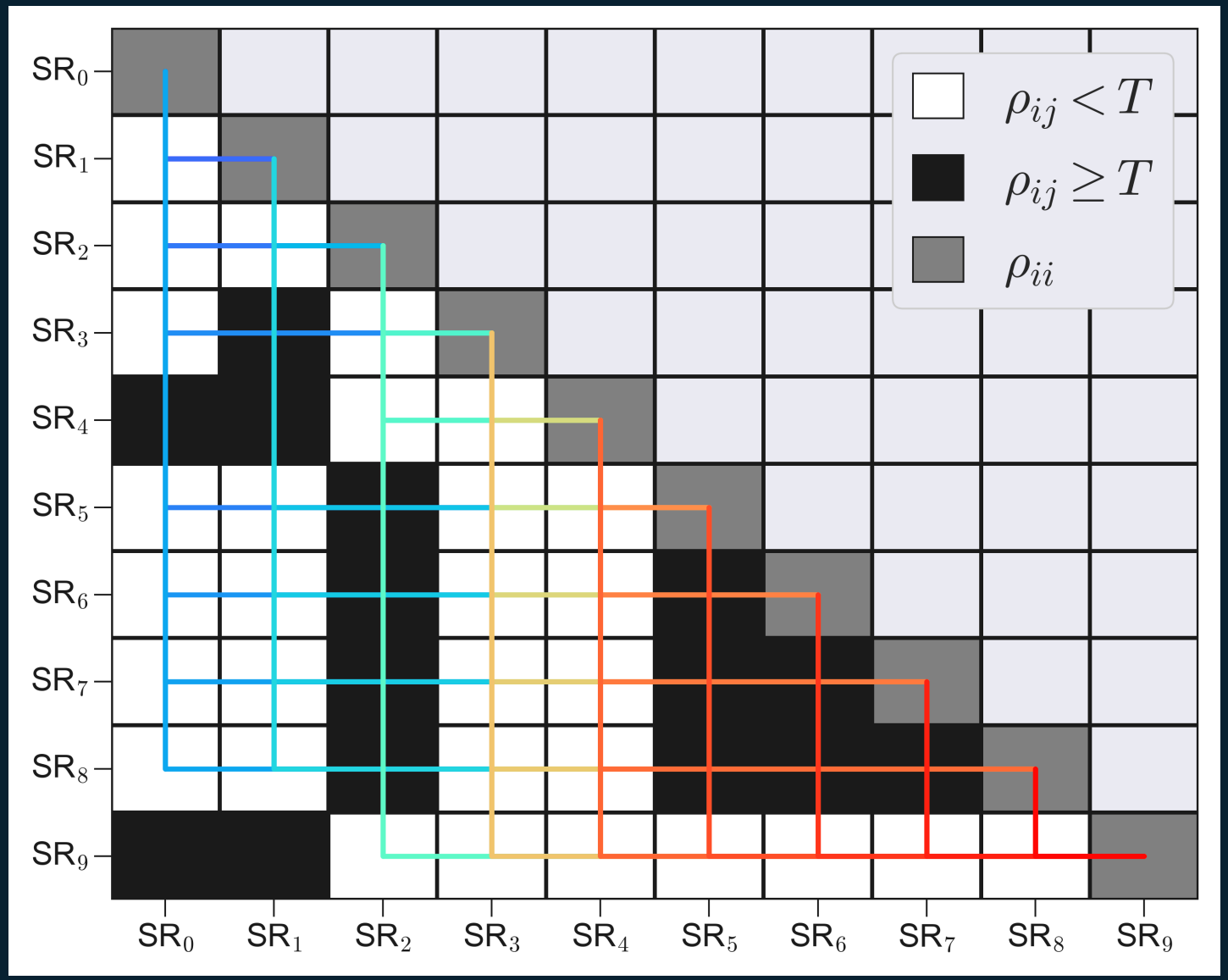
SR_1 SR_1

$\underbrace{\text{SR}_2}$ $\underbrace{\text{SR}_5}$

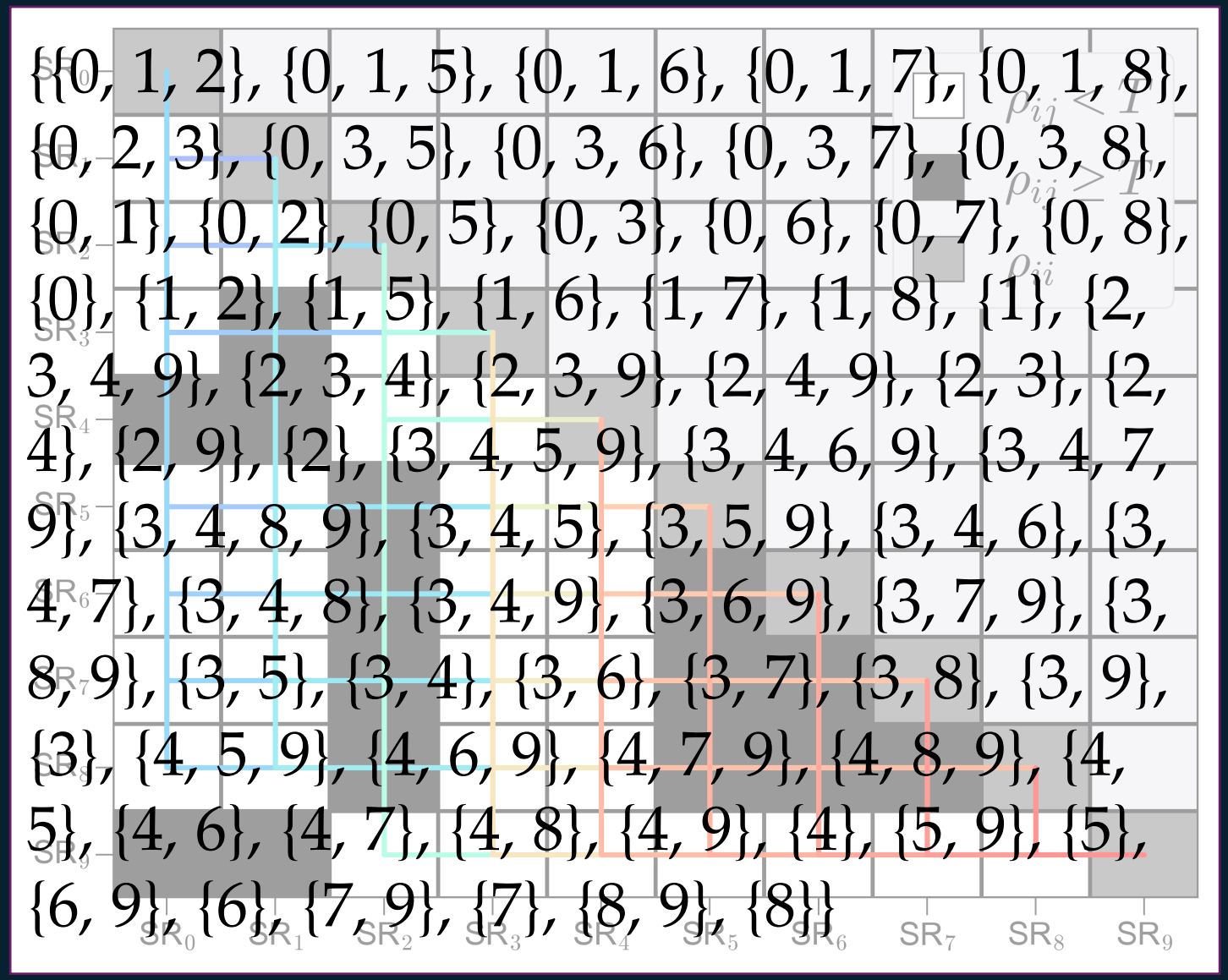


Full Set of paths starting from SR_0 ($SR_N = N$)

{{0}, {0, 1},
{0, 2}, {0, 5}, {0, 3},
{0, 6}, {0, 7}, {0, 8},
{0, 1, 2}, {0, 1, 5},
{0, 1, 6}, {0, 1, 7},
{0, 1, 8}, {0, 2, 3},
{0, 3, 5}, {0, 3, 6},
{0, 3, 7}, {0, 3, 8}}



71 allowed combinations
($SR_N = N$)



71 allowed combinations
($SR_N = N$)

Directed Acyclic Graph

Node -> Signal Region

Hereditary Depth First Search

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Hereditary Depth First Search

When building a set of signal regions, any additional signal region must have minimum overlap with all previous signal regions in the set.

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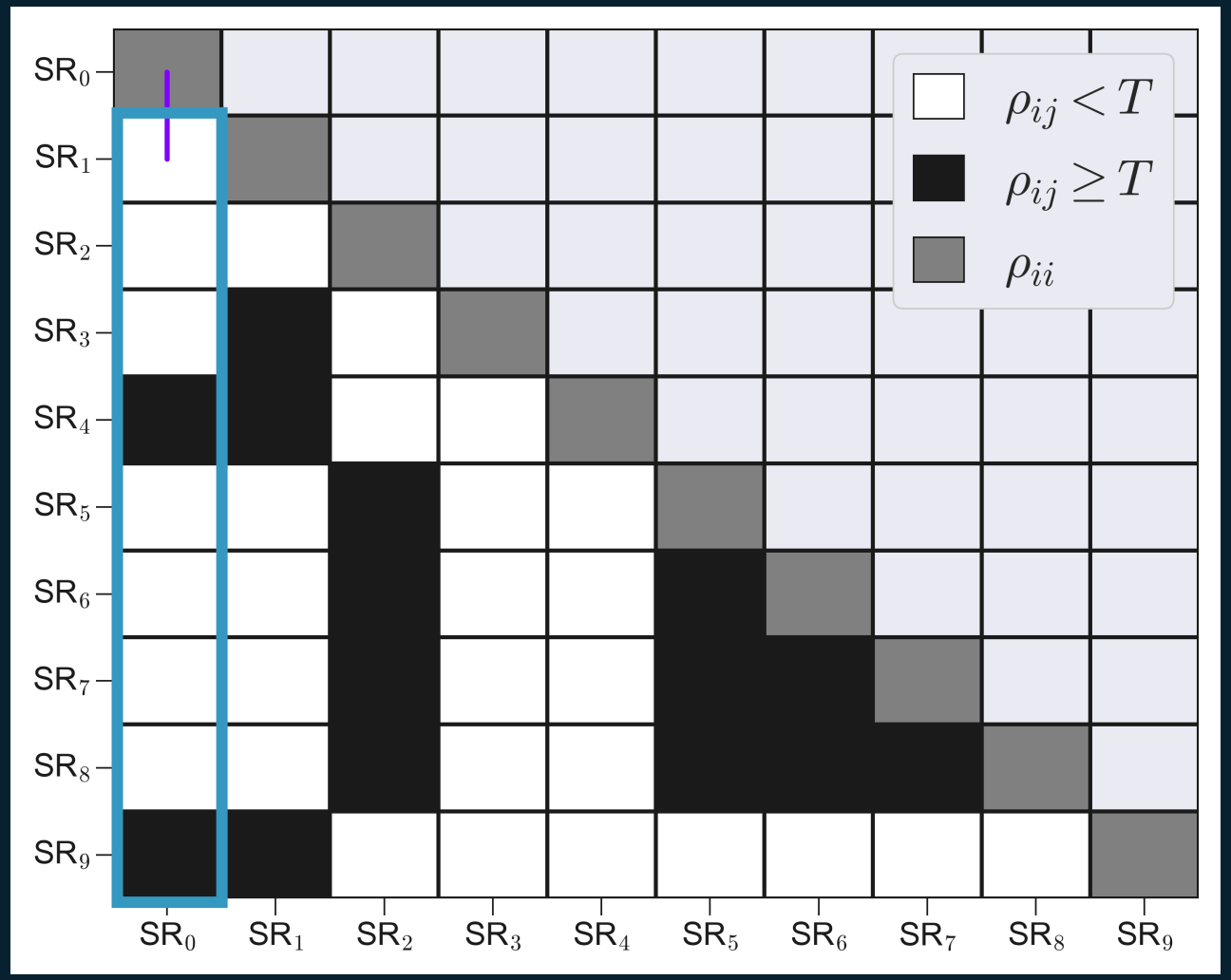
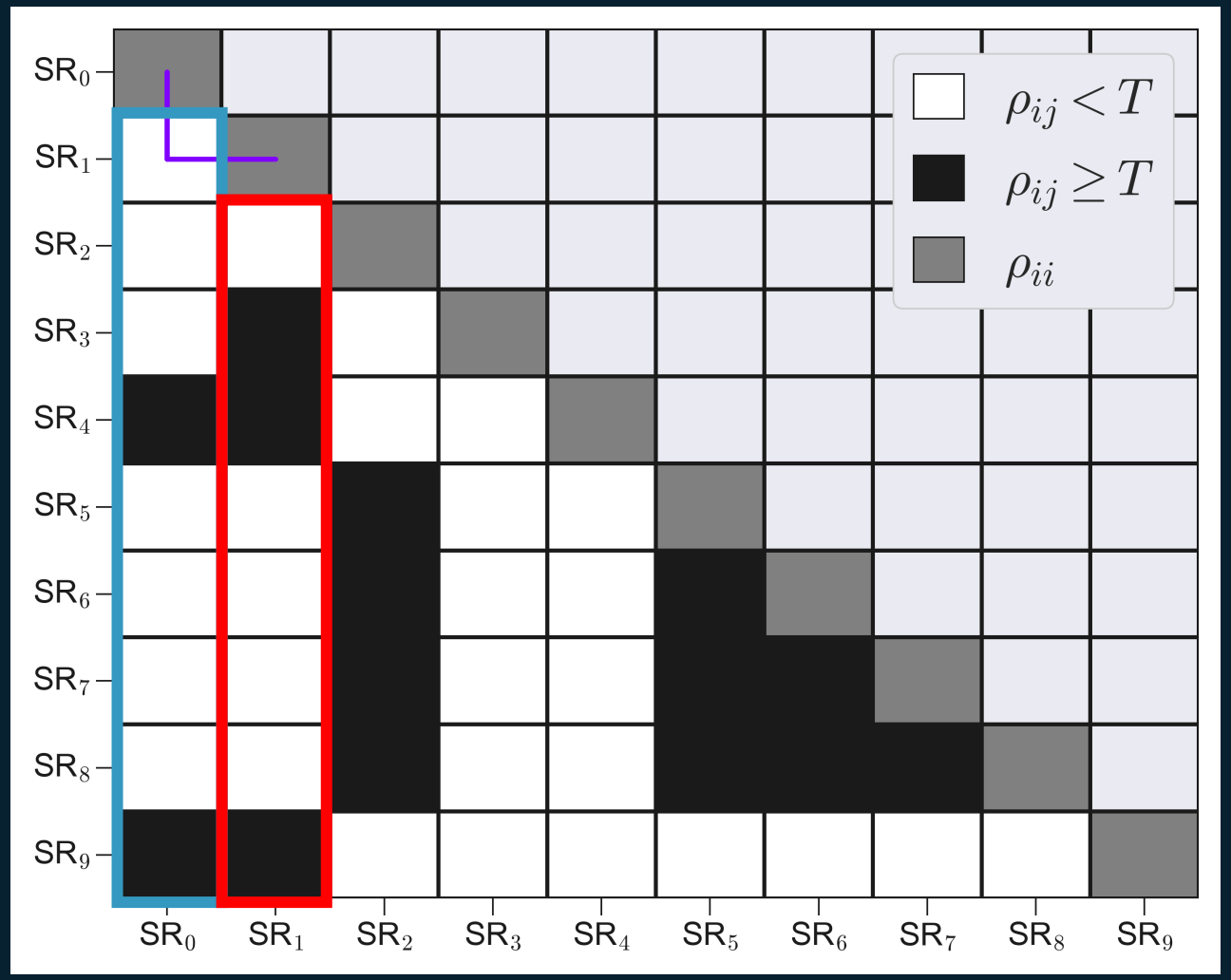
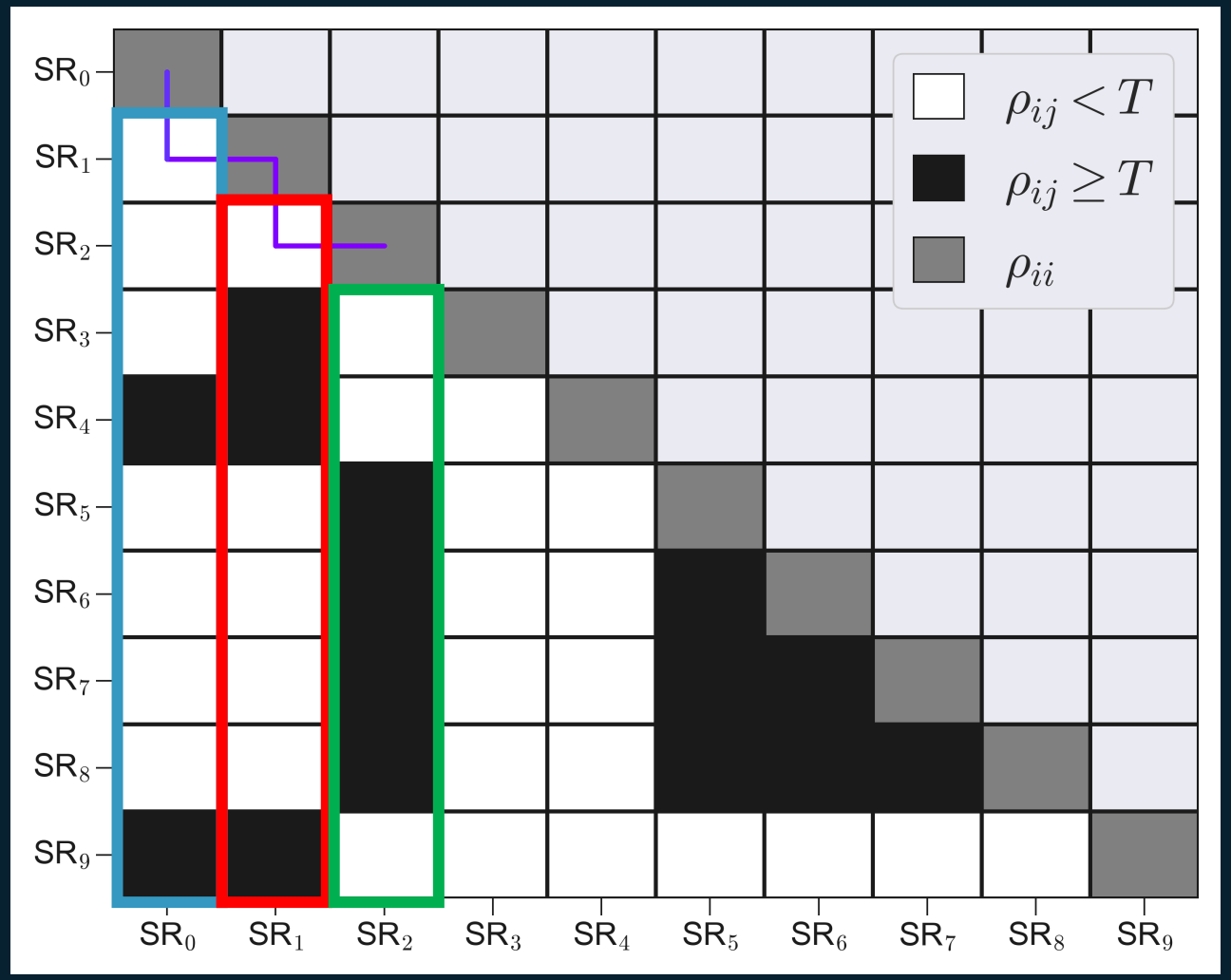

SR0
SR1
SR2
SR3
SR4
SR5
SR6
SR7
SR8
SR9
$\rho_{ij} < T$
$\rho_{ij} \geq T$
ρ_{ii}


SR0
SR1
SR2
SR3
SR4
SR5
SR6
SR7
SR8
SR9
$\rho_{ij} < T$
$\rho_{ij} \geq T$
ρ_{ii}


SR0
SR1
SR2
SR3
SR4
SR5
SR6
SR7
SR8
SR9
$\rho_{ij} < T$
$\rho_{ij} \geq T$
ρ_{ii}
SR0
SR1
SR2
SR3
SR4
SR5
SR6
SR7
SR8
SR9

□ ∩ □ ∩ □

= {}

Hereditary Depth First Search

Algorithm available in the paper and on the TACO GitLab

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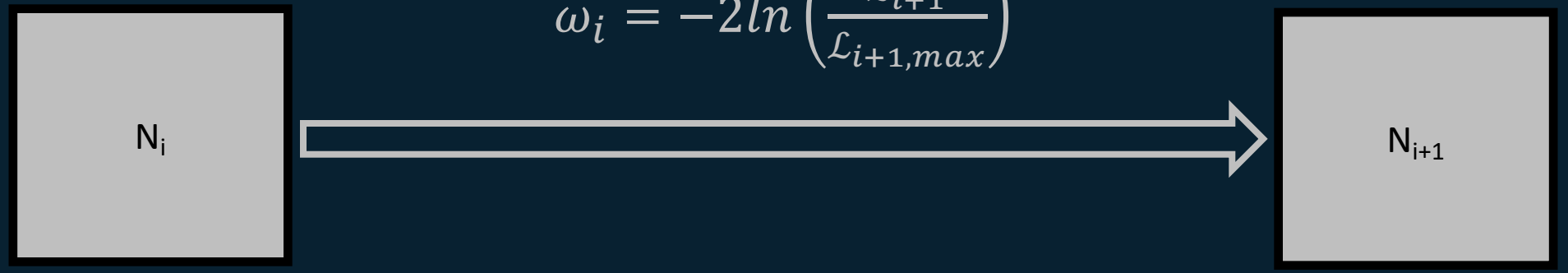
Weighted Edge:

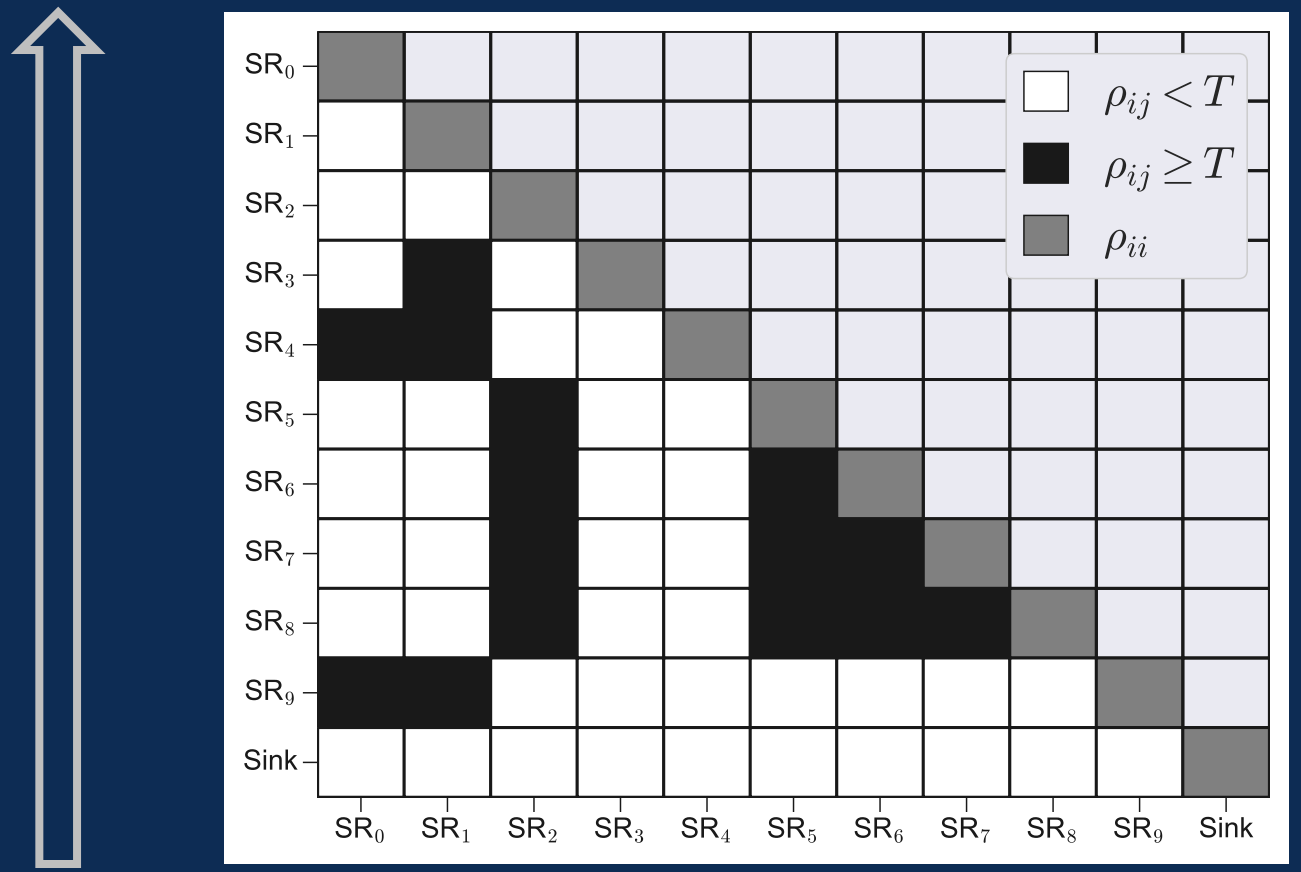
$$\omega_i = -2ln\left(\frac{\mathcal{L}_{i+1}}{\mathcal{L}_{i+1,max}}\right)$$

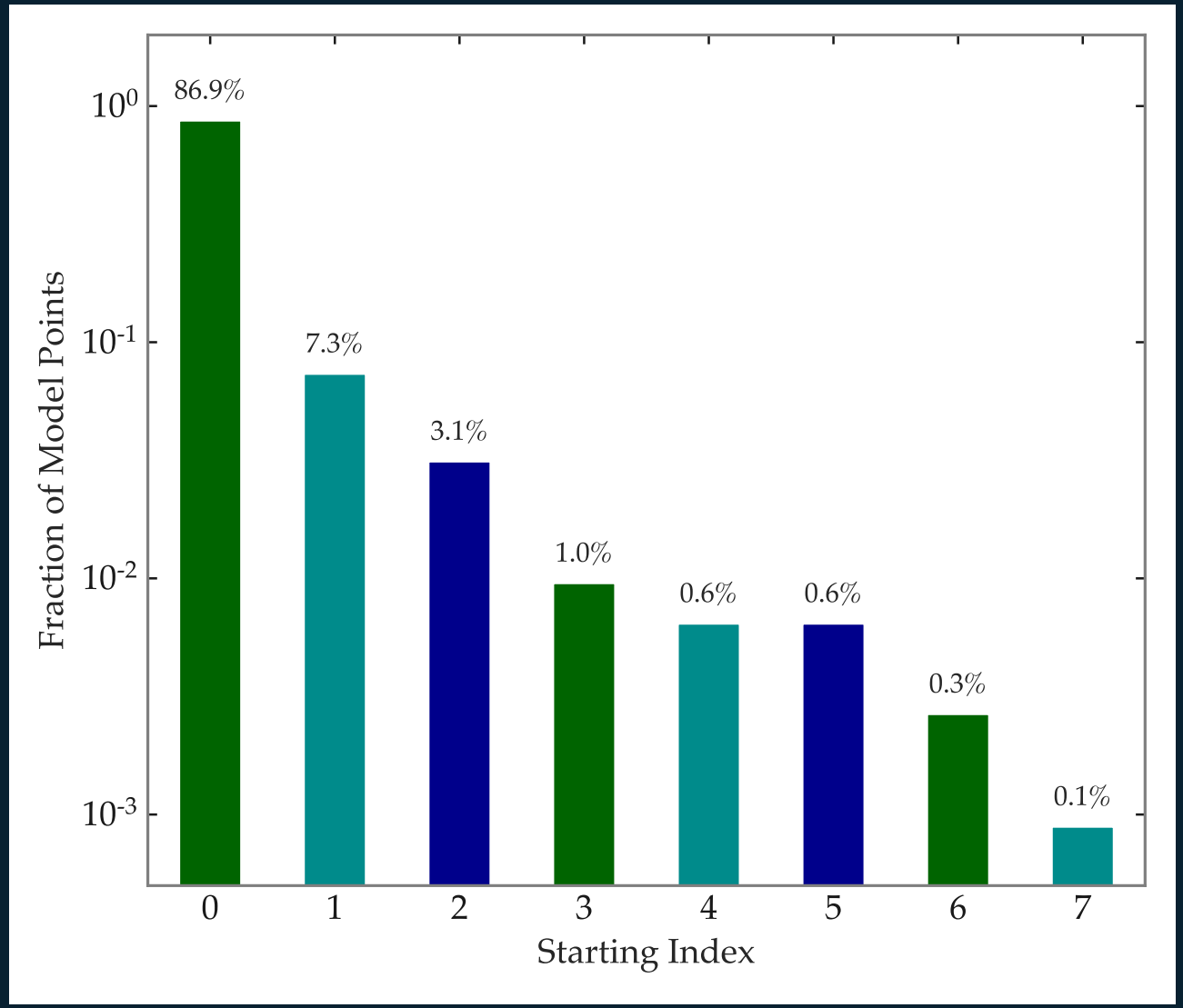


Weighted Edge:

$$\text{Best Path} = \max\left\{\left\{\sum_{i \in p_j} \omega_i\right\}_j\right\}$$

Rank matrix in order of preference for each model point i.e. upper limit or r-value




86.9%
7.3%
3.1%
1.0%
0.6%
0.6%
0.3%
0.1%
10^{0}
10^{-1}
10^{-2}
10^{-3}
Fraction of Model Points
0
1
2
3
4
5
6
7
Starting Index

Weighted Hereditary Depth First Search

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Weighted Hereditary Depth First Search

When building a set of signal regions, an upper limit on the available weight can be evaluated by calculating the LLR sum of the remaining signal regions with minimum overlap with the current set.

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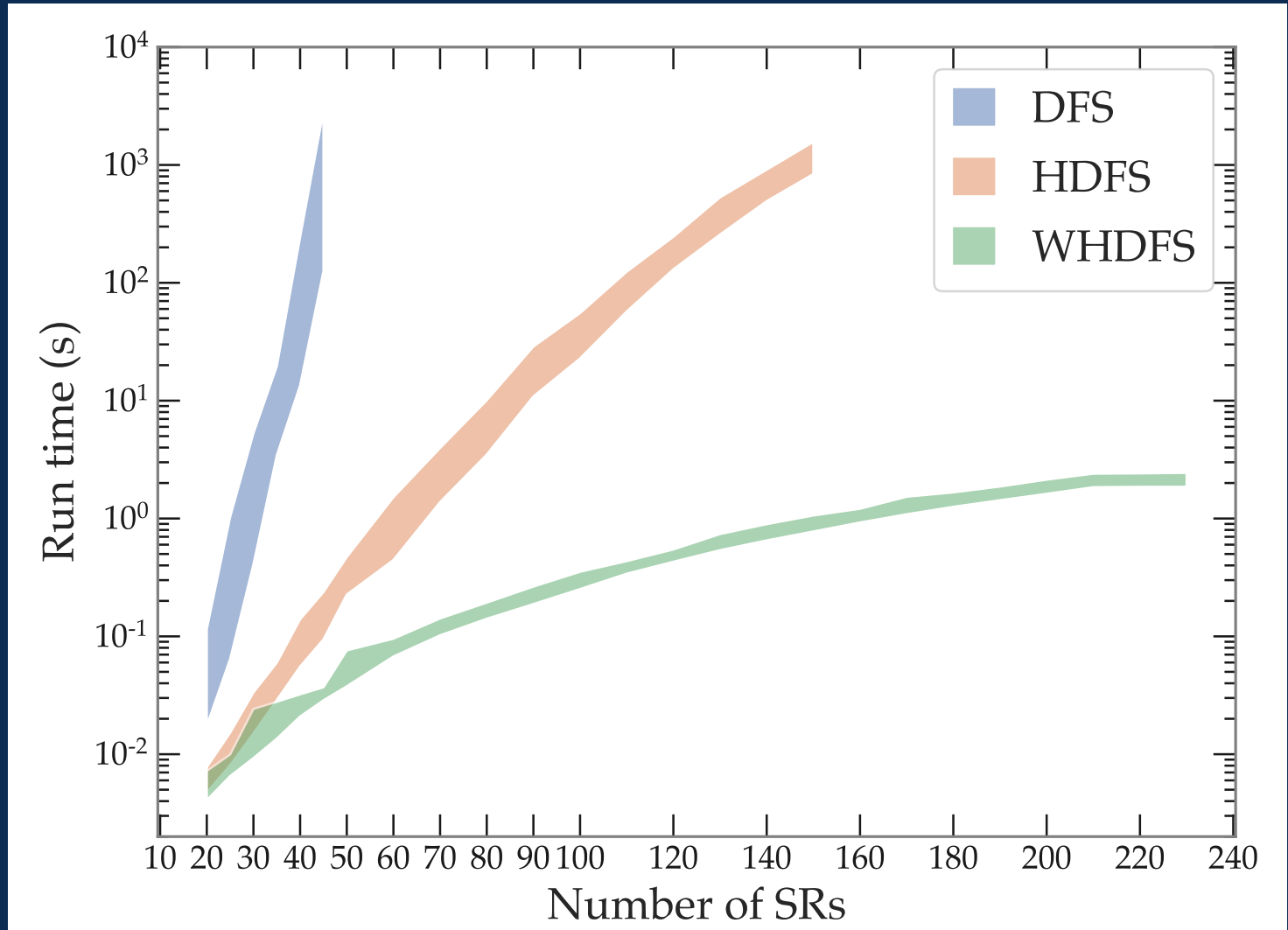
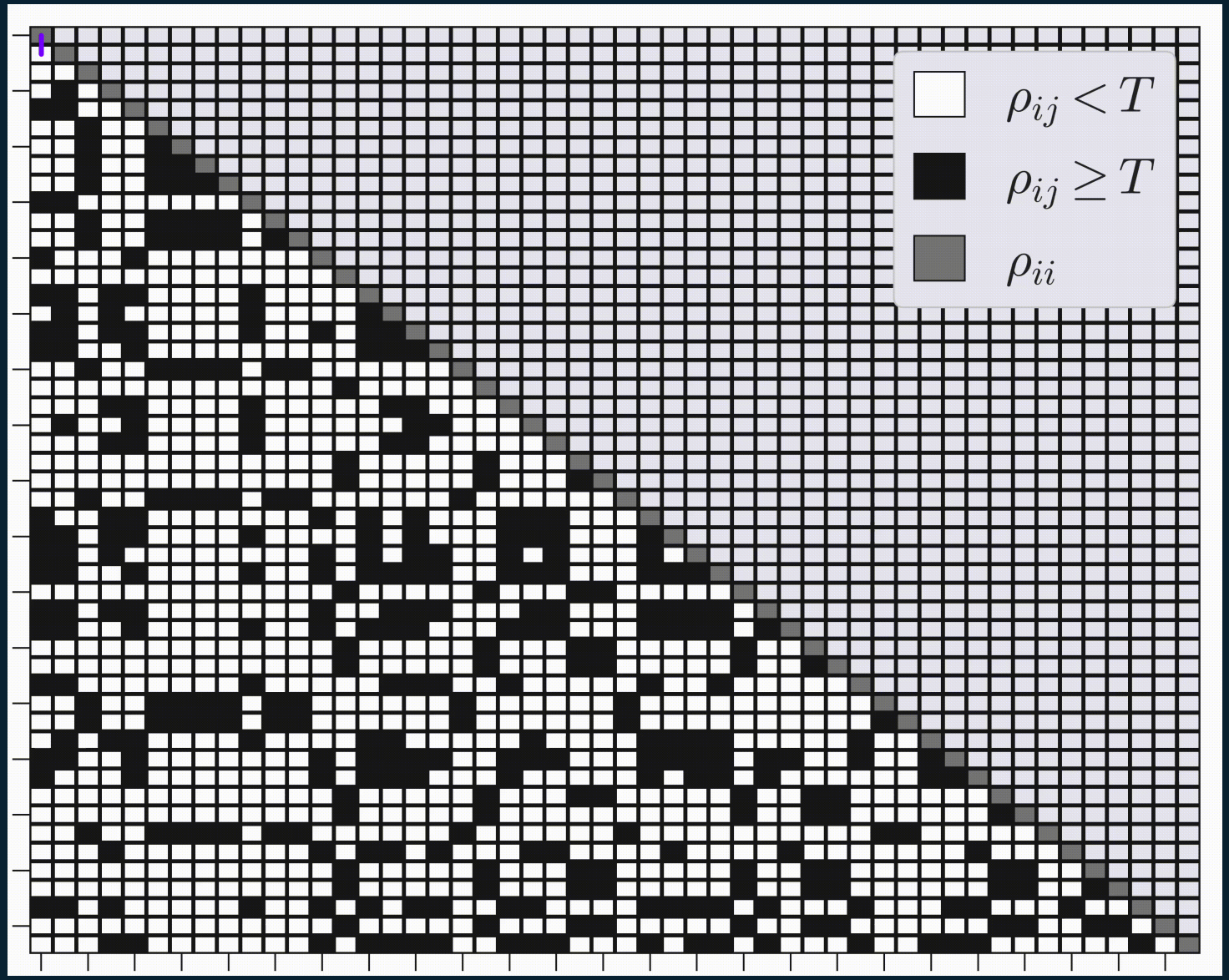
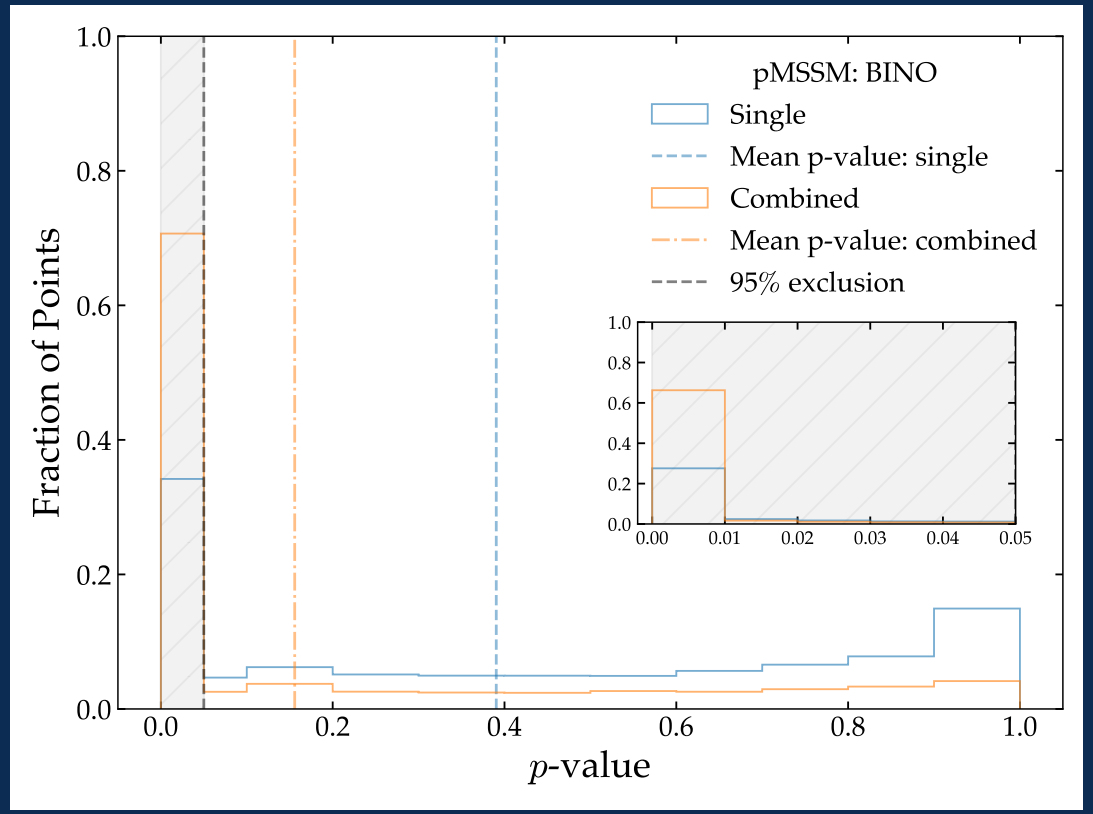

DFS
HDFS
WHDFS
Run time (s)
10^4
10^3
10^2
10^1
10^0
10^{-1}
10^{-2}
10 20 30 40 50 60 70 80 90 100 120 140 160 180 200 220 240
Number of SRs


$\rho_{ij} < T$
$\rho_{ij} \geq T$
ρ_{ii}

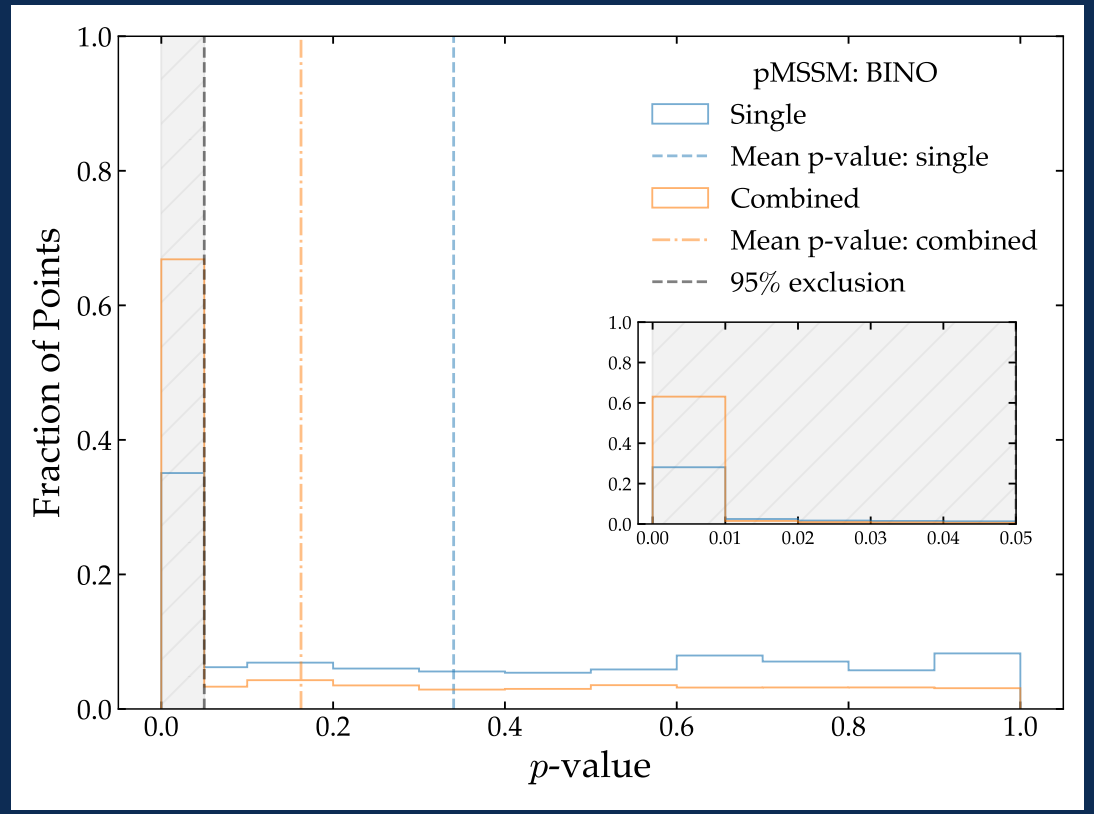
pMSSM-19 Reinterpretation: Bino

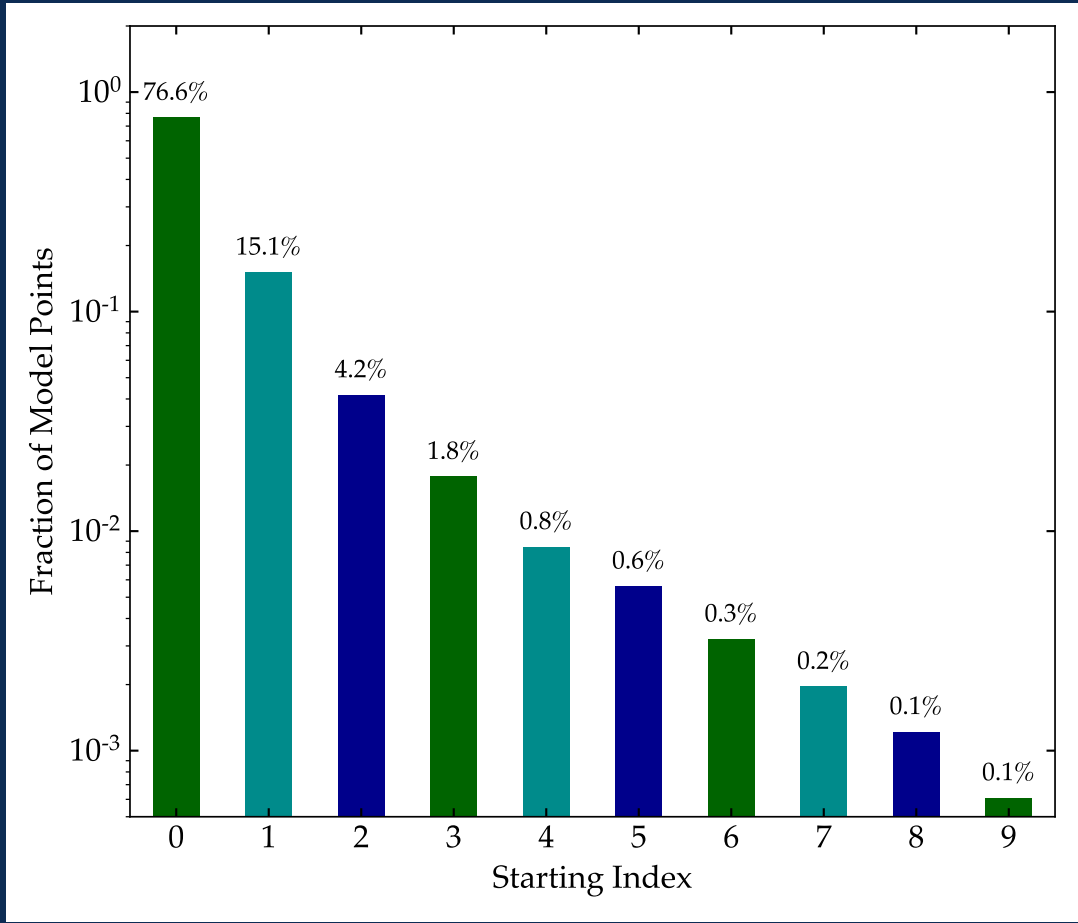
pMSSM-19: Bino

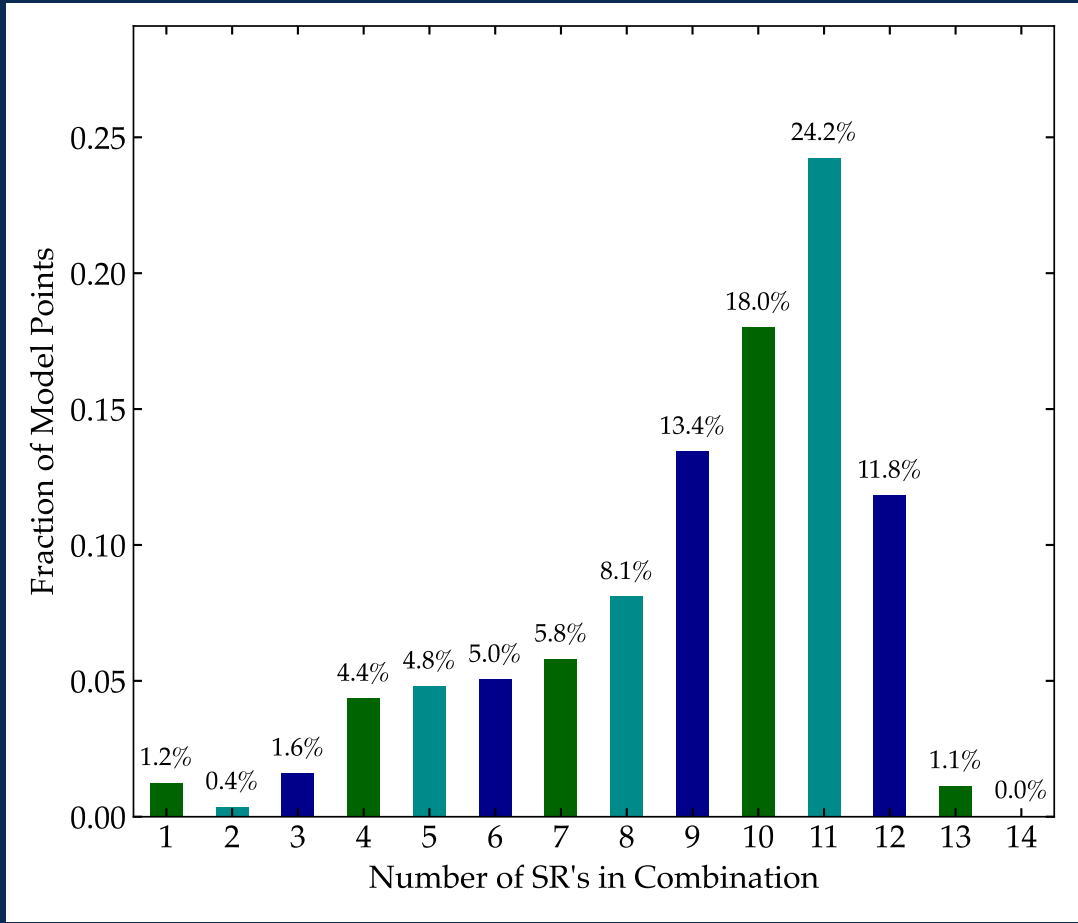
Expected



Observed




Fraction of Model Points
10^0
10^{-1}
10^{-2}
10^{-3}
76.6%
15.1%
4.2%
1.8%
0.8%
0.6%
0.3%
0.2%
0.1%
0.1%
0 1 2 3 4 5 6 7 8 9
Starting Index


Fraction of Model Points
0.25
0.20
0.15
0.10
0.05
0.00
1.2%
0.4%
1.6%
4.4%
4.8%
5.0%
5.8%
8.1%
13.4%
18.0%
24.2%
11.8%
1.1%
0.0%
1 2 3 4 5 6 7 8 9 10 11 12 13 14
Number of SR's in Combination

The Combinations can be viewed as a directed acyclic graph, on which a weighted hereditary longest-path computation can be used to identify the best-expected SR
combination for limit-setting on any given BSM model.

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Thank You

Any Questions?

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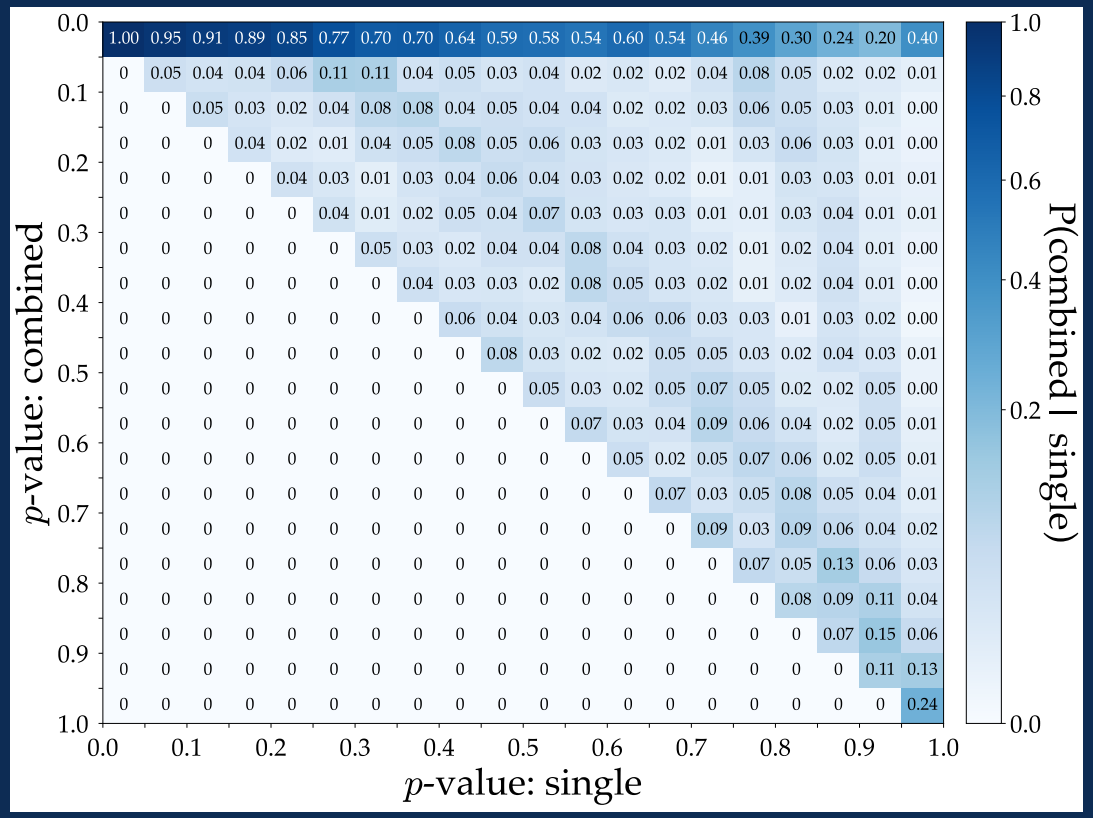
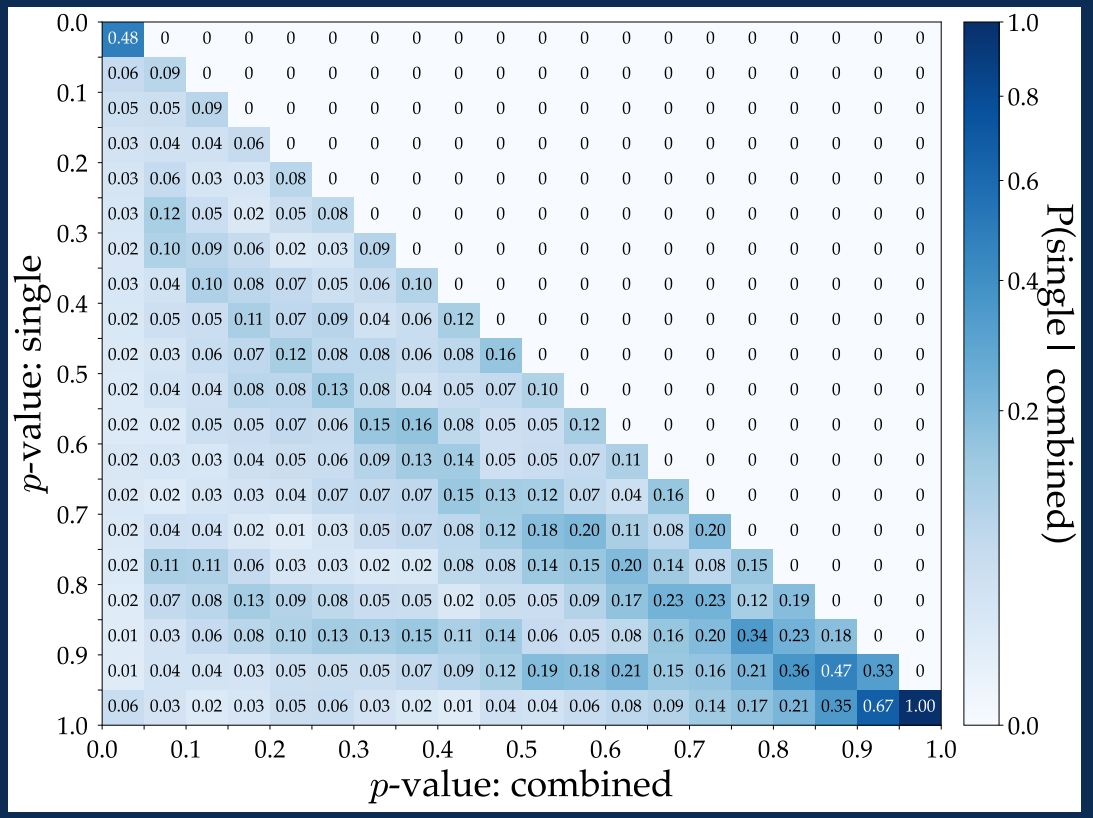
pMSSM-19: Bino

Expected

P(combined | single)



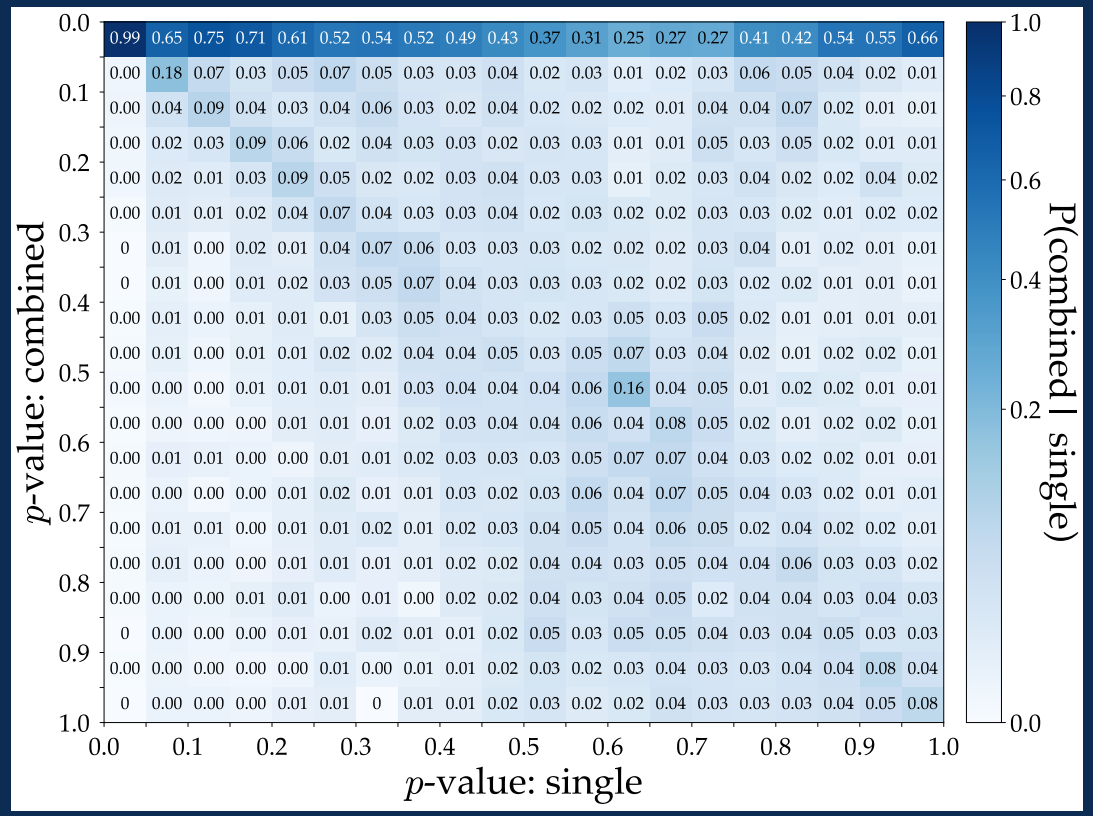
P(single | combined)



pMSSM-19: Bino

Observed

P(combined | single)



P(single | combined)