Labeled Optimal Partitioning

Toby Dylan Hocking
toby.hocking@nau.edu
joint work with Anuraag Srivastava
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Introduction: supervised changepoint detection for cancer diagnosis with DNA copy number data

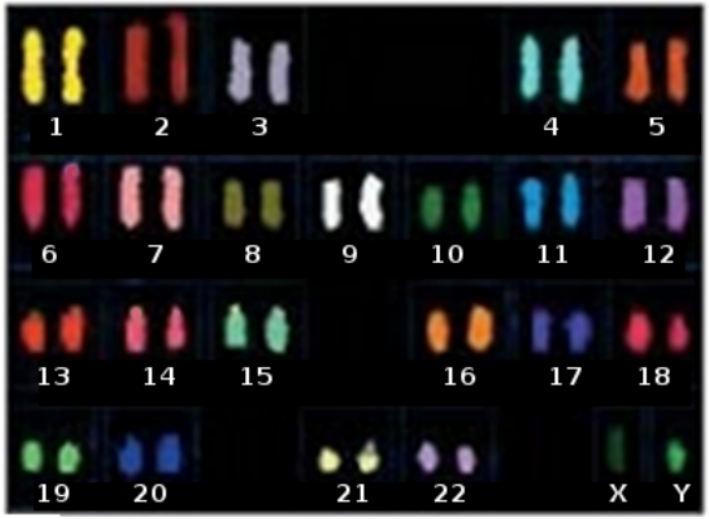
Labeled Optimal Partitioning (LOPART)

LOPART Demo

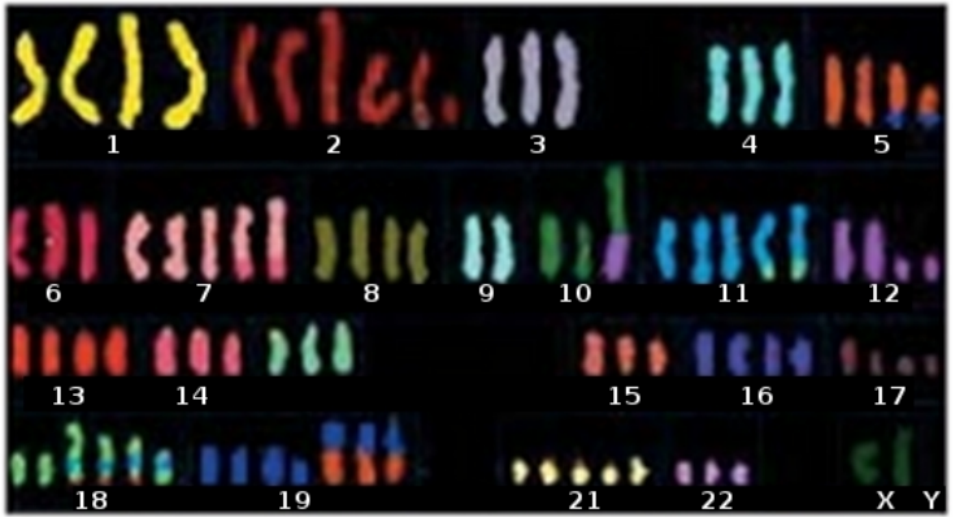
Results and Discussion

Cancer cells show chromosomal copy number alterations

Spectral karyotypes show the number of copies of the sex chromosomes (X,Y) and autosomes (1-22).
Source: Alberts *et al.* 2002.

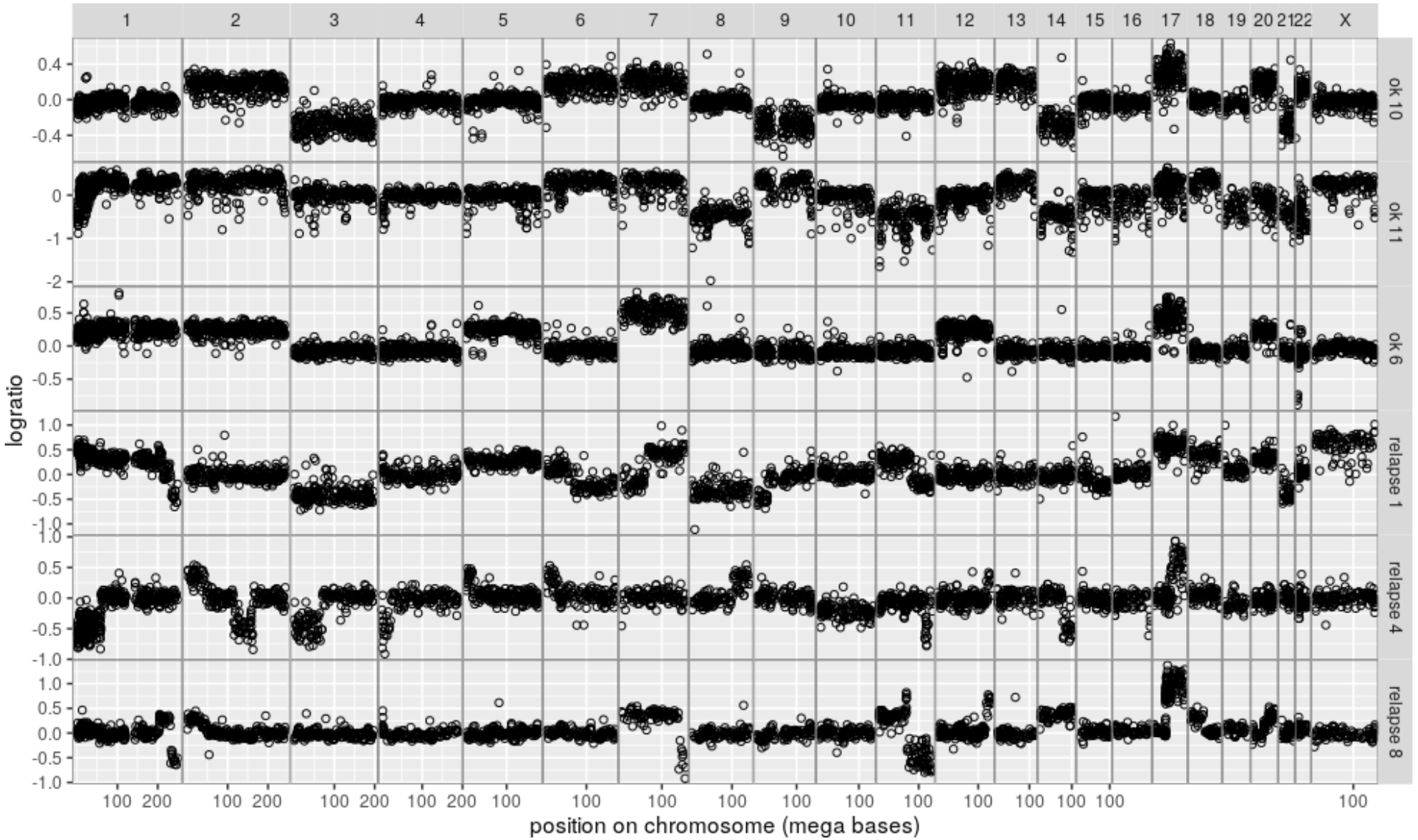


Normal cell with 2 copies of each autosome.

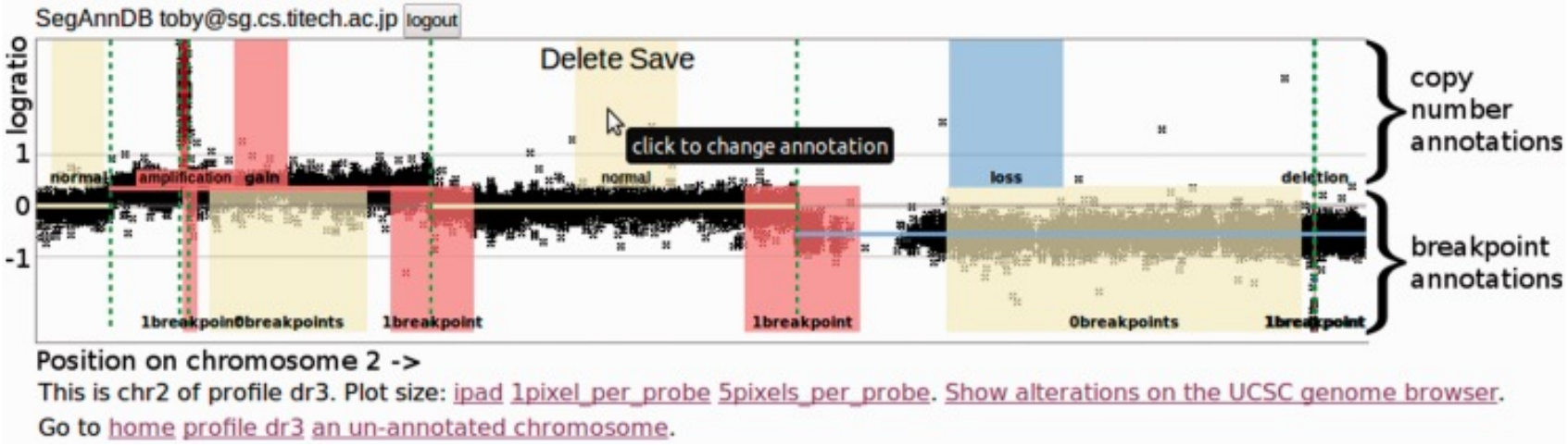


Cancer cell with many copy number alterations.

DNA copy number profiles from neuroblastoma patients with or without relapse



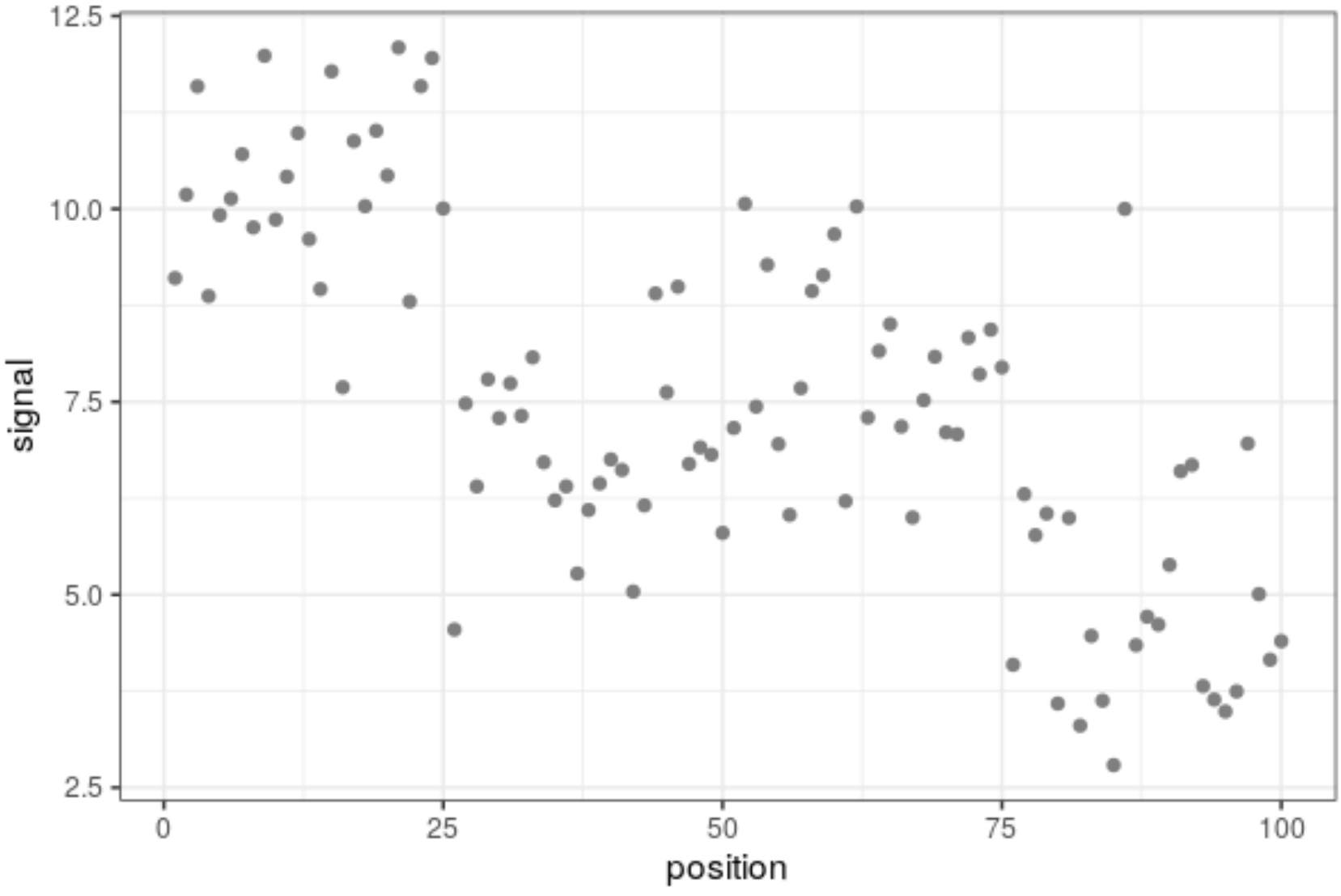
Previous work: SegAnnDB interactive machine learning system



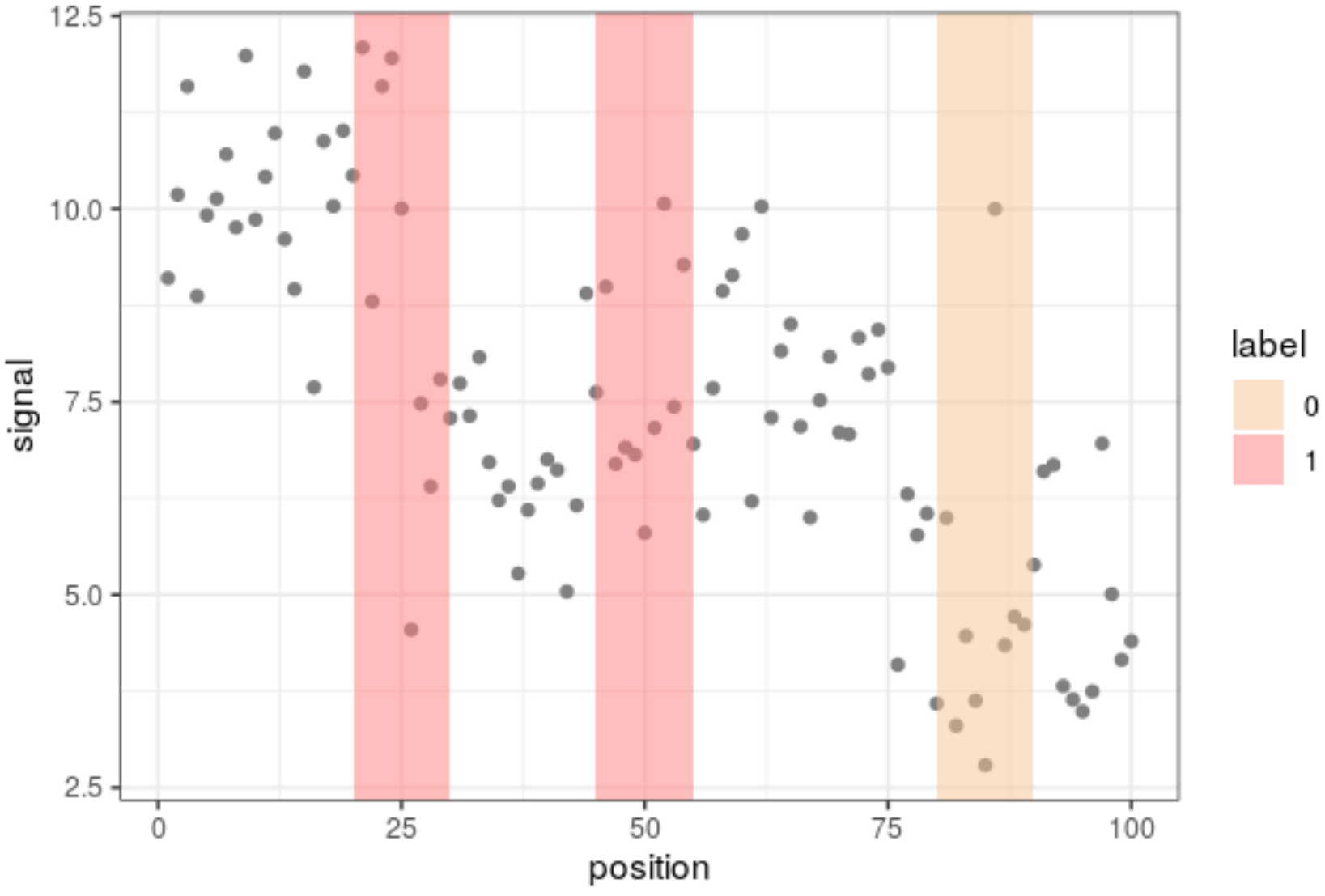
Hocking *et al.*, 2014.

- User uploads noisy data sets for machine learning analysis.
- User can provide labels which indicate presence(1) or absence(0) of changepoints in specific regions of data sets.
- Classic optimal changepoint model (max penalized Gaussian likelihood) used if it has zero label errors. OPART algorithm, Jackson *et al.*, 2005. FPOP algorithm, Maidstone *et al.*, 2016.
- Label-aware SegAnnot algorithm used otherwise (Hocking and Rigaill, 2012). Always zero train label errors, but never predicts any changepoints outside of positive(1) labels.

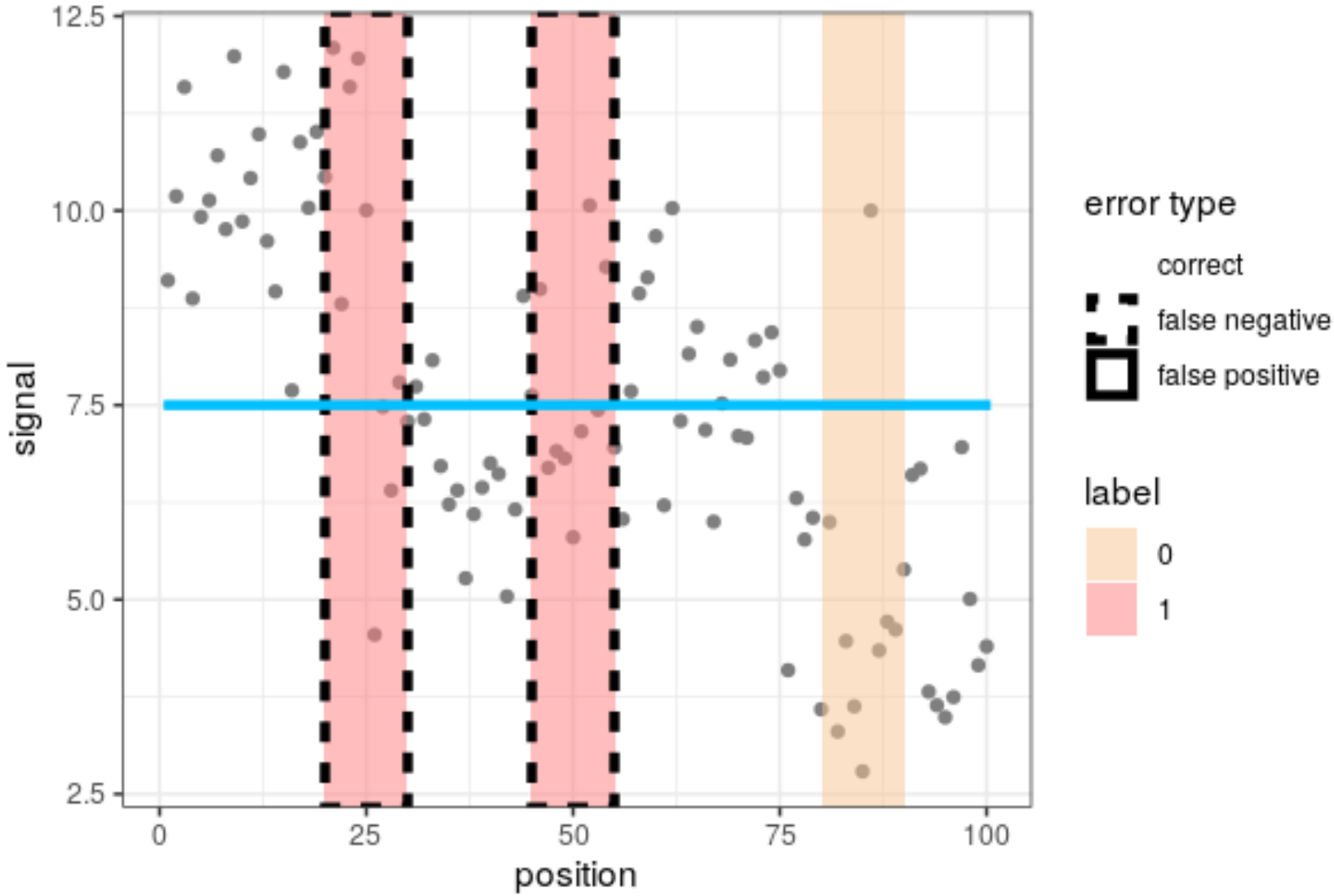
Example noisy data sequence



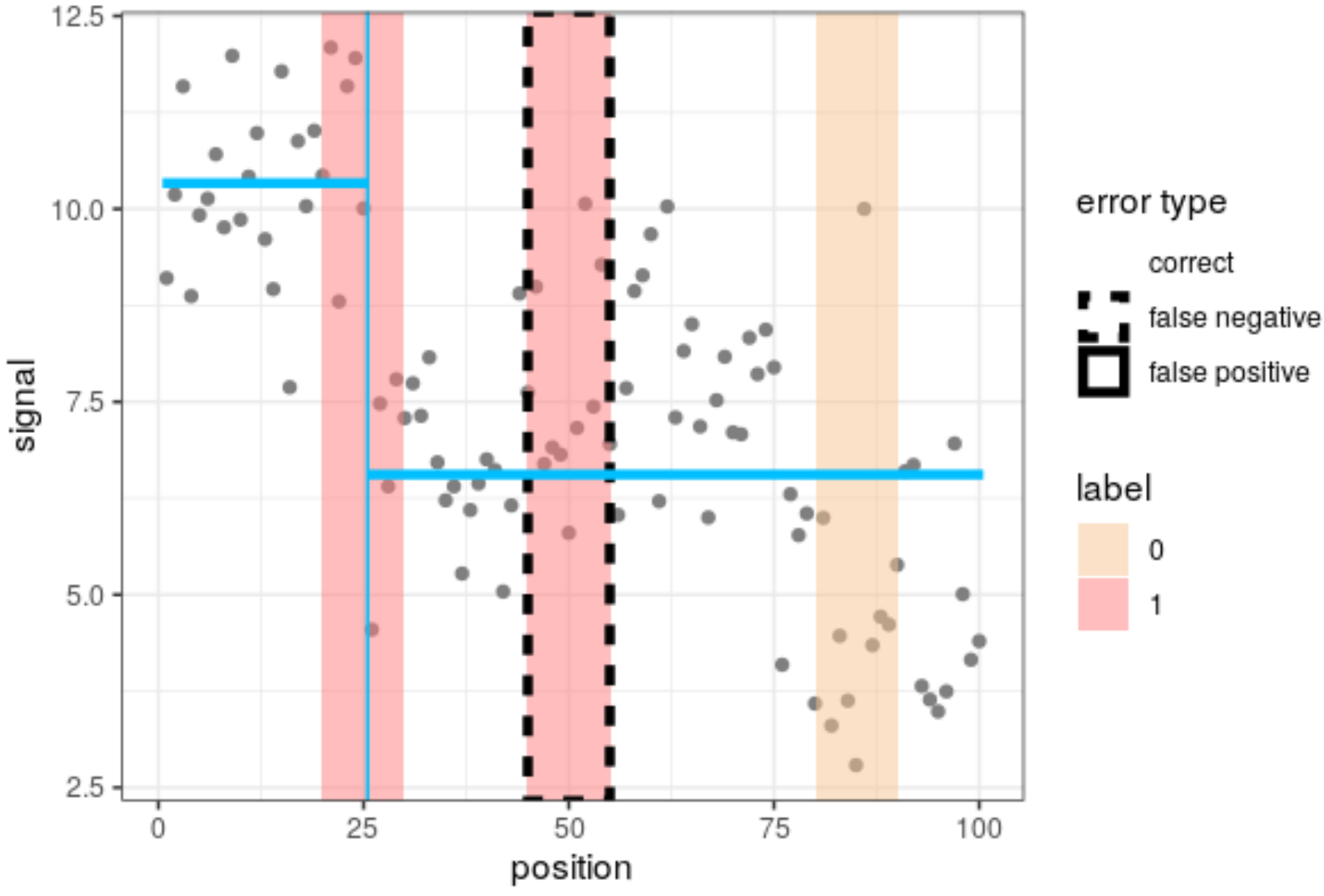
Example noisy data sequence with labels



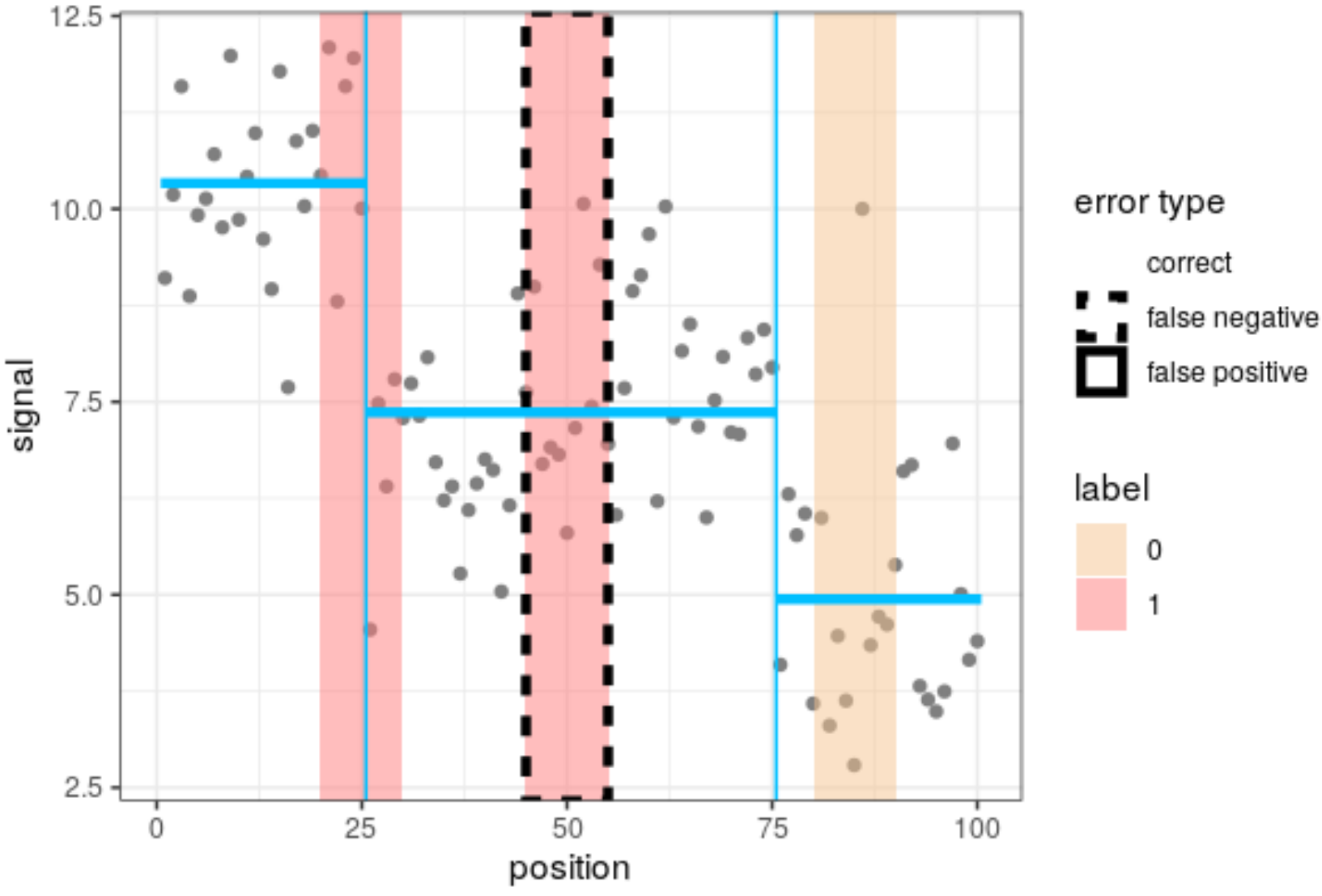
OPART with penalty $\lambda = 1000$ (ignores labels)



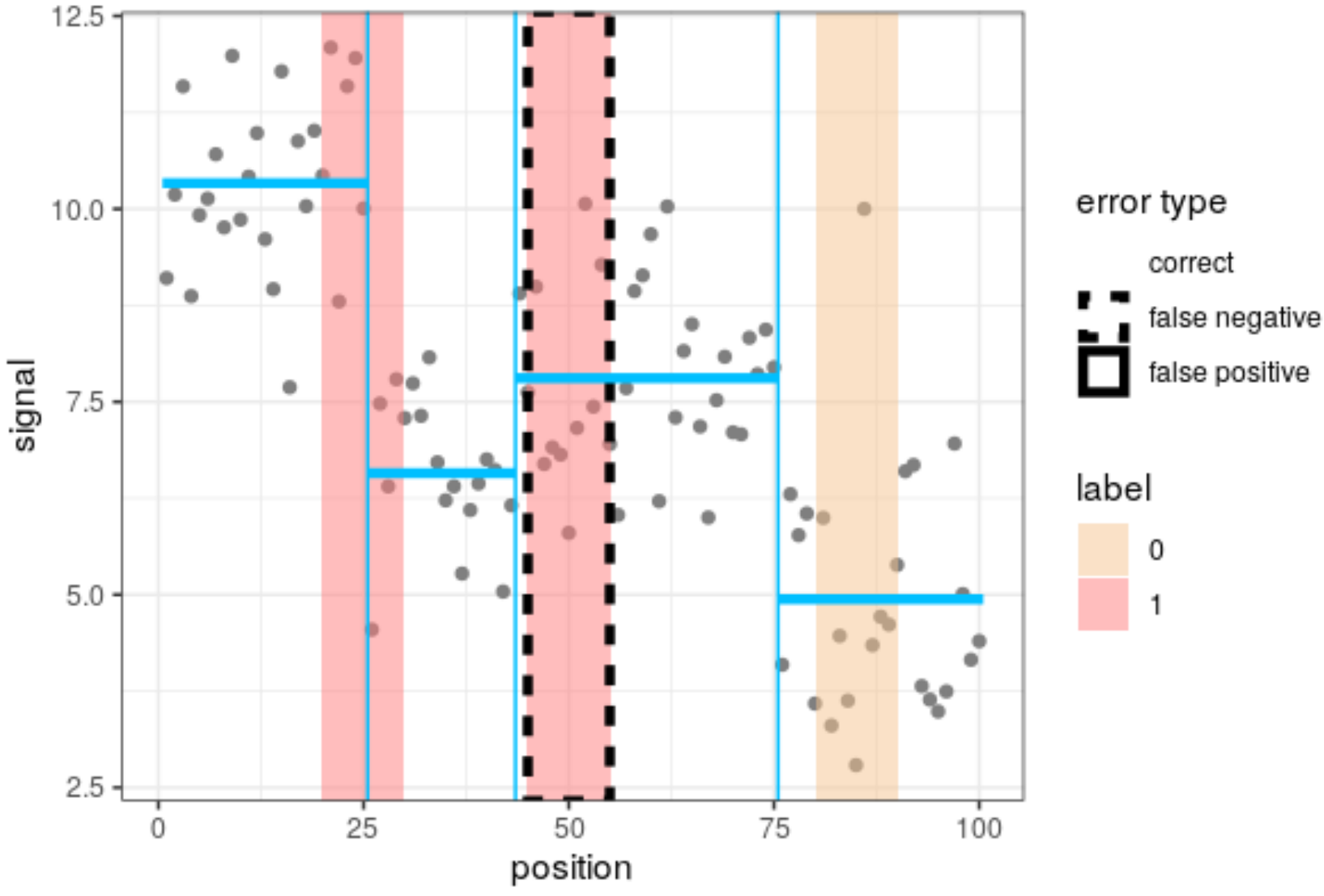
OPART with penalty $\lambda = 100$ (ignores labels)



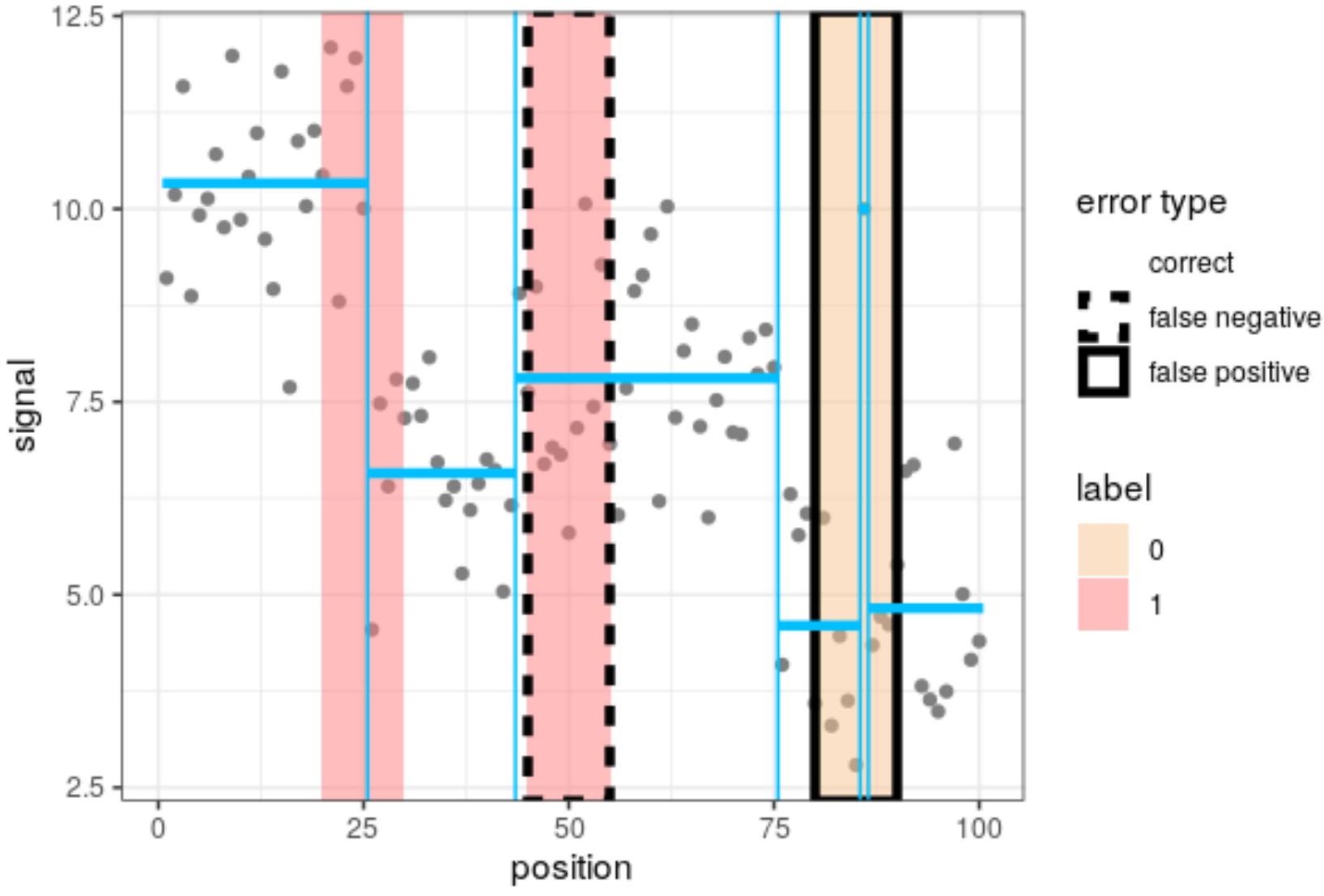
OPART with penalty $\lambda = 20$ (ignores labels)



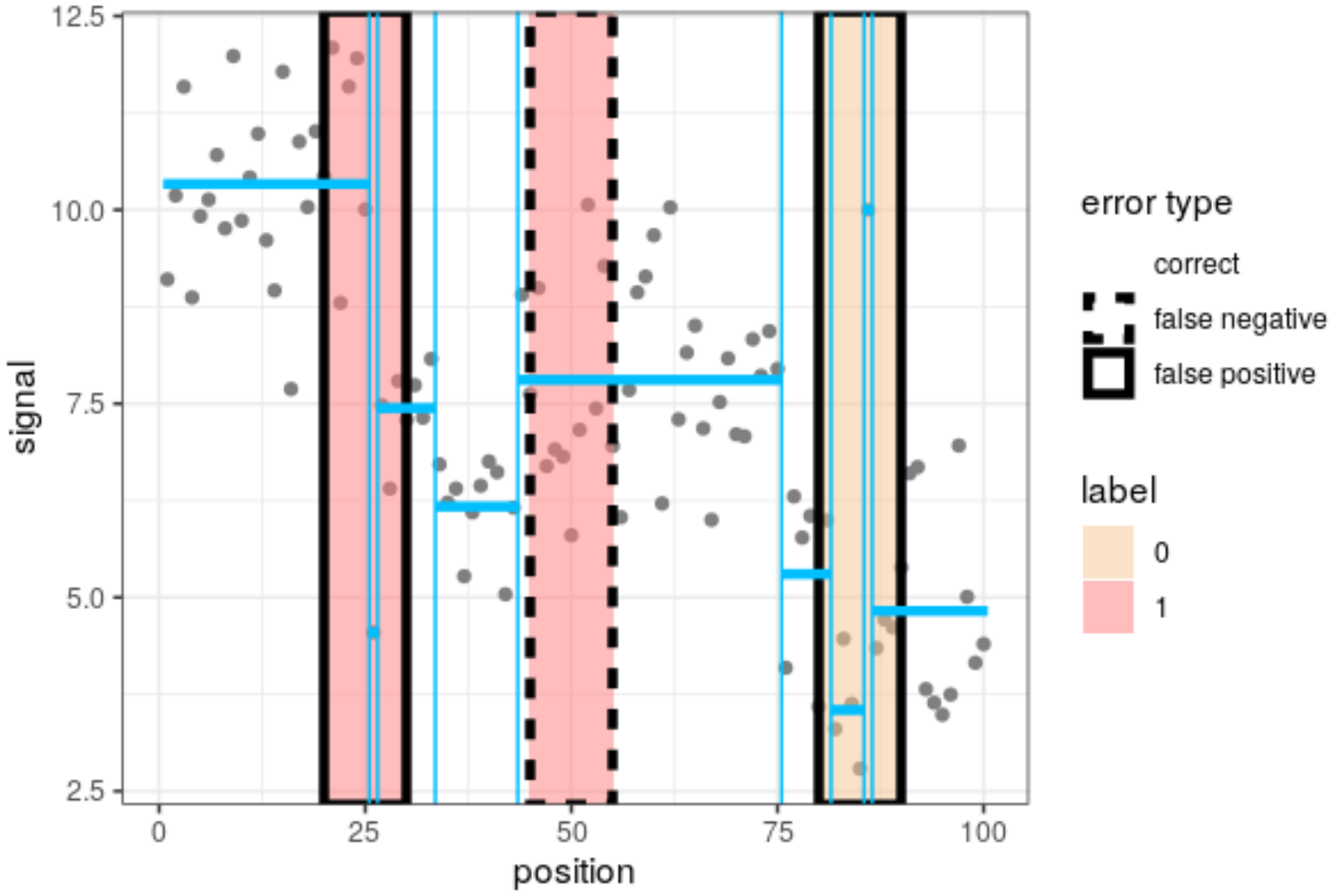
OPART with penalty $\lambda = 15$ (ignores labels)



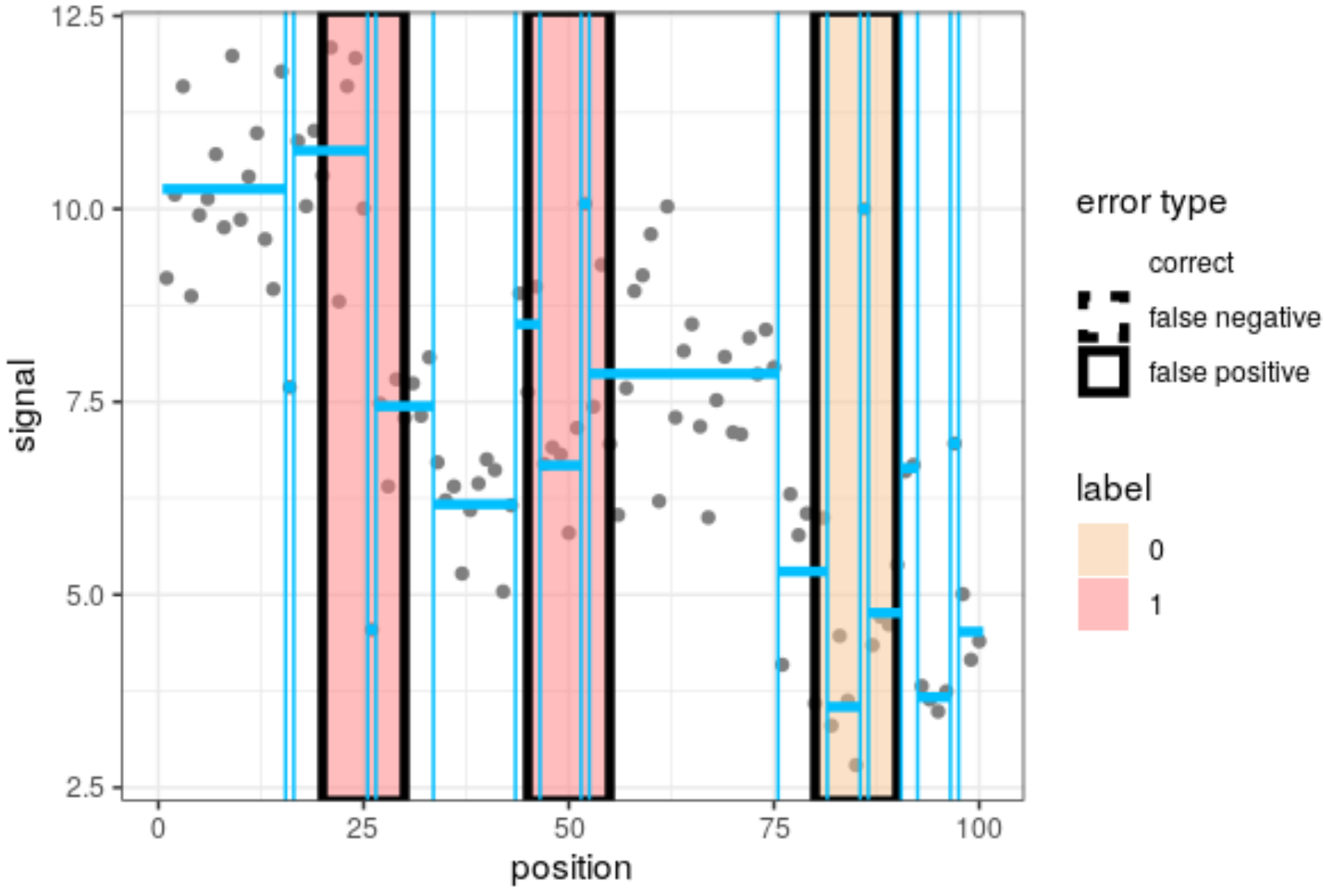
OPART with penalty $\lambda = 10$ (ignores labels)



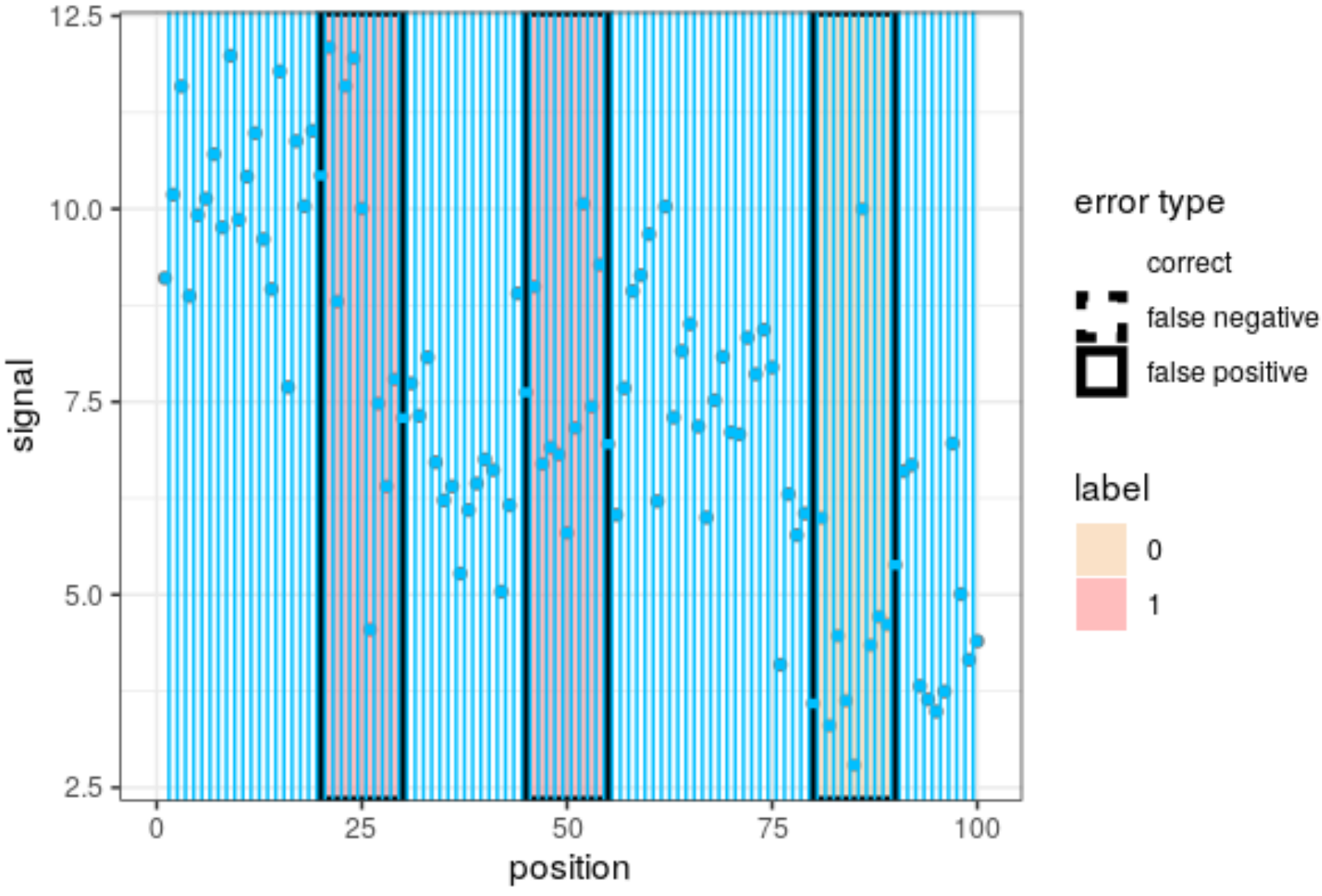
OPART with penalty $\lambda = 5$ (ignores labels)



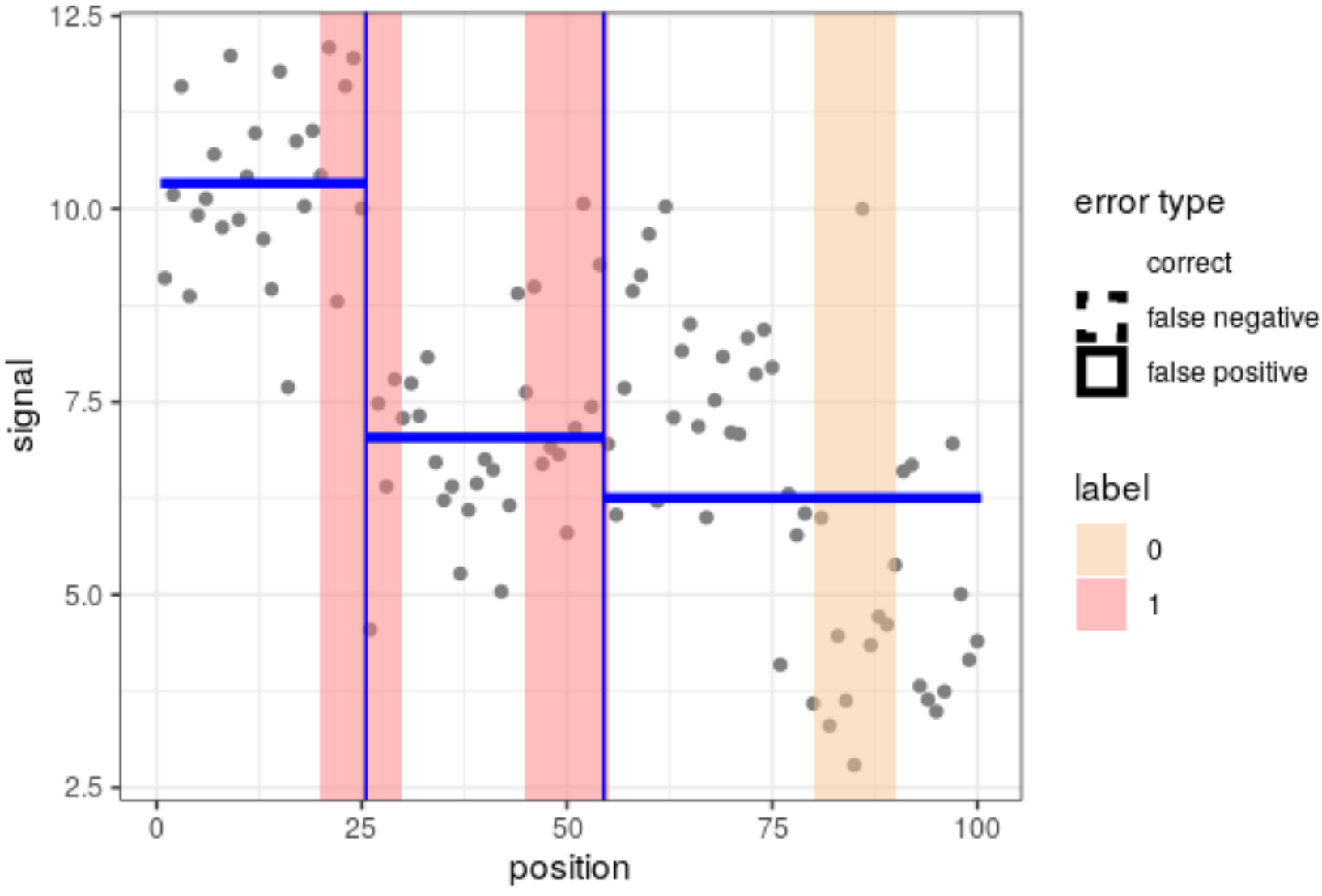
OPART with penalty $\lambda = 4$ (ignores labels)



OPART with penalty $\lambda = 0$ (ignores labels)



SegAnnot (no changes in unlabeled regions)



Introduction: supervised changepoint detection for cancer diagnosis with DNA copy number data

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Results and Discussion

Baseline/previous OPART algorithm

Assume

- $\mathbf{x} = [x_1 \cdots x_N]$ is the sequence of N data,
- ℓ is a loss function (e.g. square loss),
- I the indicator function counts the number of changes,
- λ is a non-negative penalty (larger for fewer changes).

Then the problem and algorithm are

$$\begin{aligned} \hat{C}_N &= \min_{\mathbf{m}\in\mathbb{R}^N} \sum_{i=1}^{N} \ell(m_i, x_i) + \lambda \sum_{i=1}^{N-1} I[m_i \neq m_{i+1}]. \\ &= \min_{\tau\in\{0,1,\ldots,N-1\}} \hat{C}_\tau + \lambda + L(\tau+1, N, \mathbf{x}). \end{aligned}$$

where

- τ is the last changepoint optimization variable,
- $\hat{C}_\tau$ is the optimal cost computed in previous iteration τ,
- L is the cost of the last segment.

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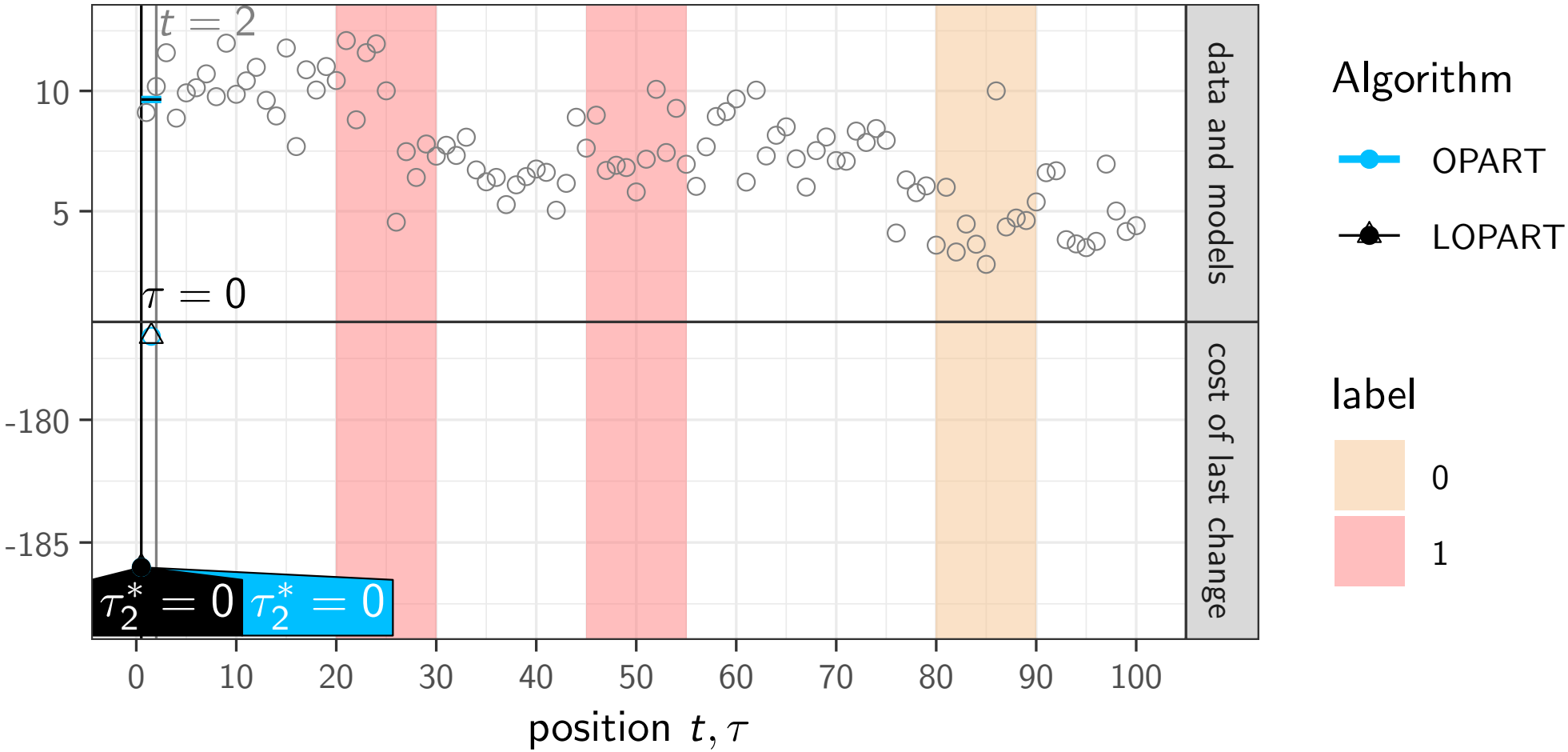
Demonstration of LOPART with penalty $\lambda = 10$



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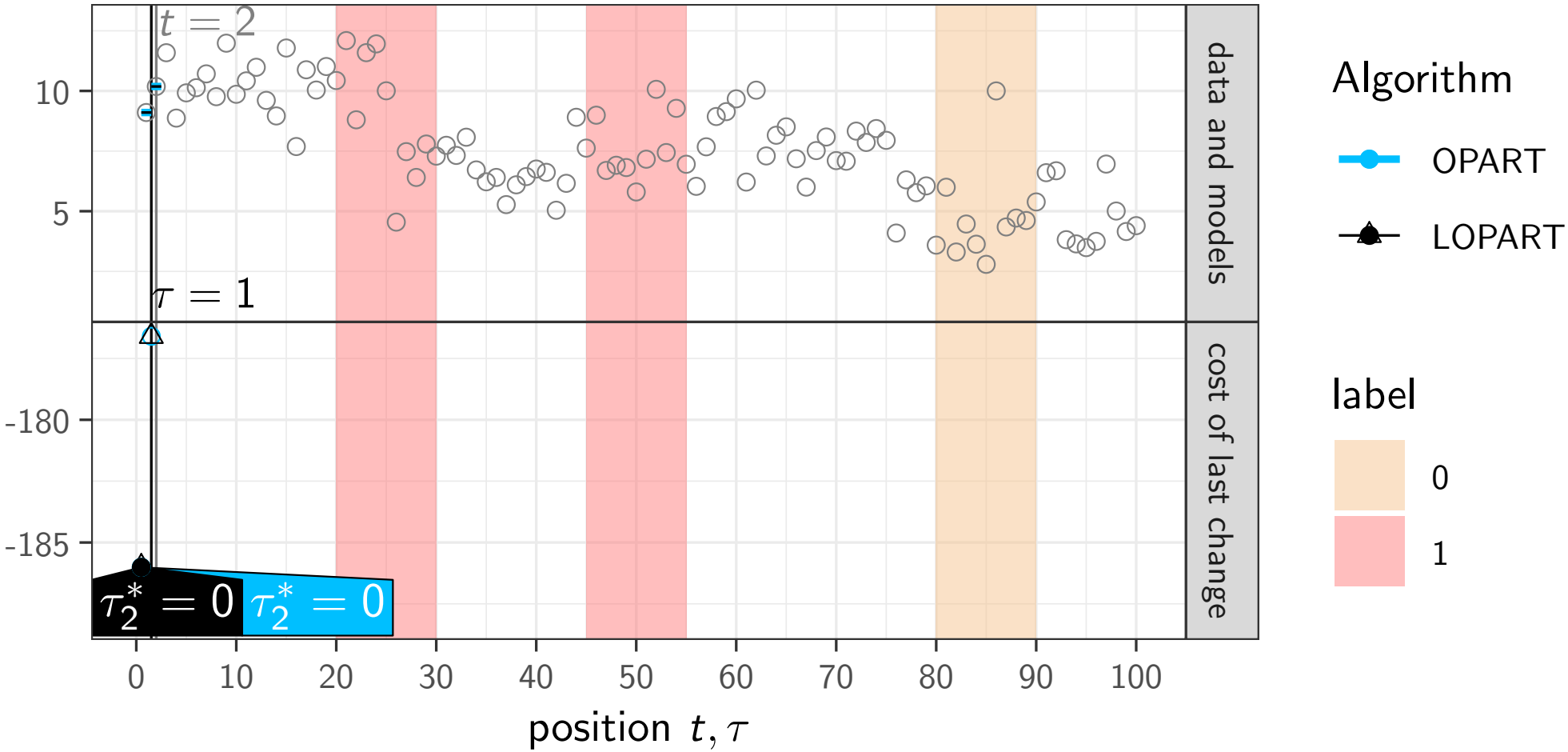

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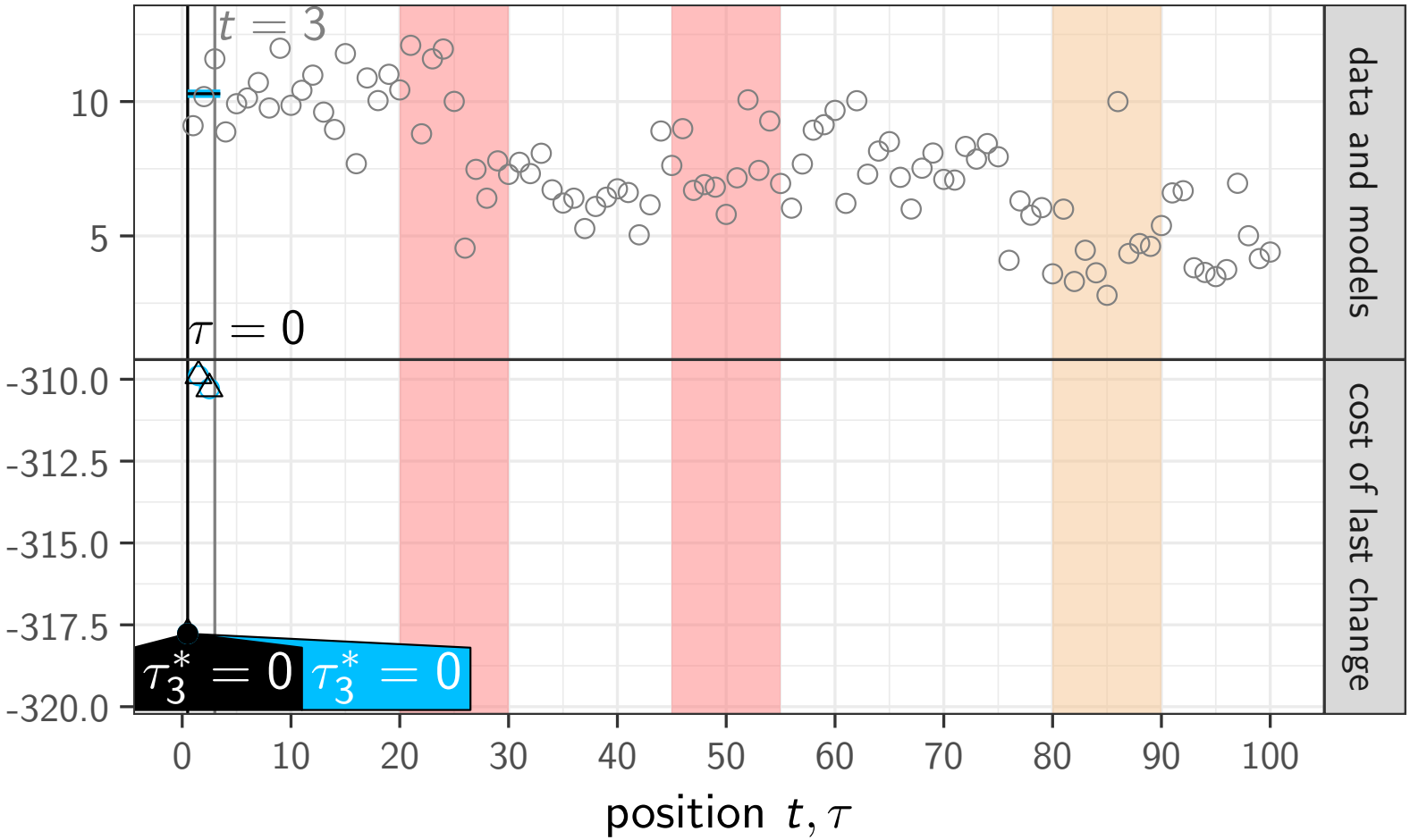

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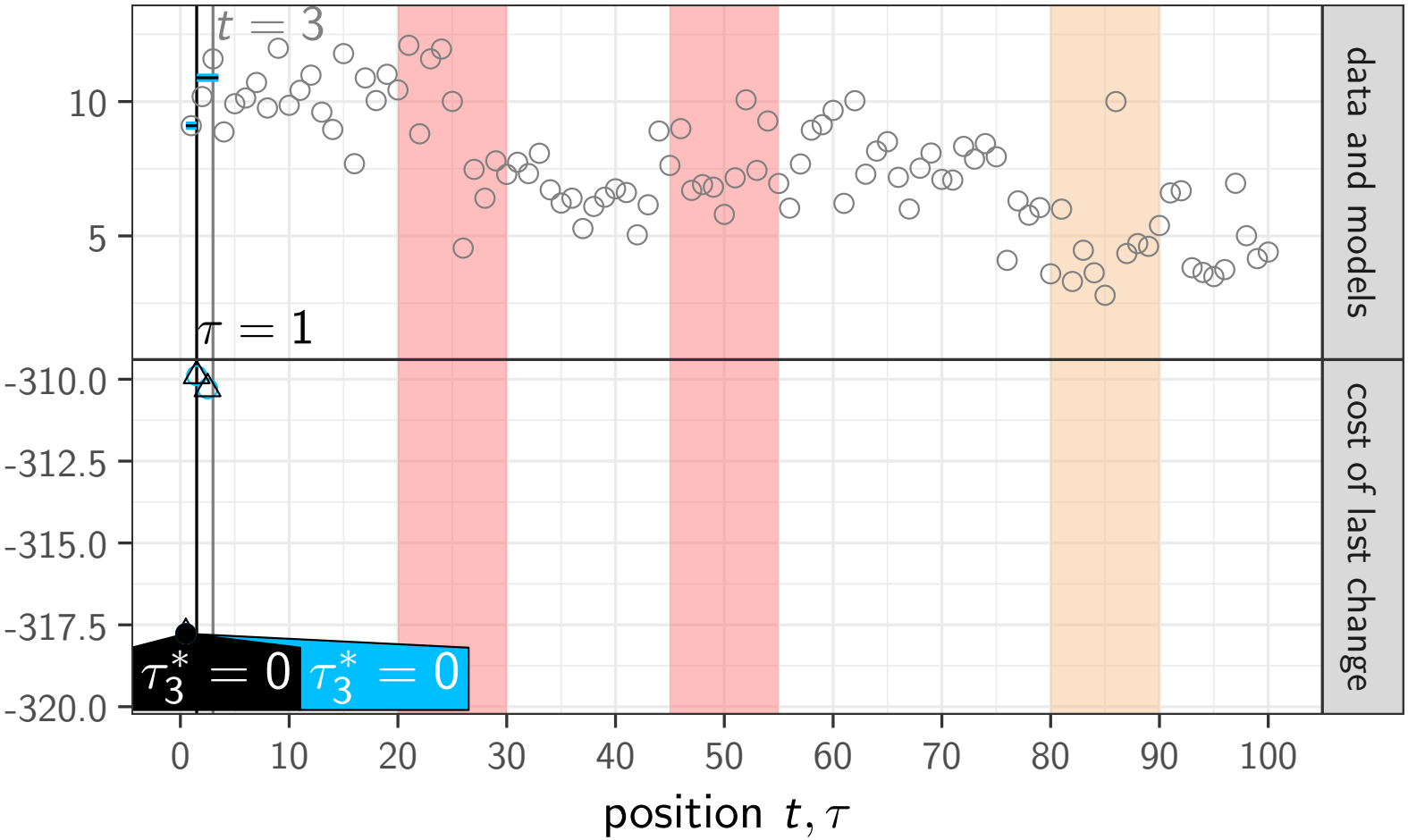

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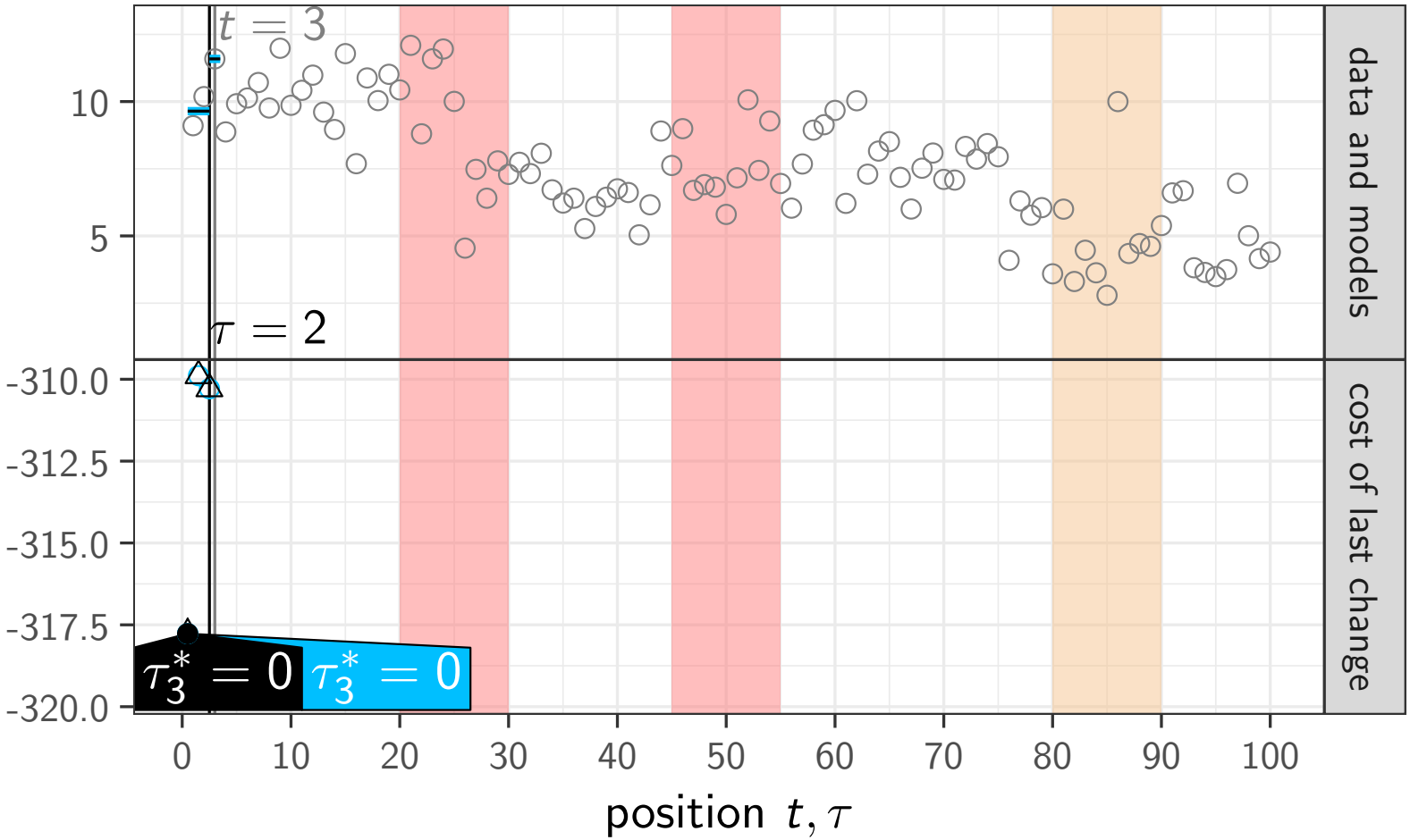

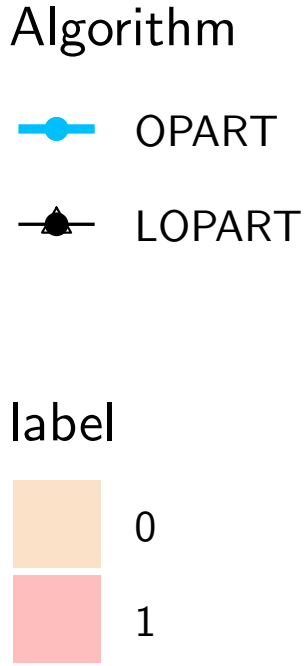

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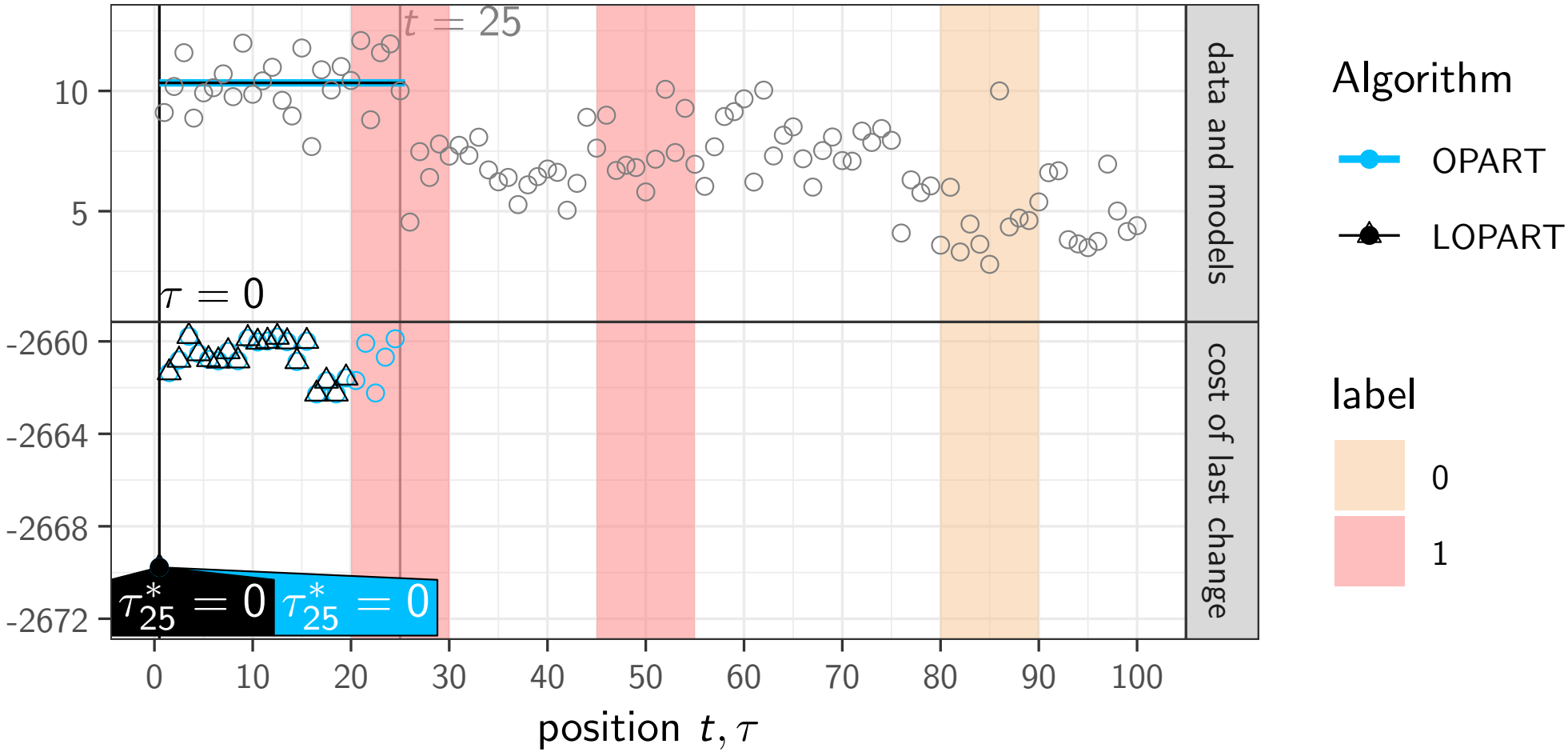

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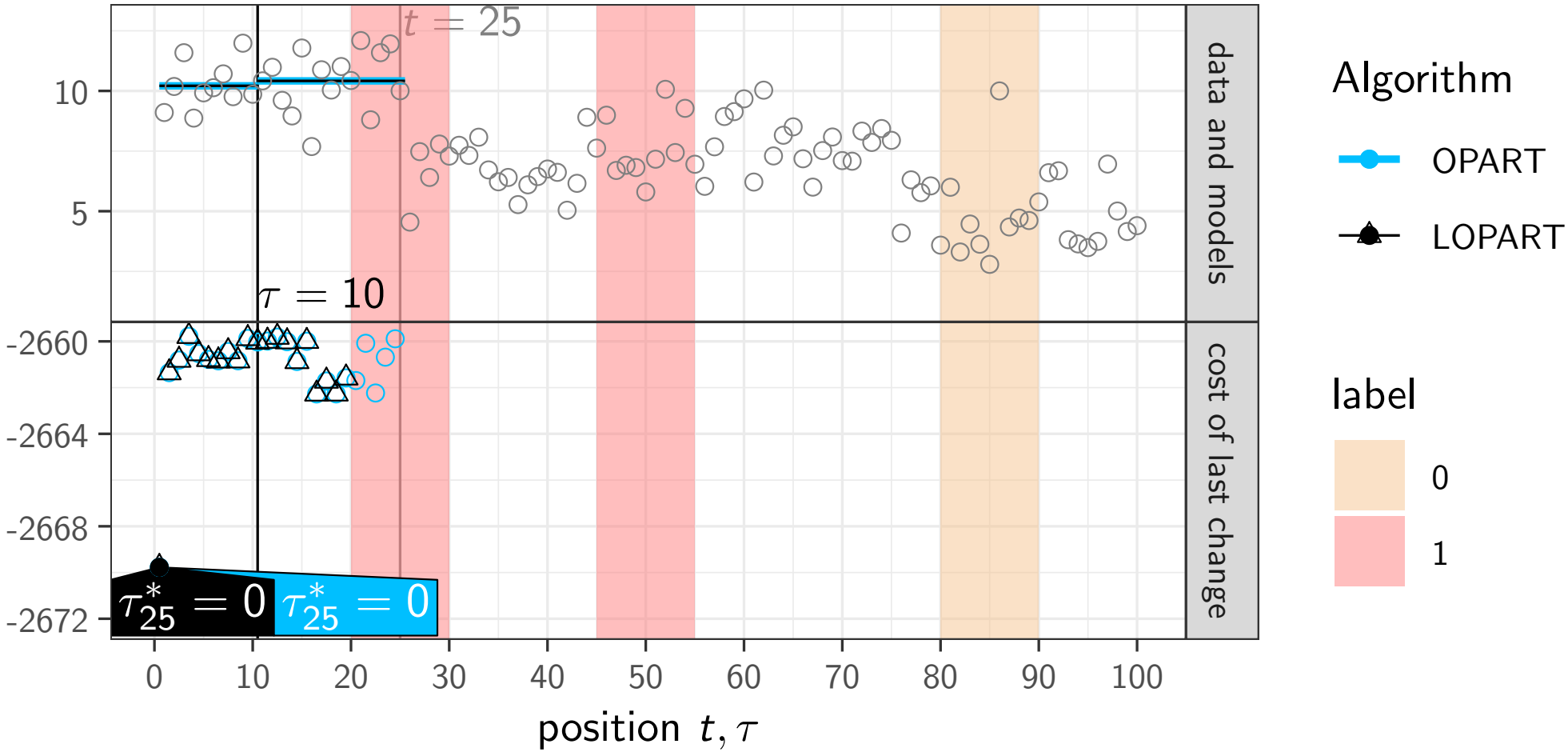

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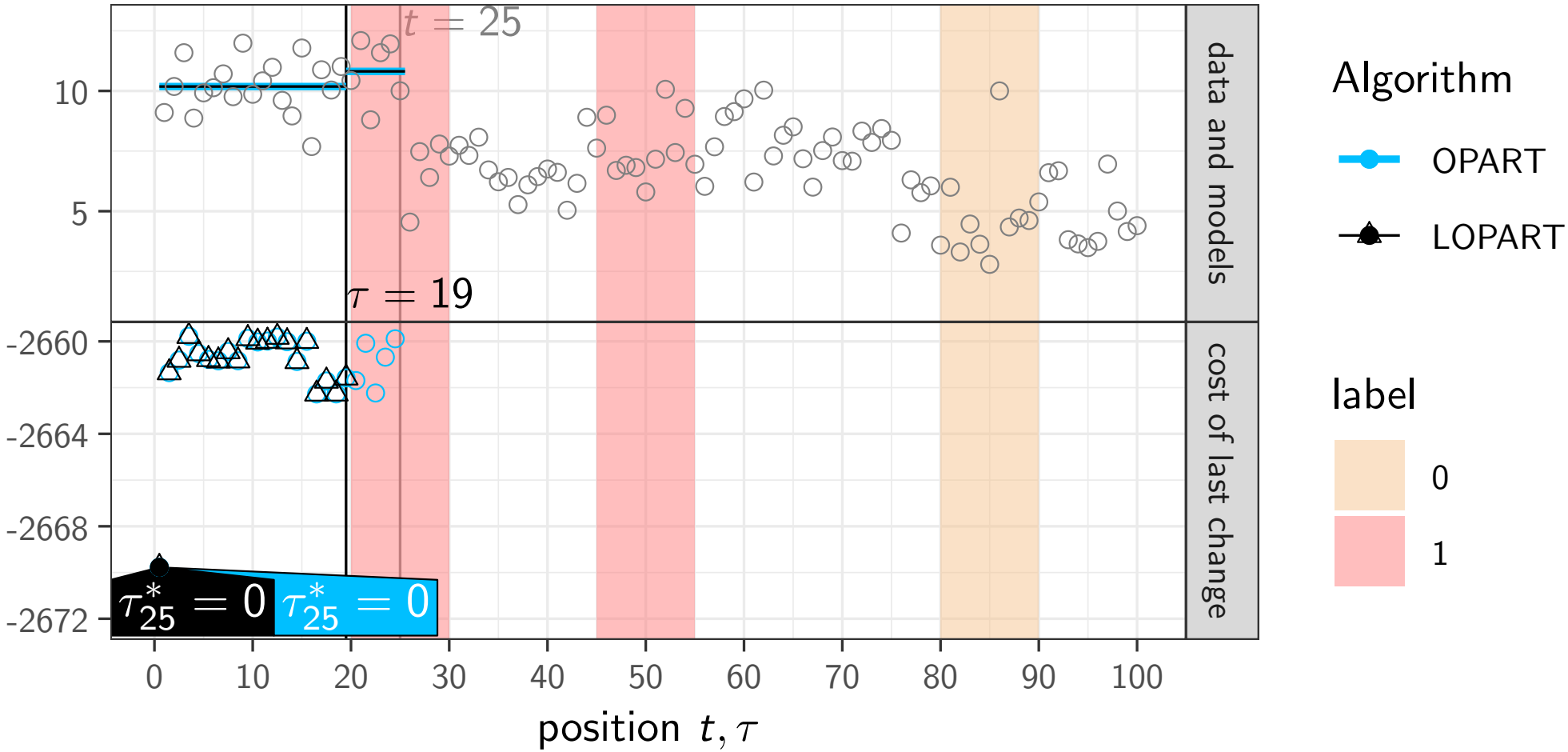

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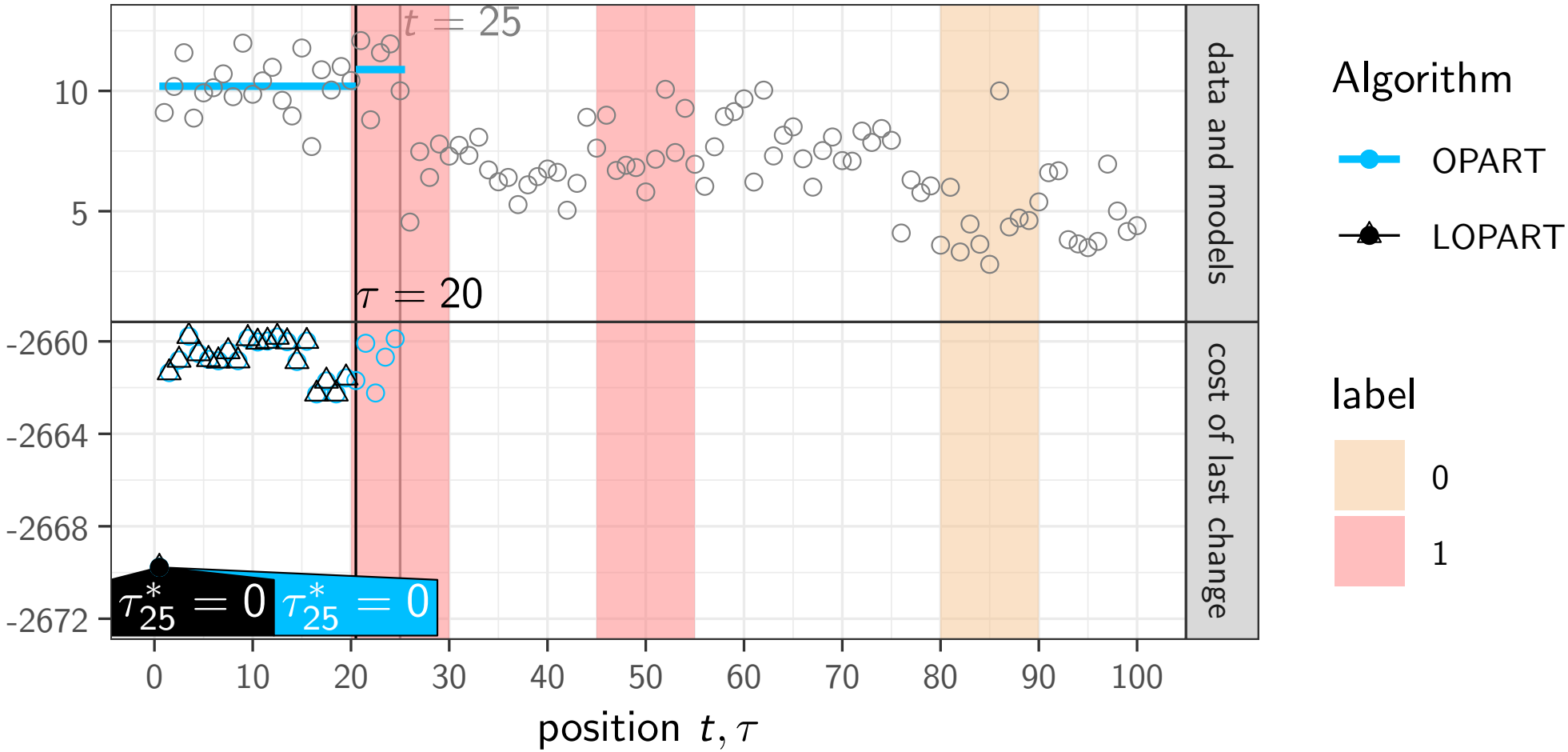

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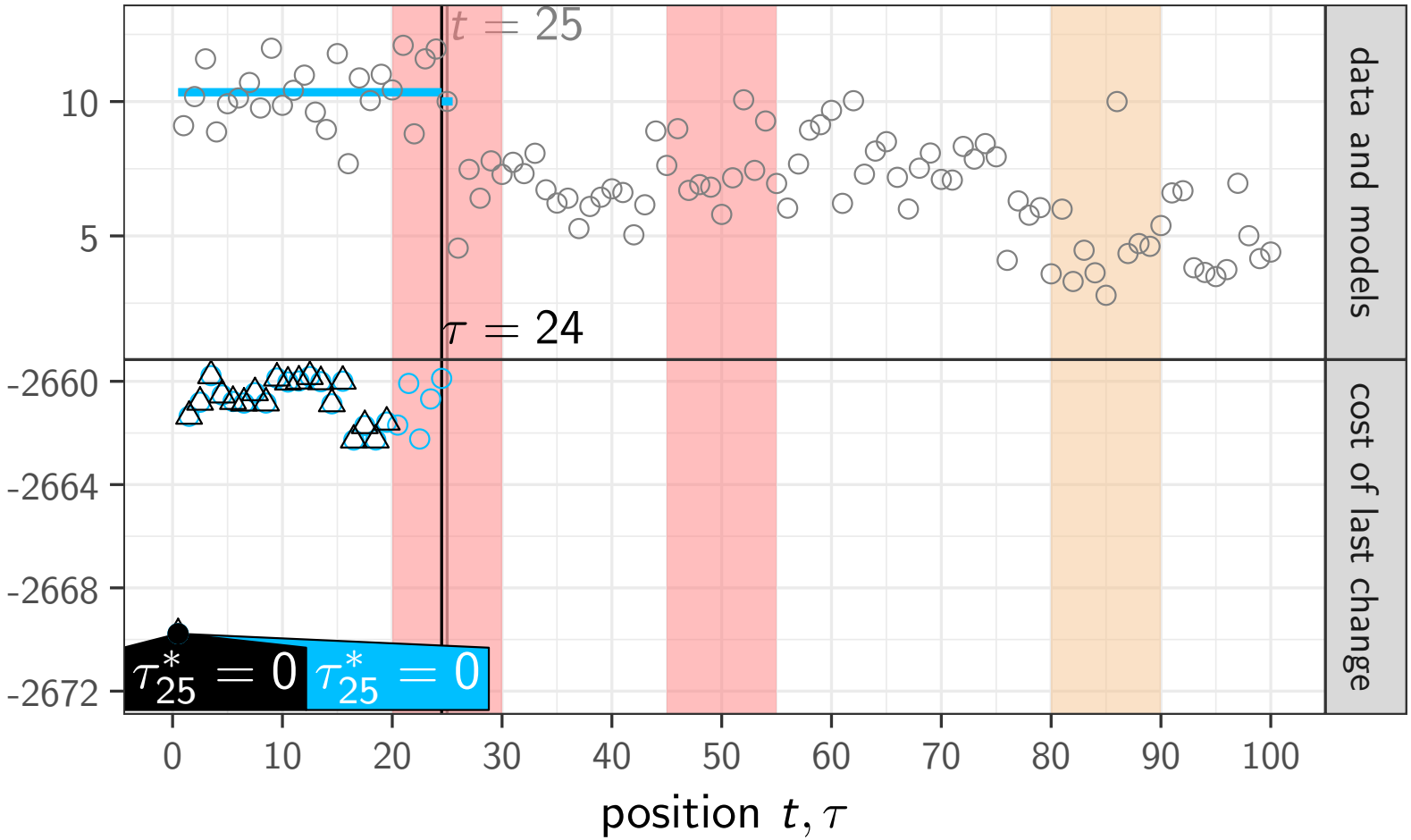

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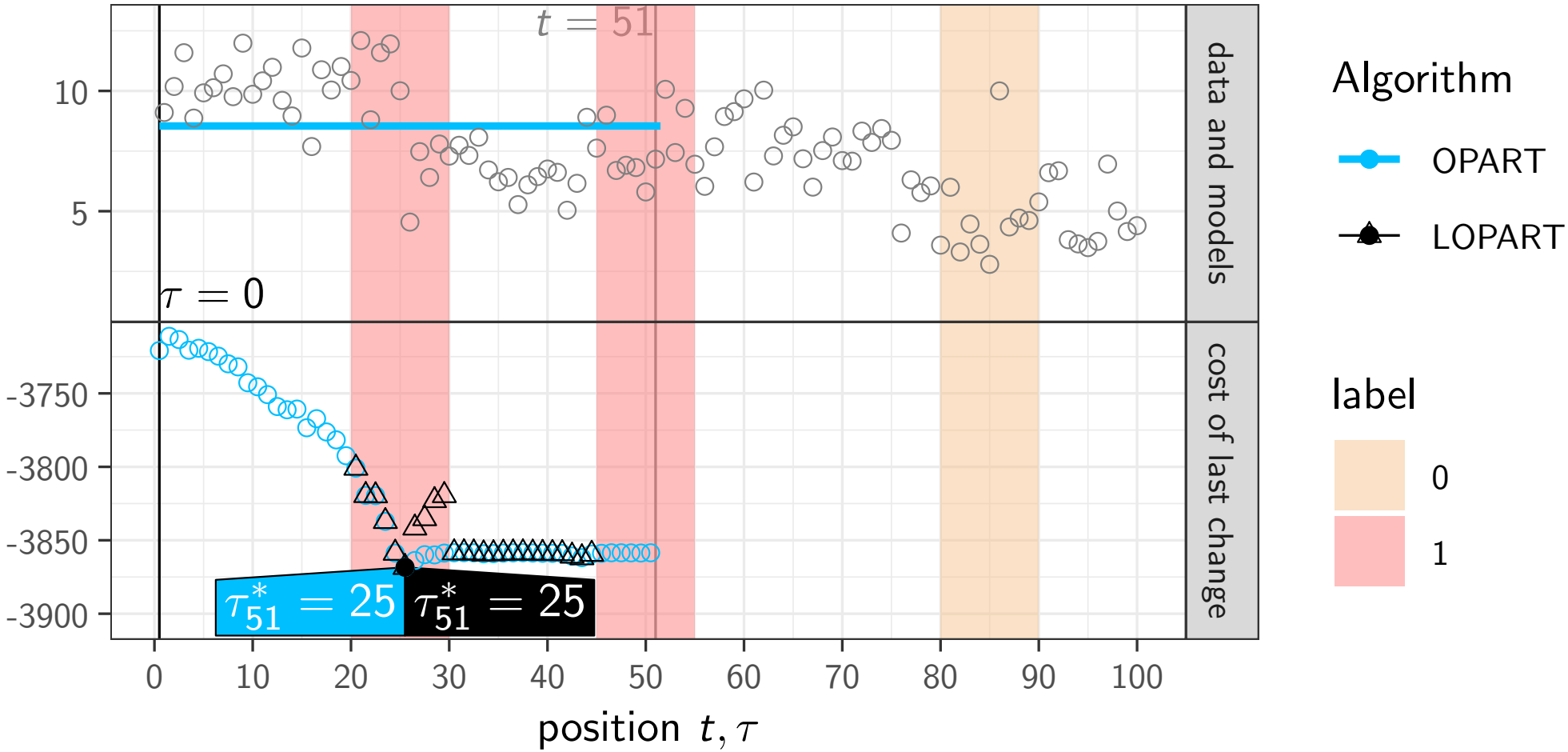

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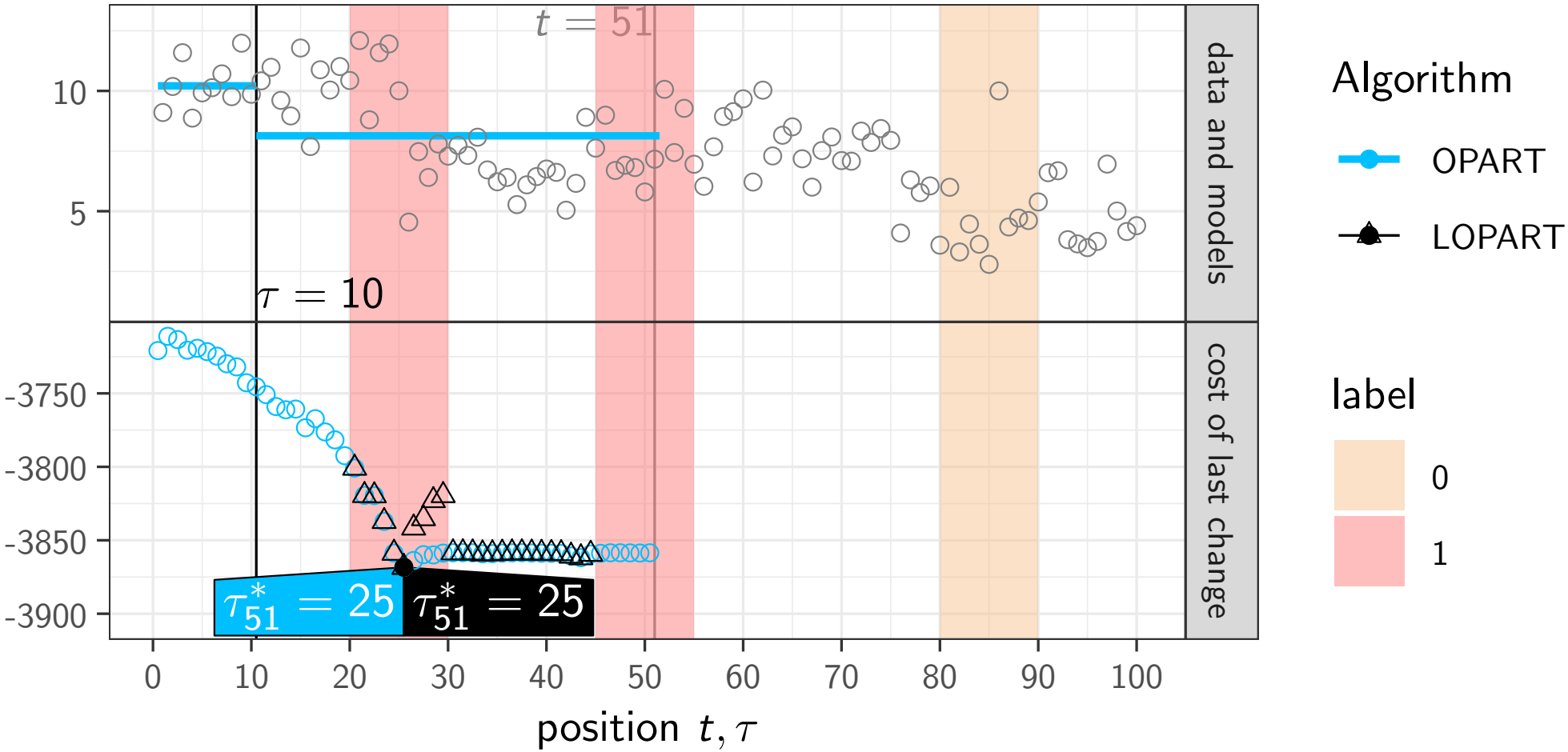

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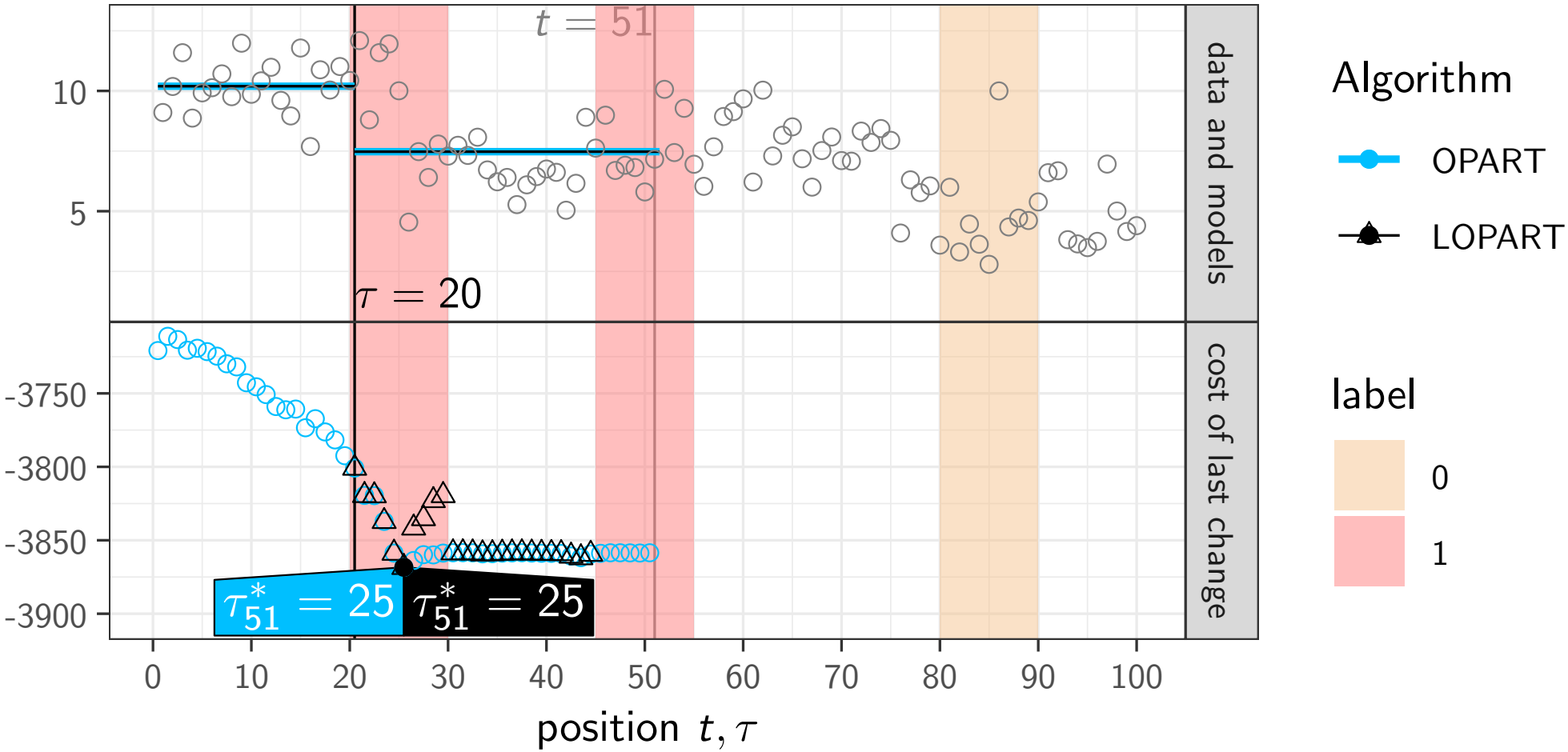

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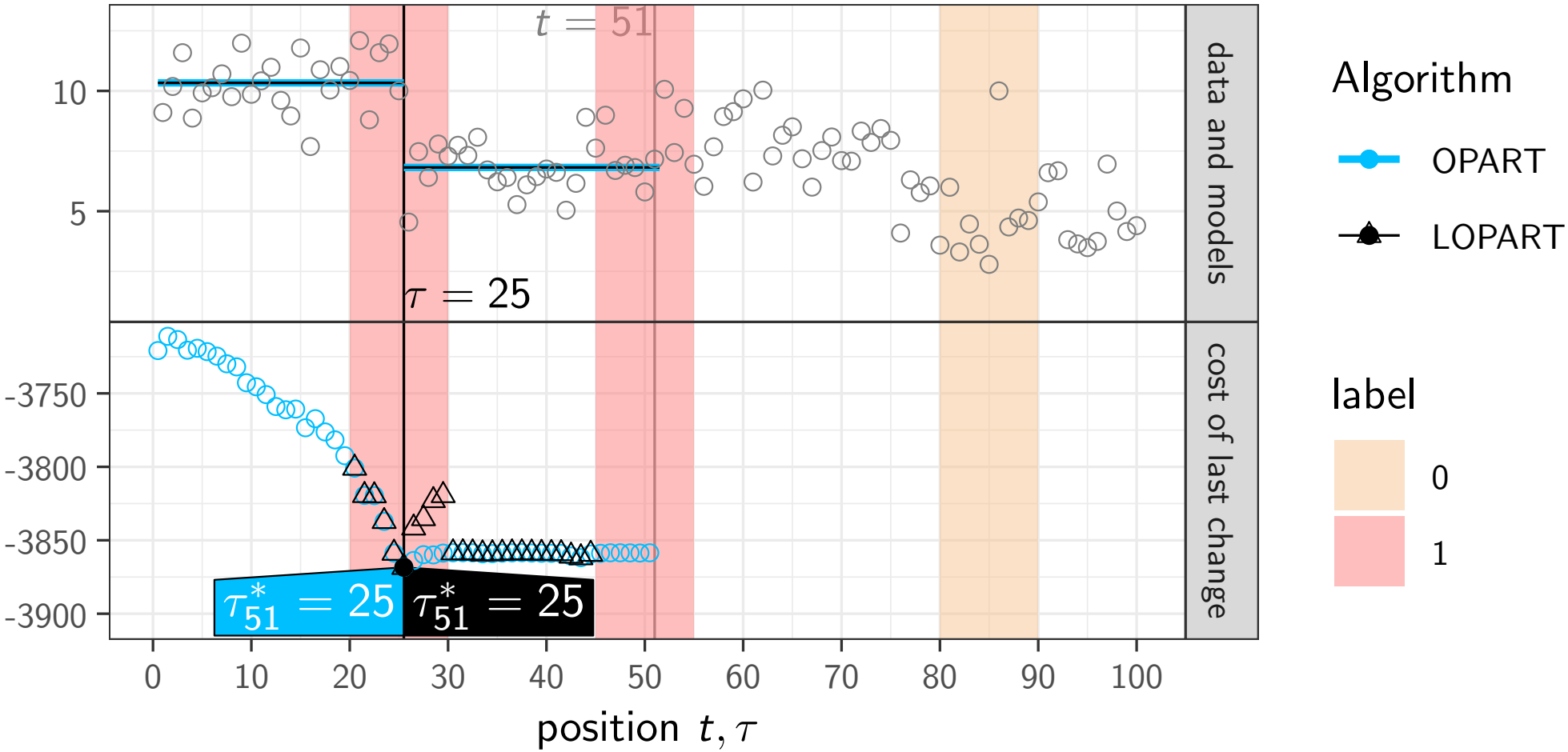

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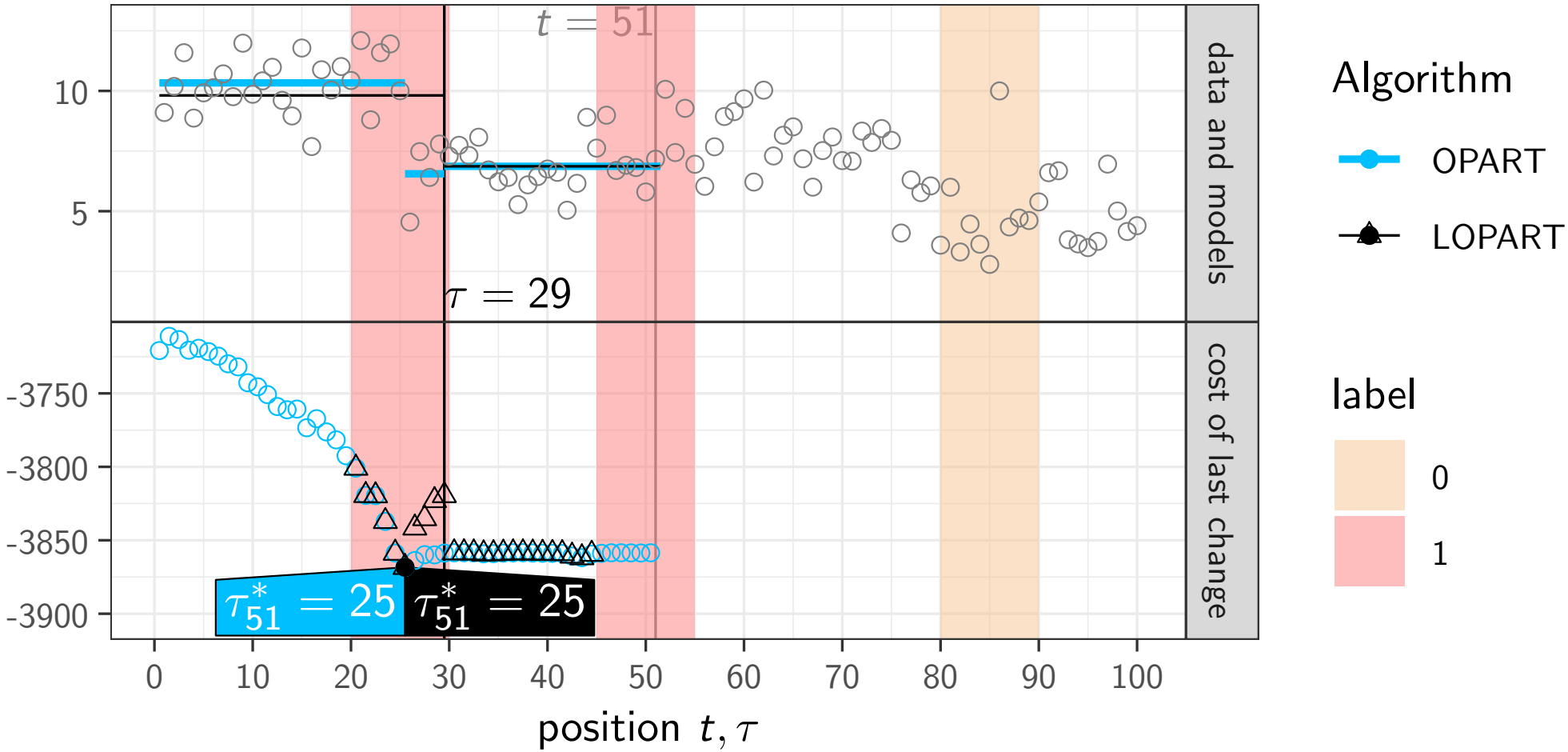

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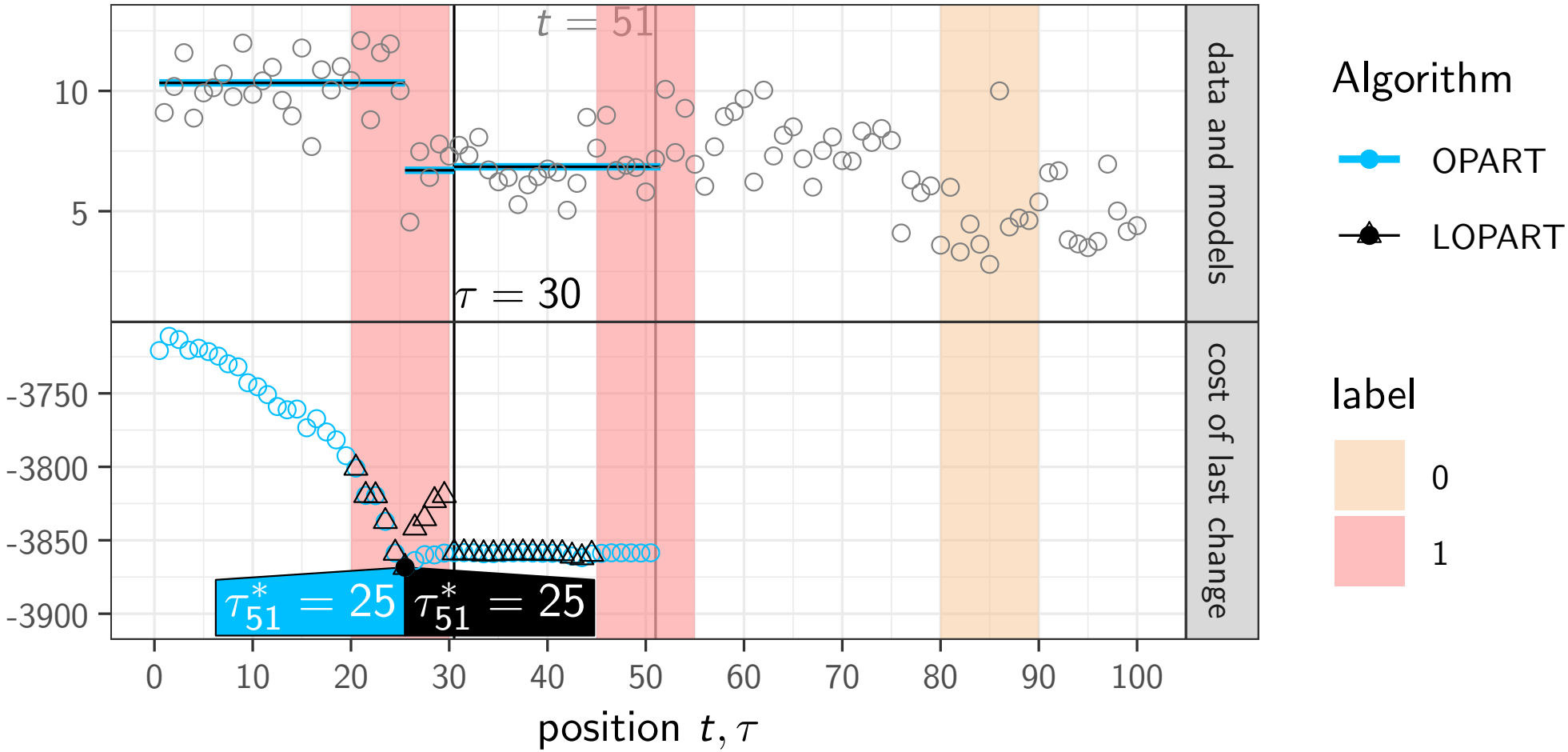

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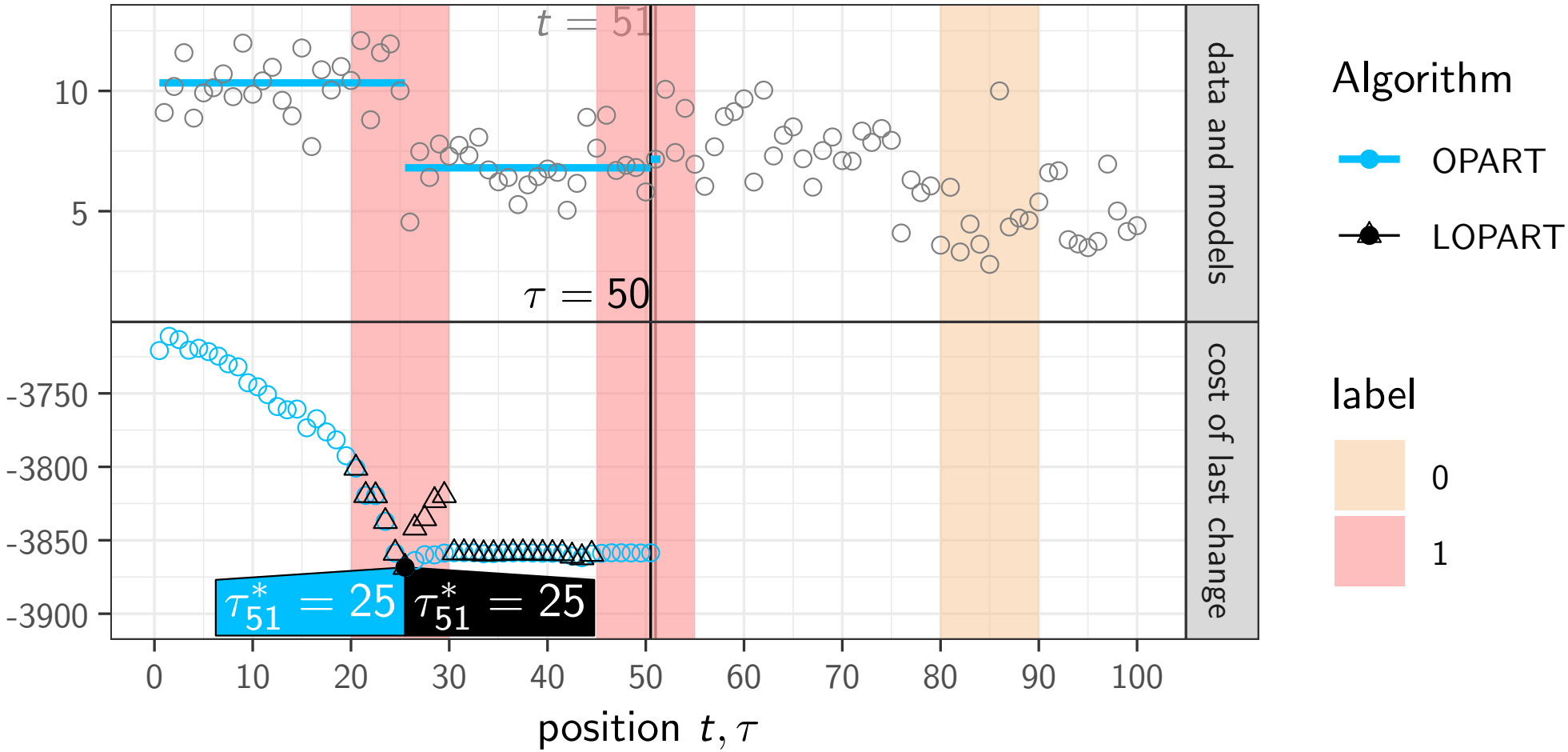

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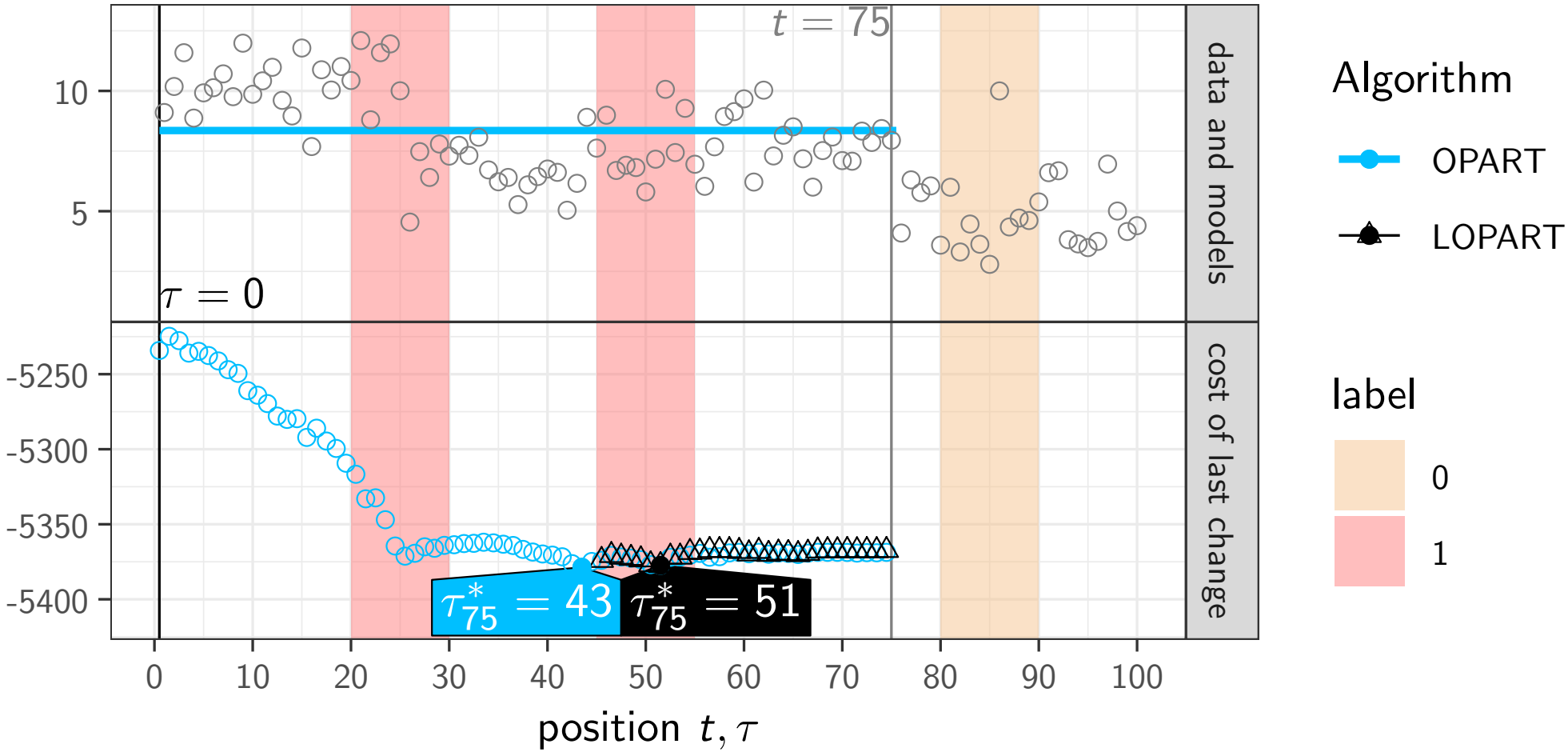

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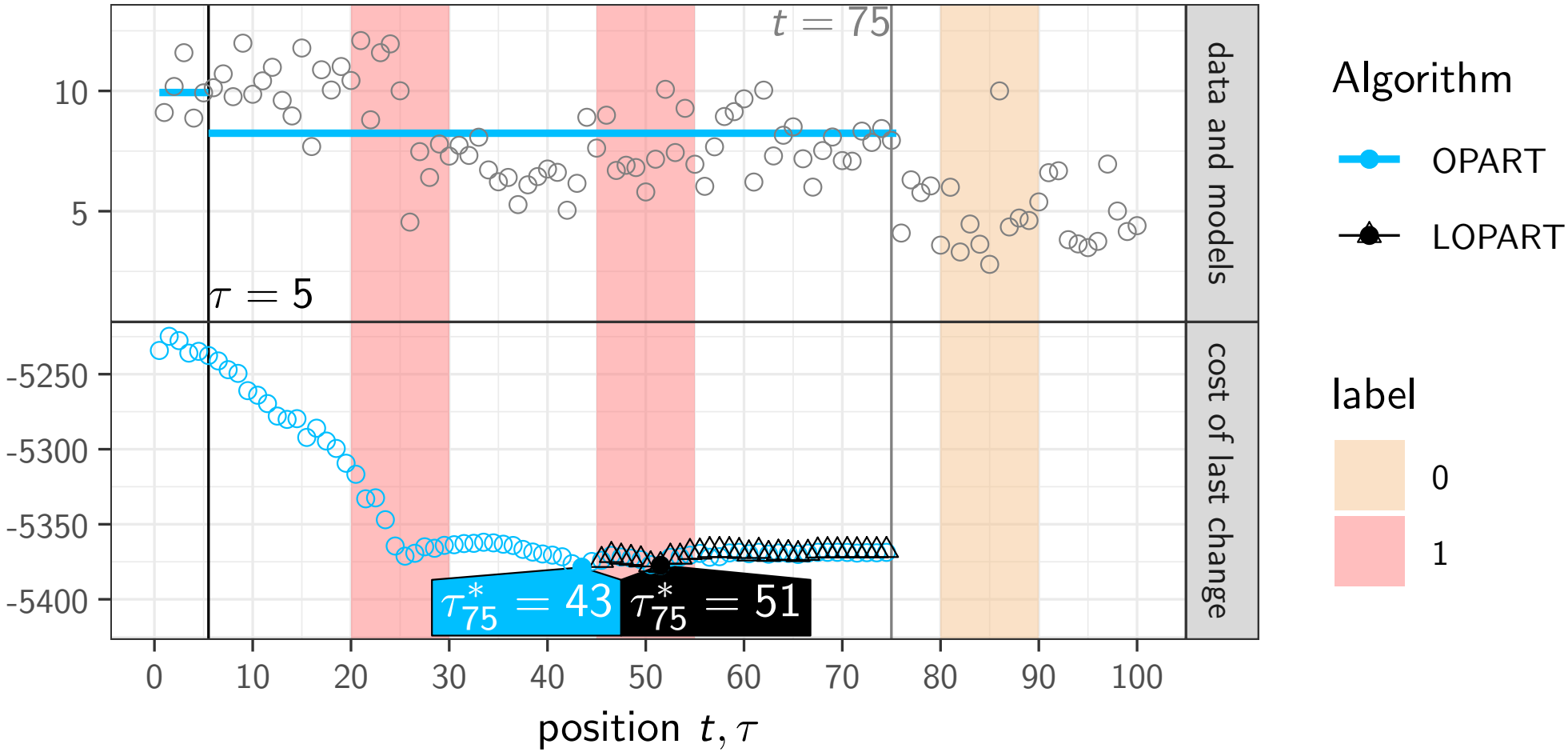

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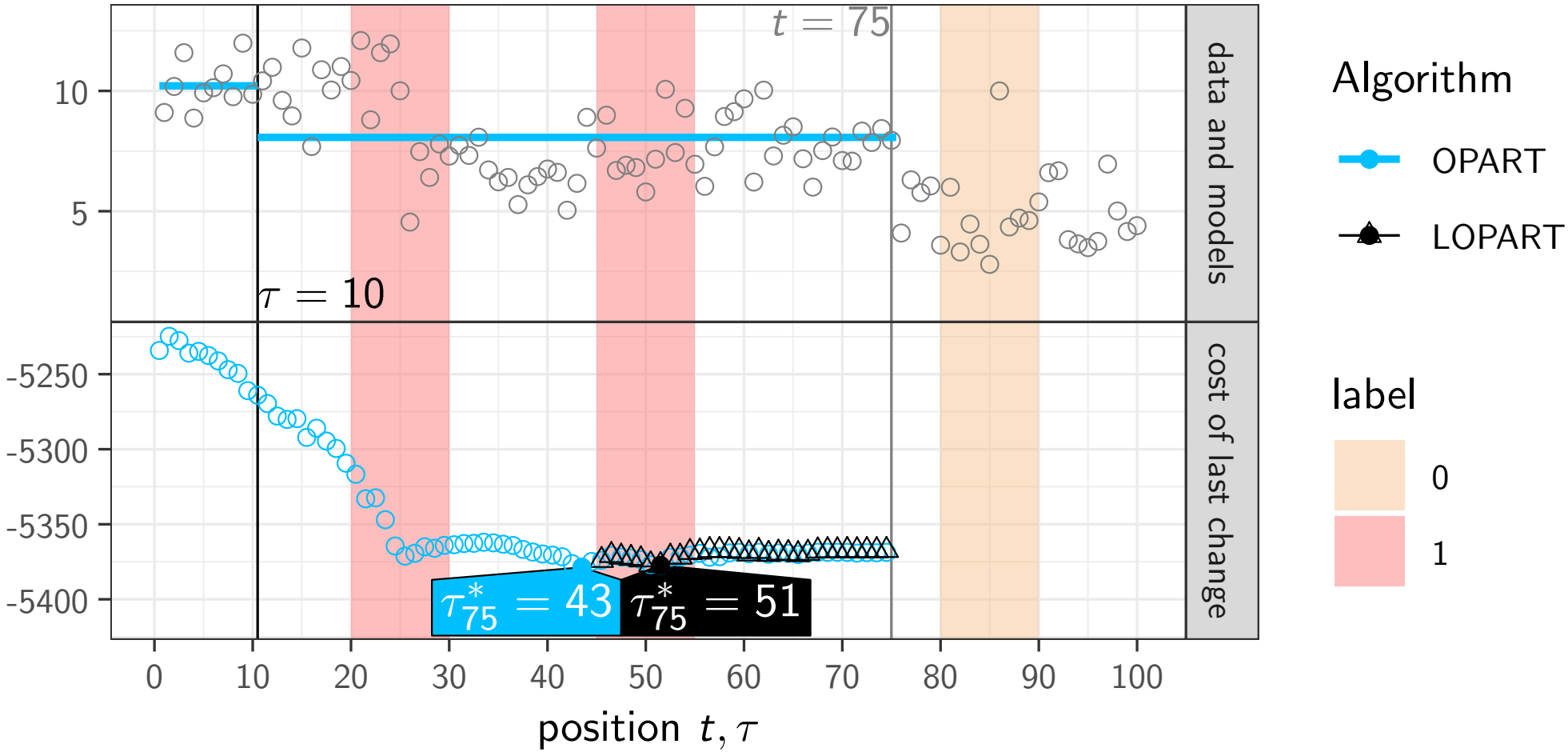

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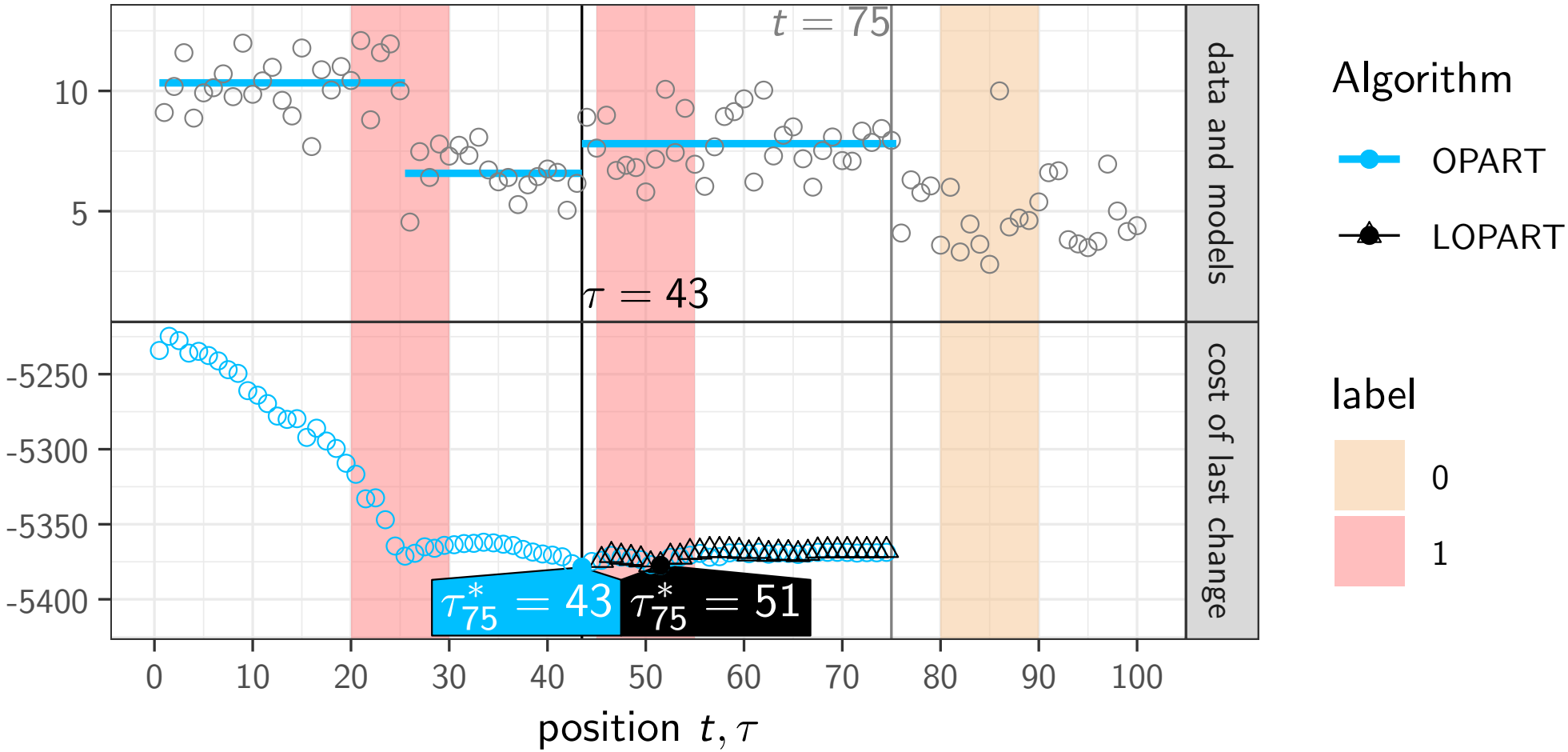

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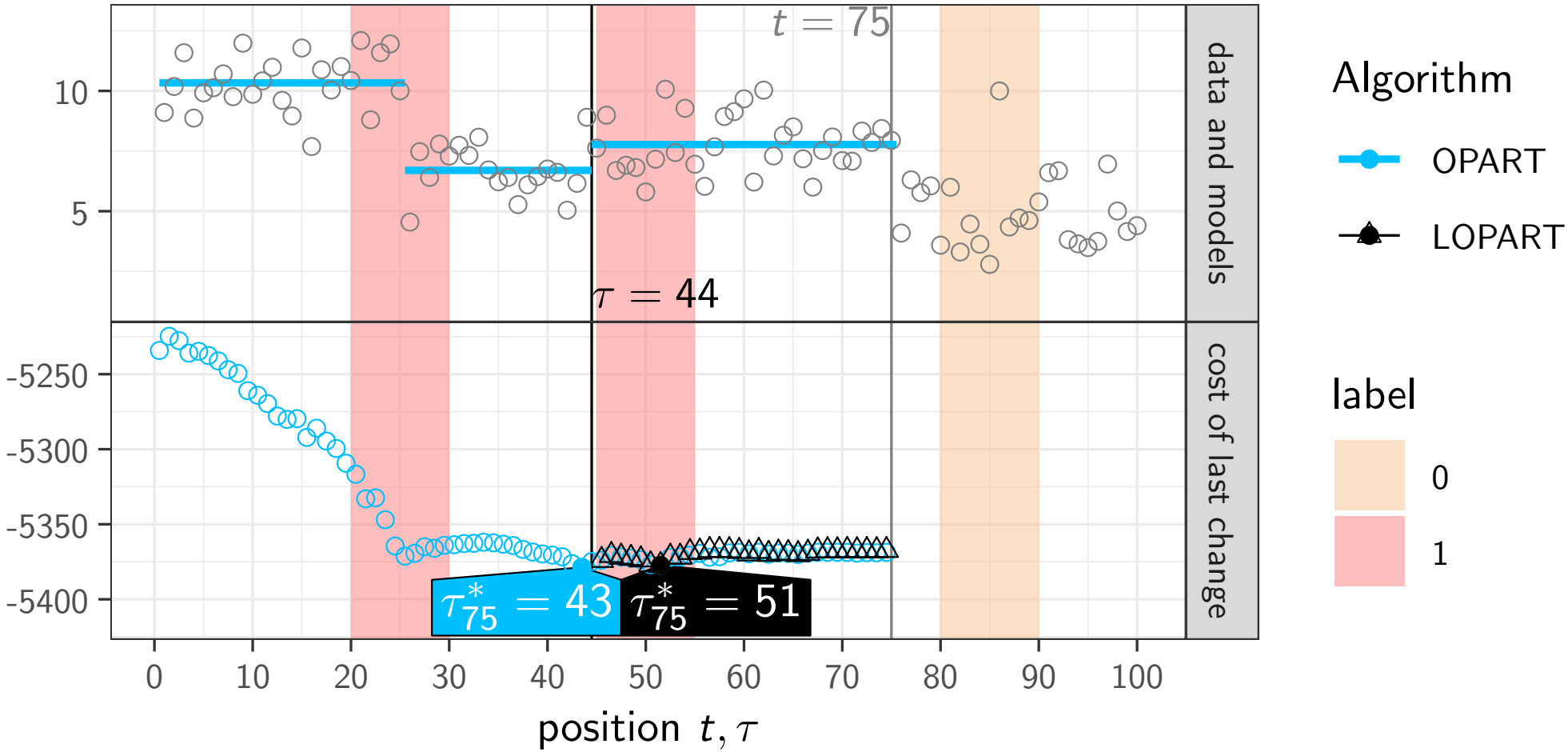

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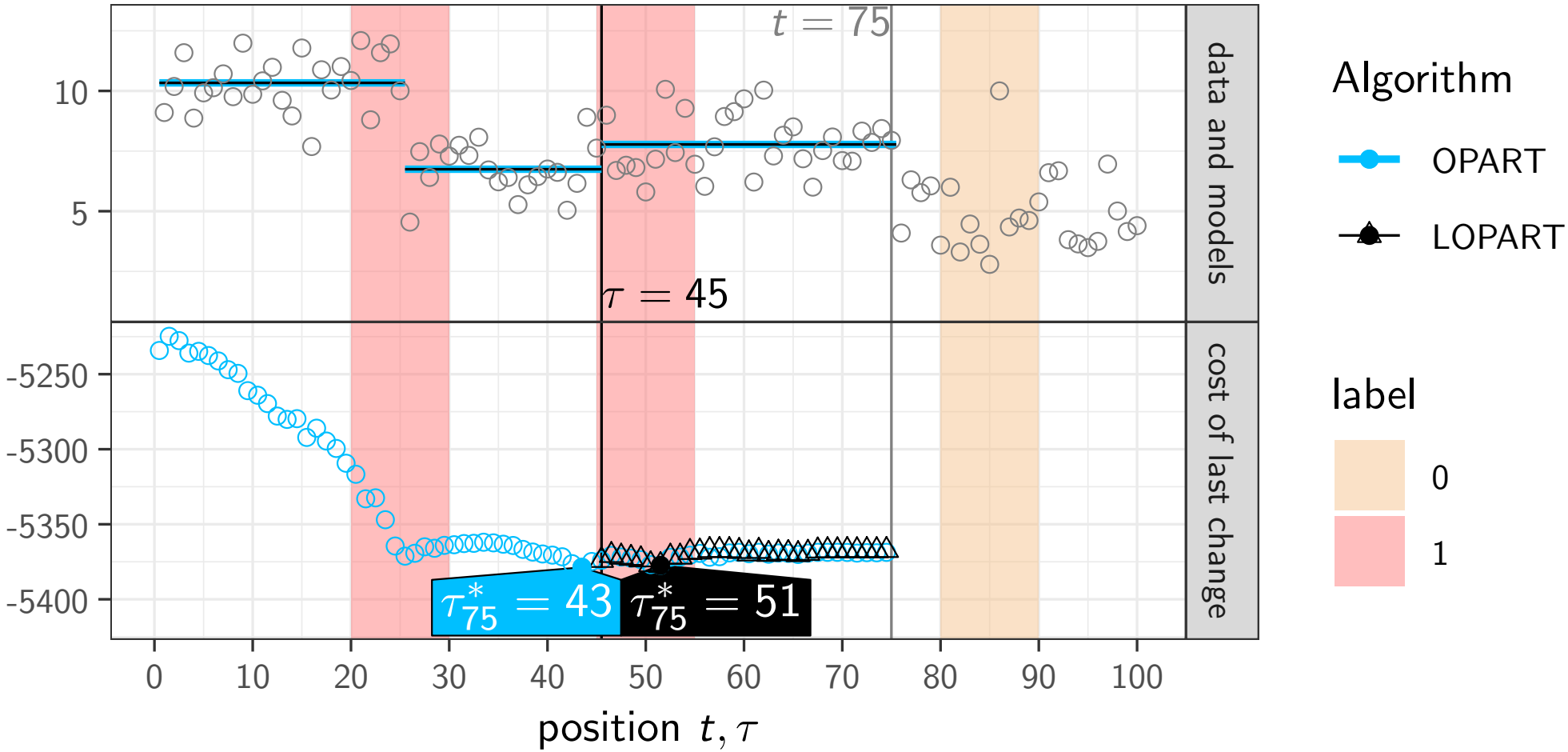

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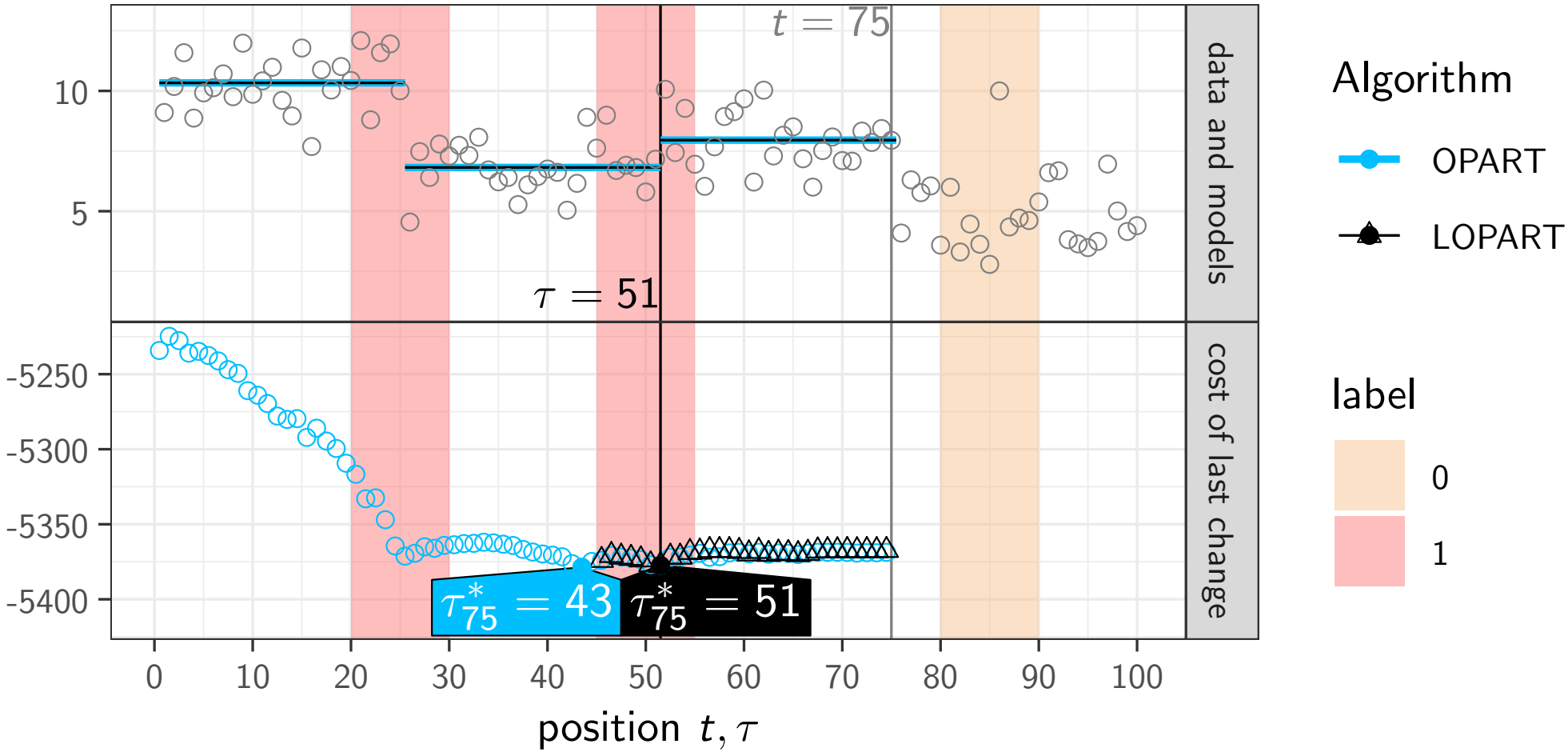

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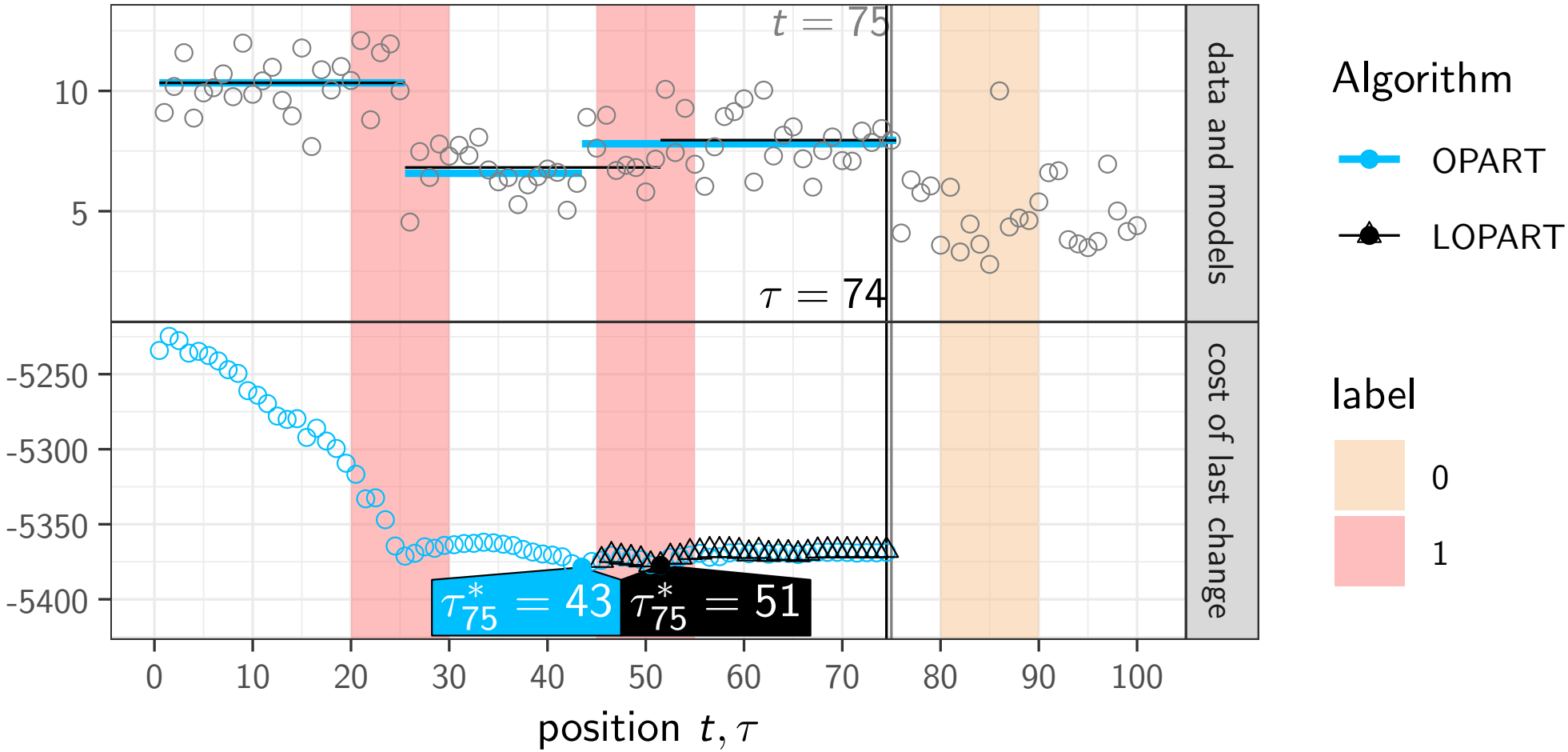

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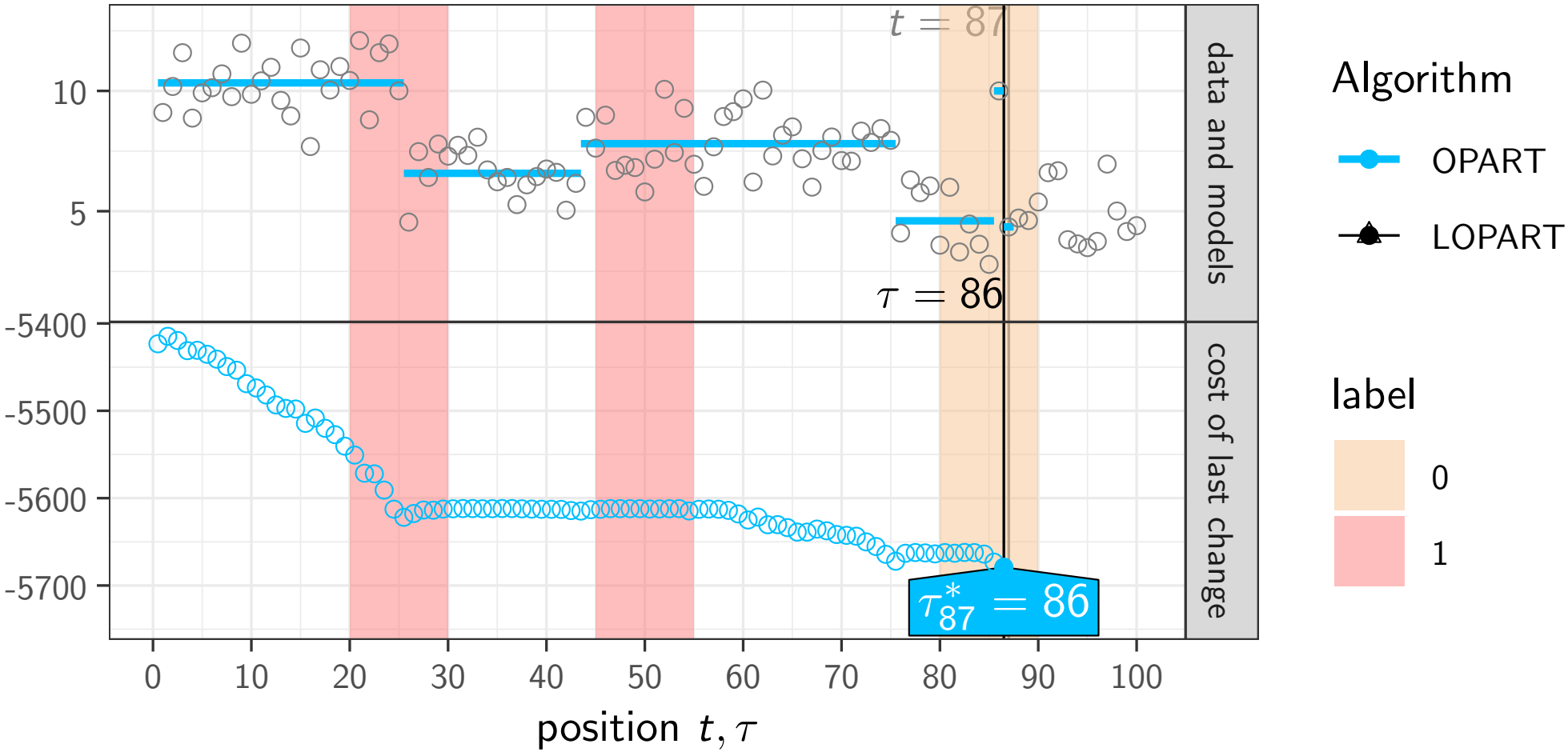

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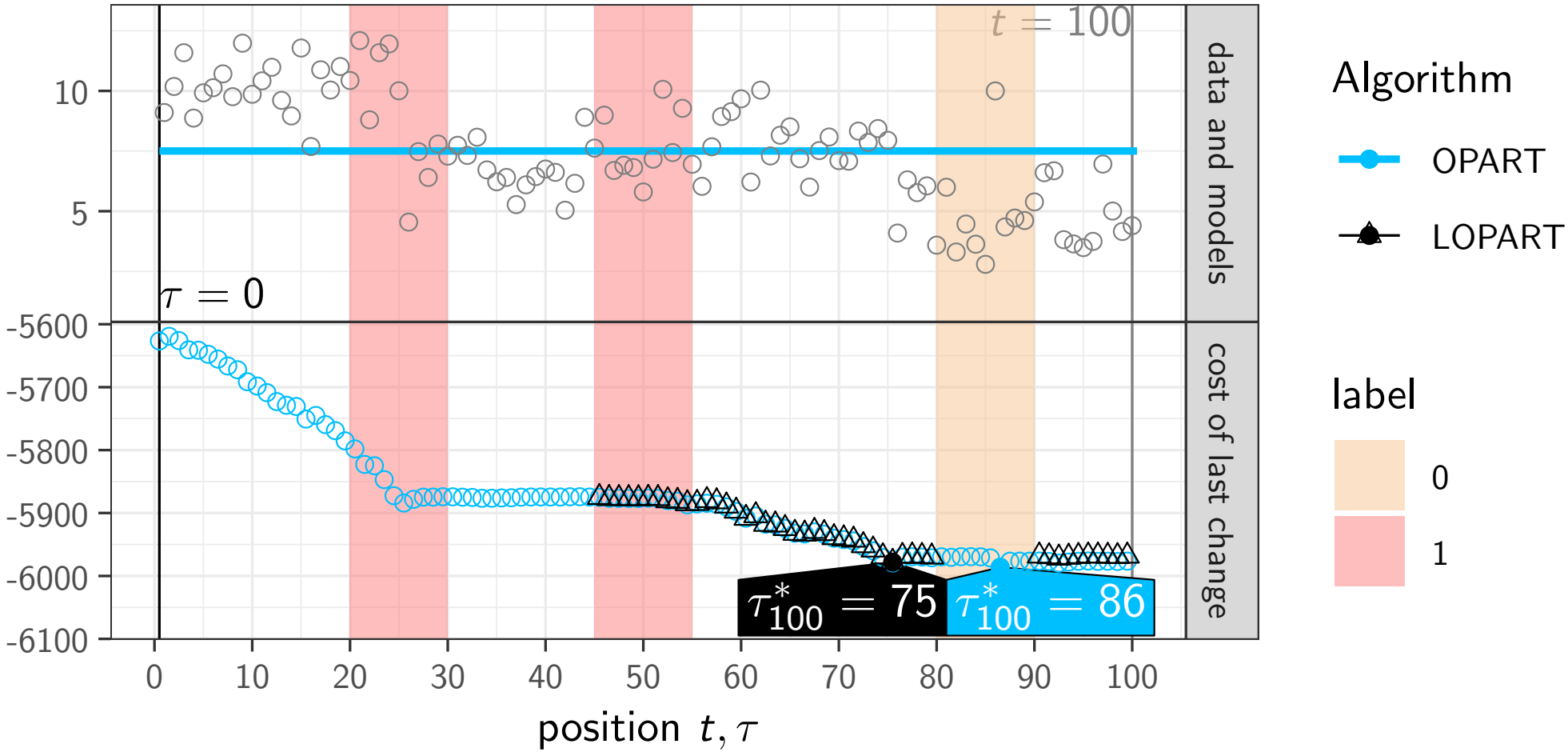

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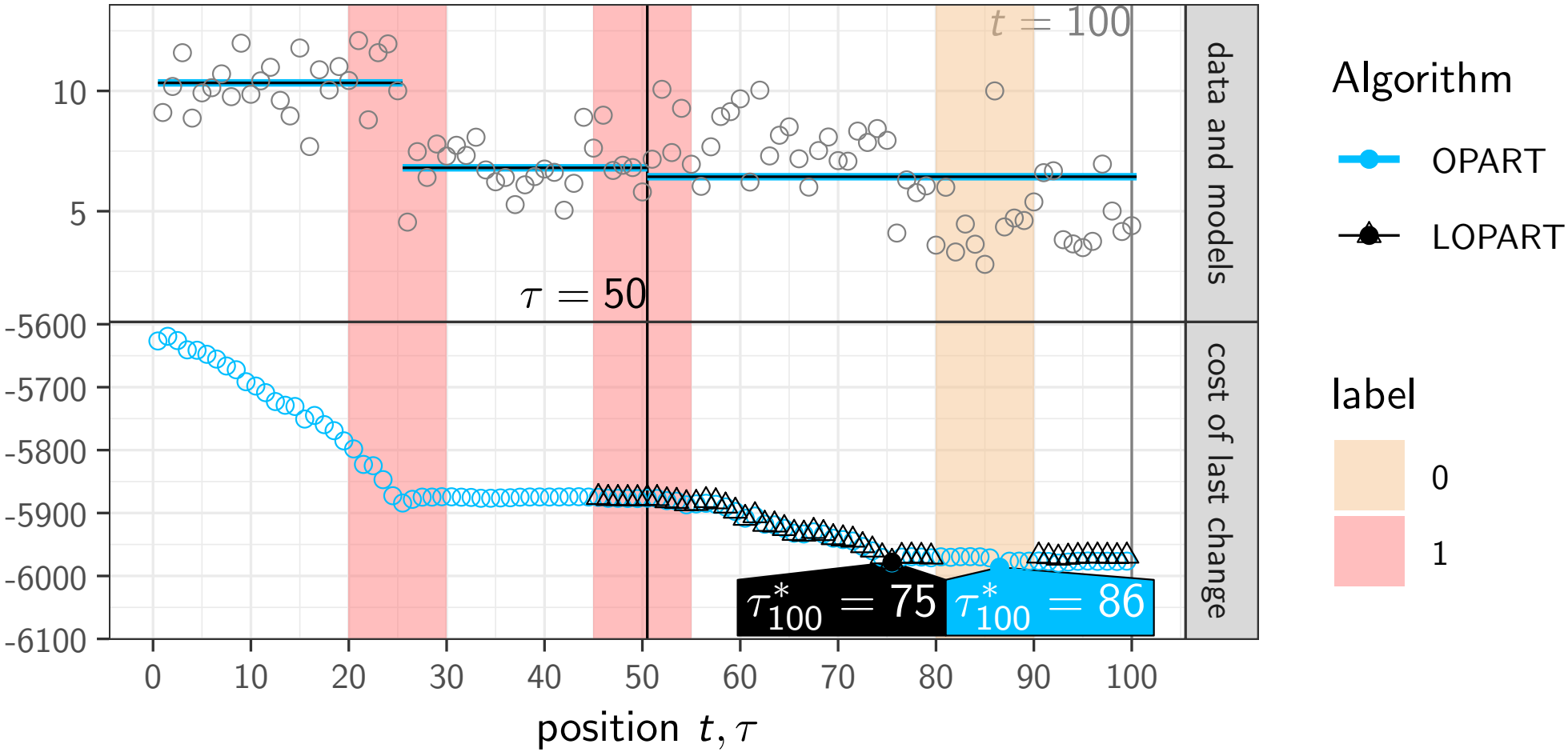

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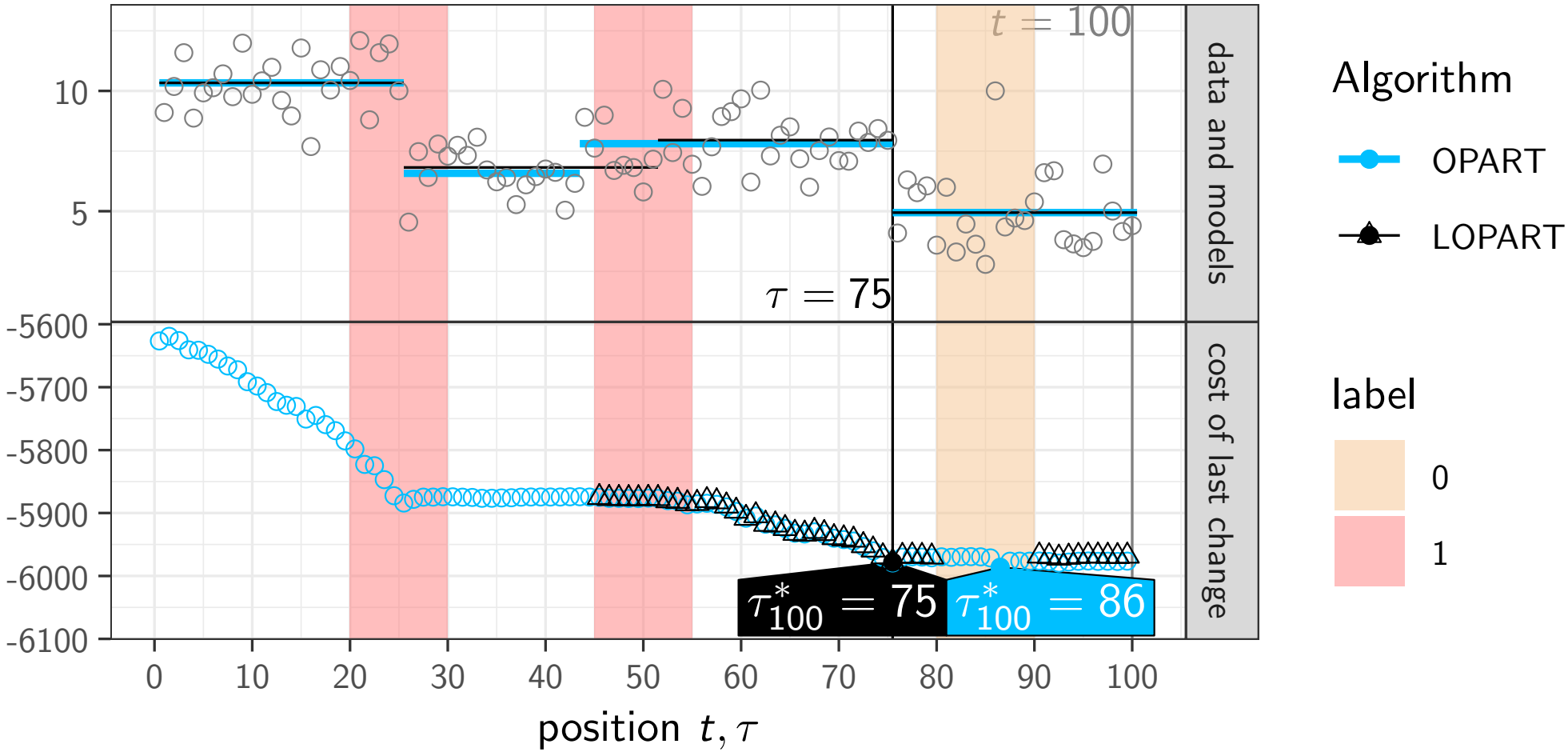

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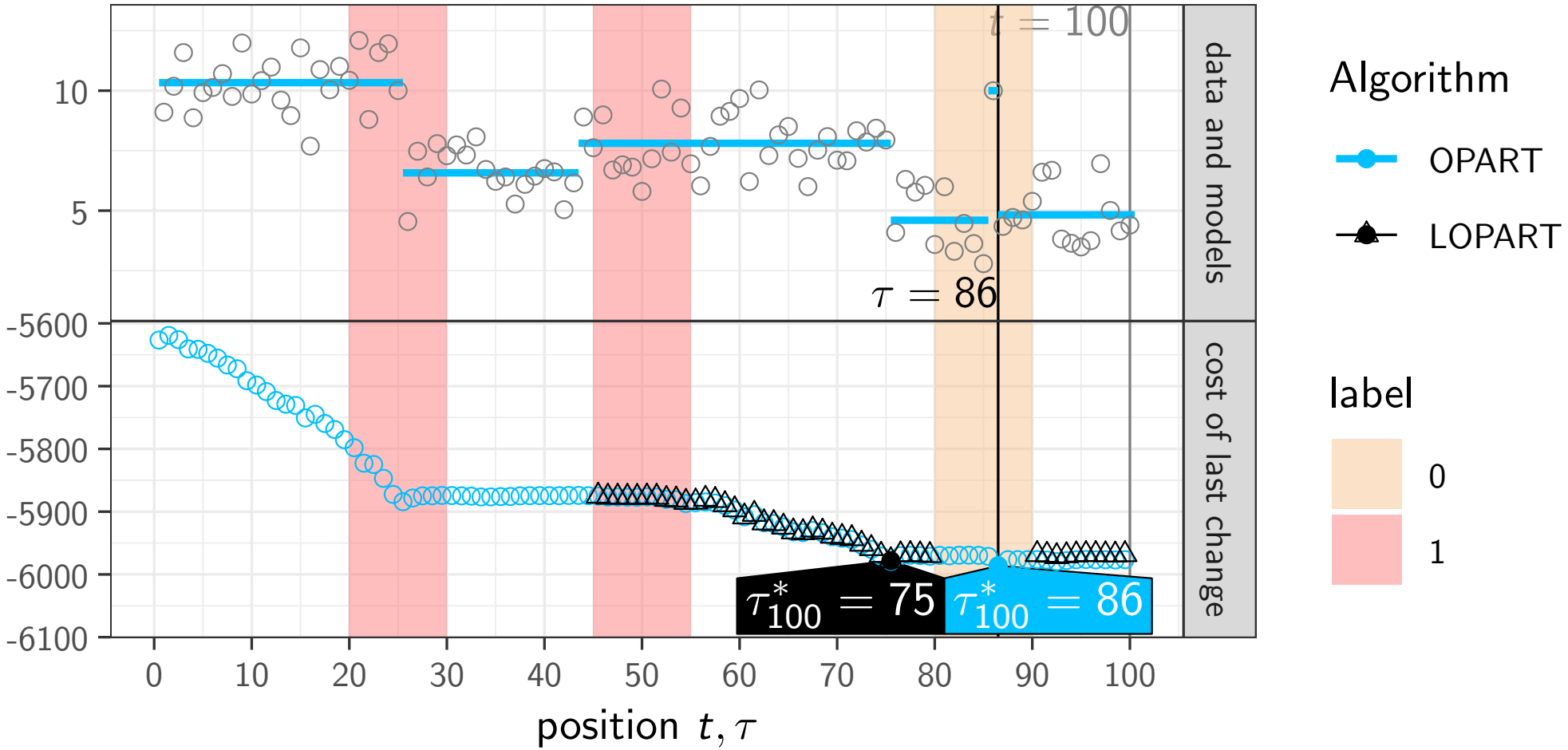

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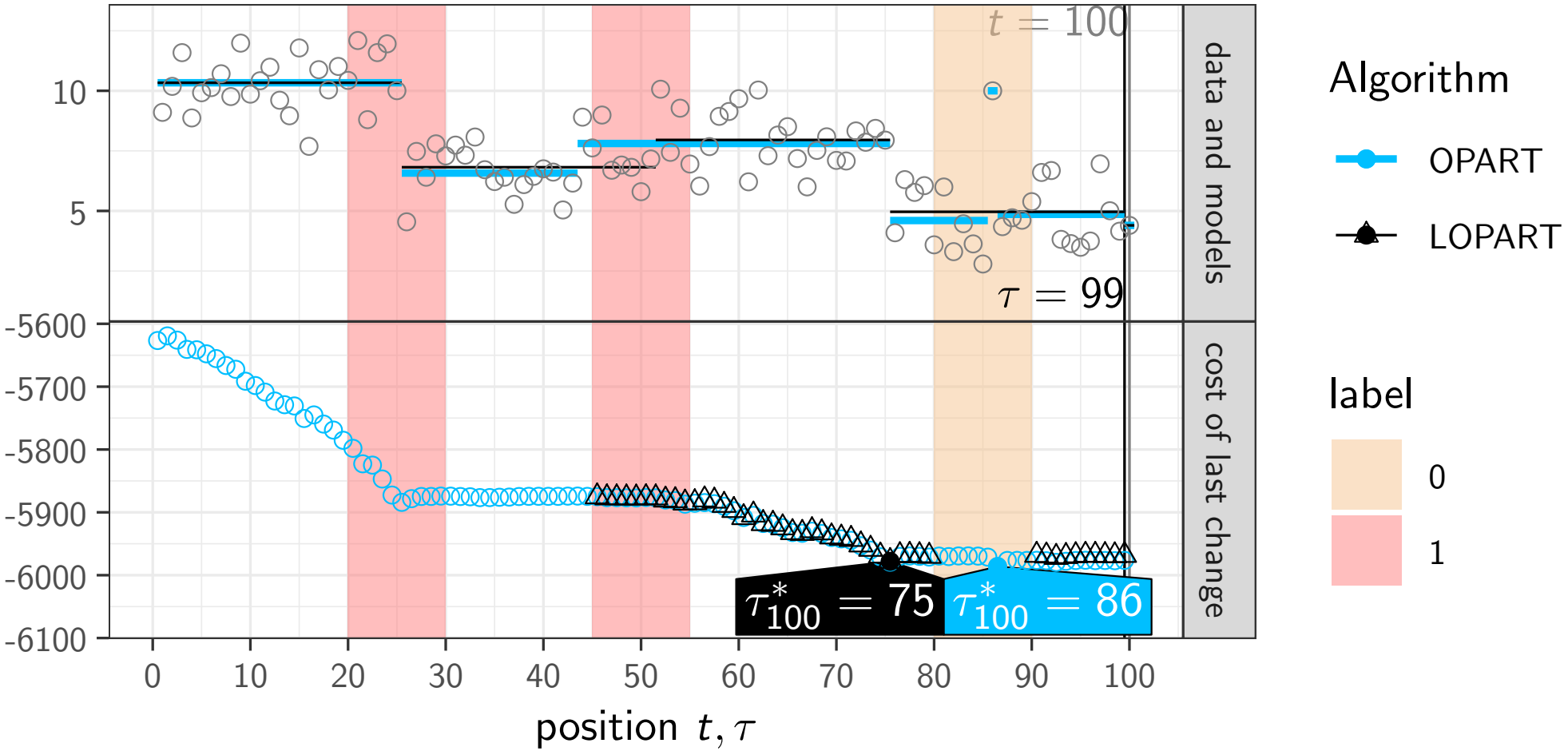

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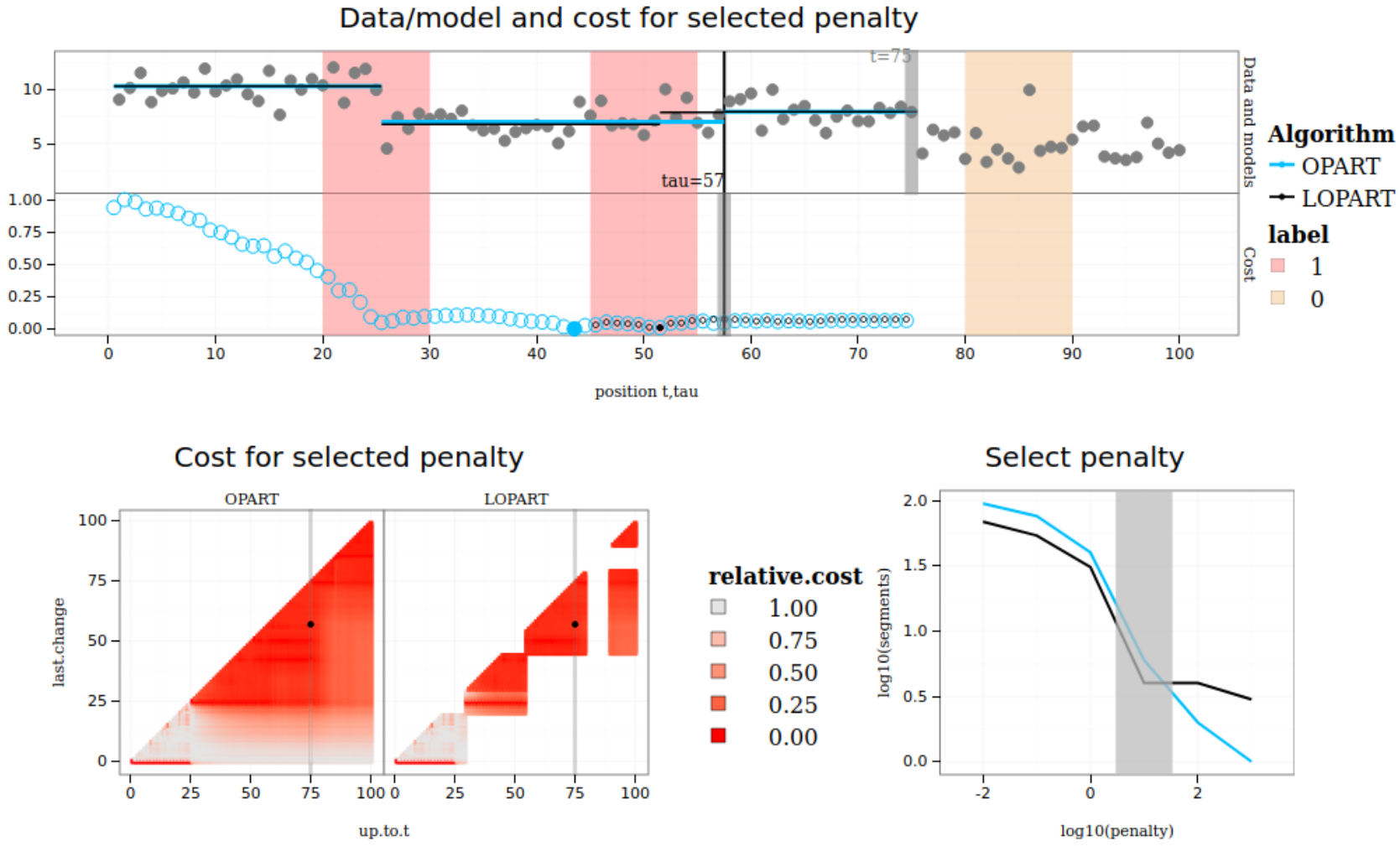
Interactive version

Try this at home:



http://members.cbio.mines-paristech.fr/~thocking/figure-candidates-interactive/

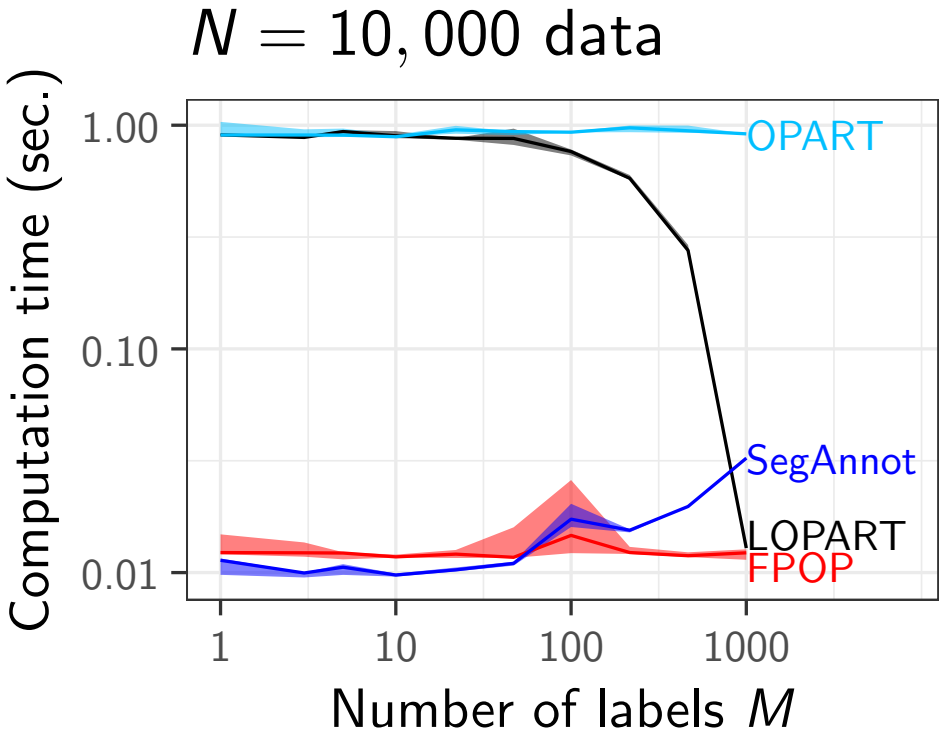
Introduction: supervised changepoint detection for cancer diagnosis with DNA copy number data

Labeled Optimal Partitioning (LOPART)

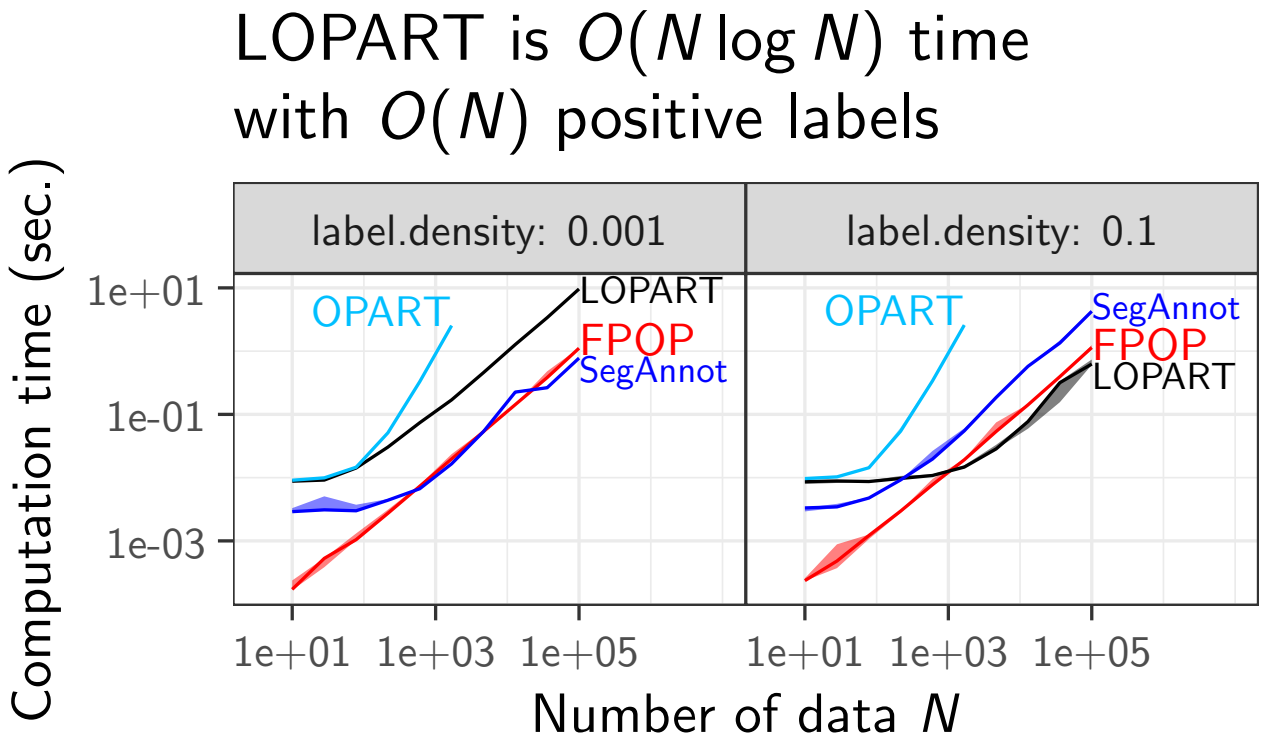
LOPART Demo

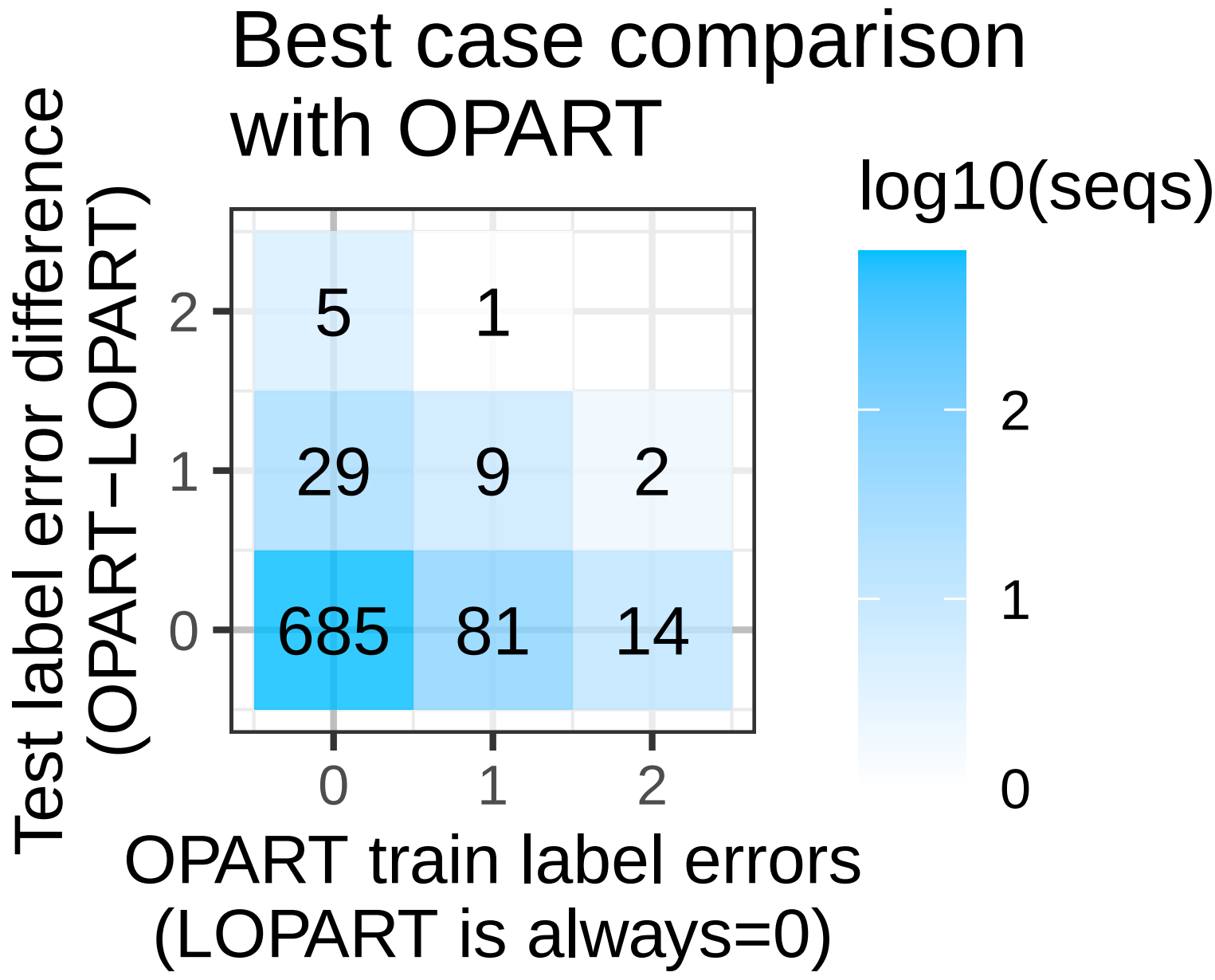
Results and Discussion

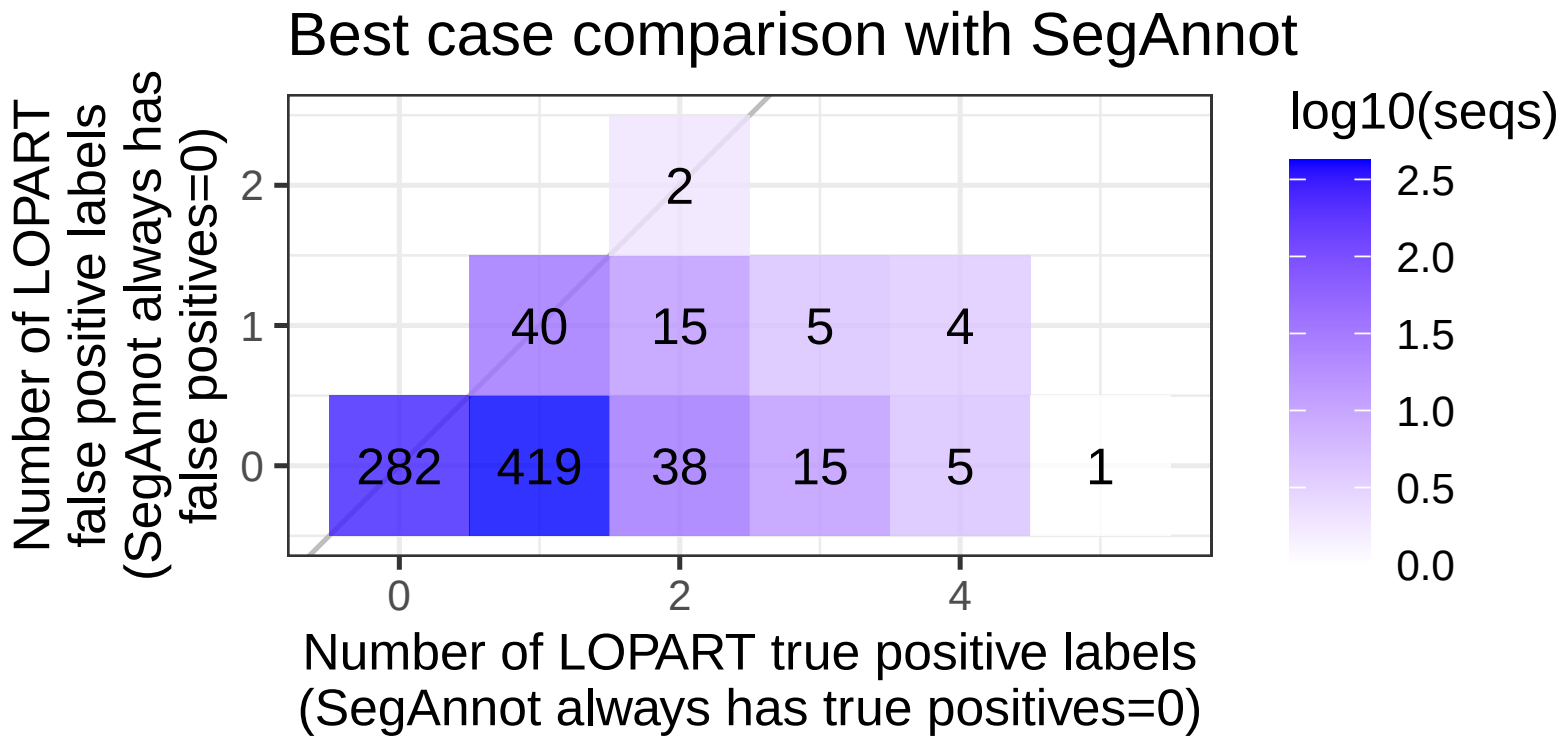
Empirical time complexity (labels)



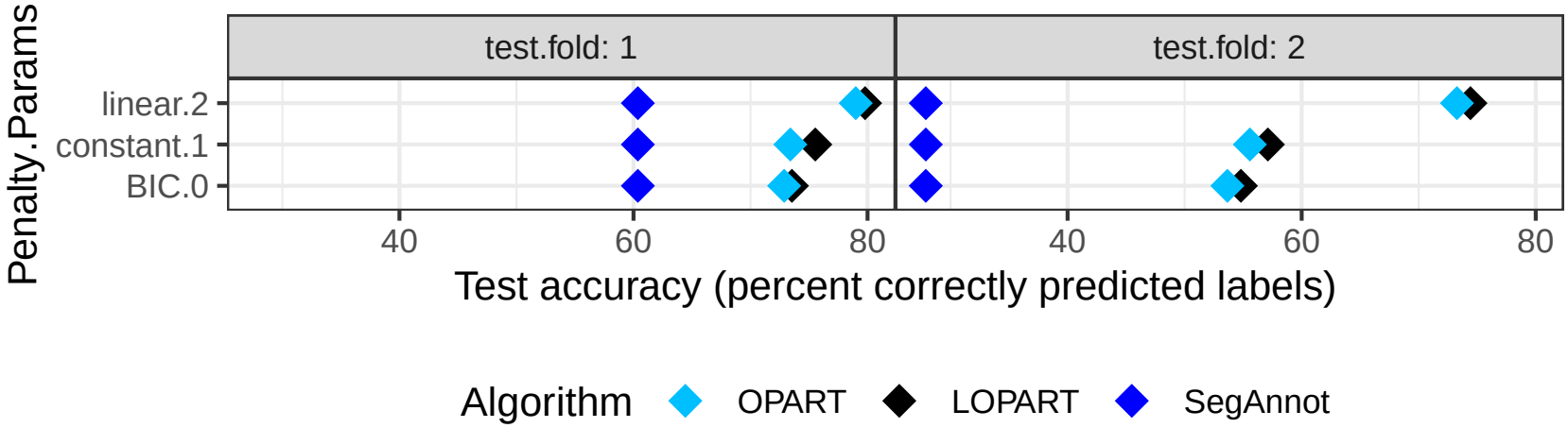
Empirical time complexity (data)



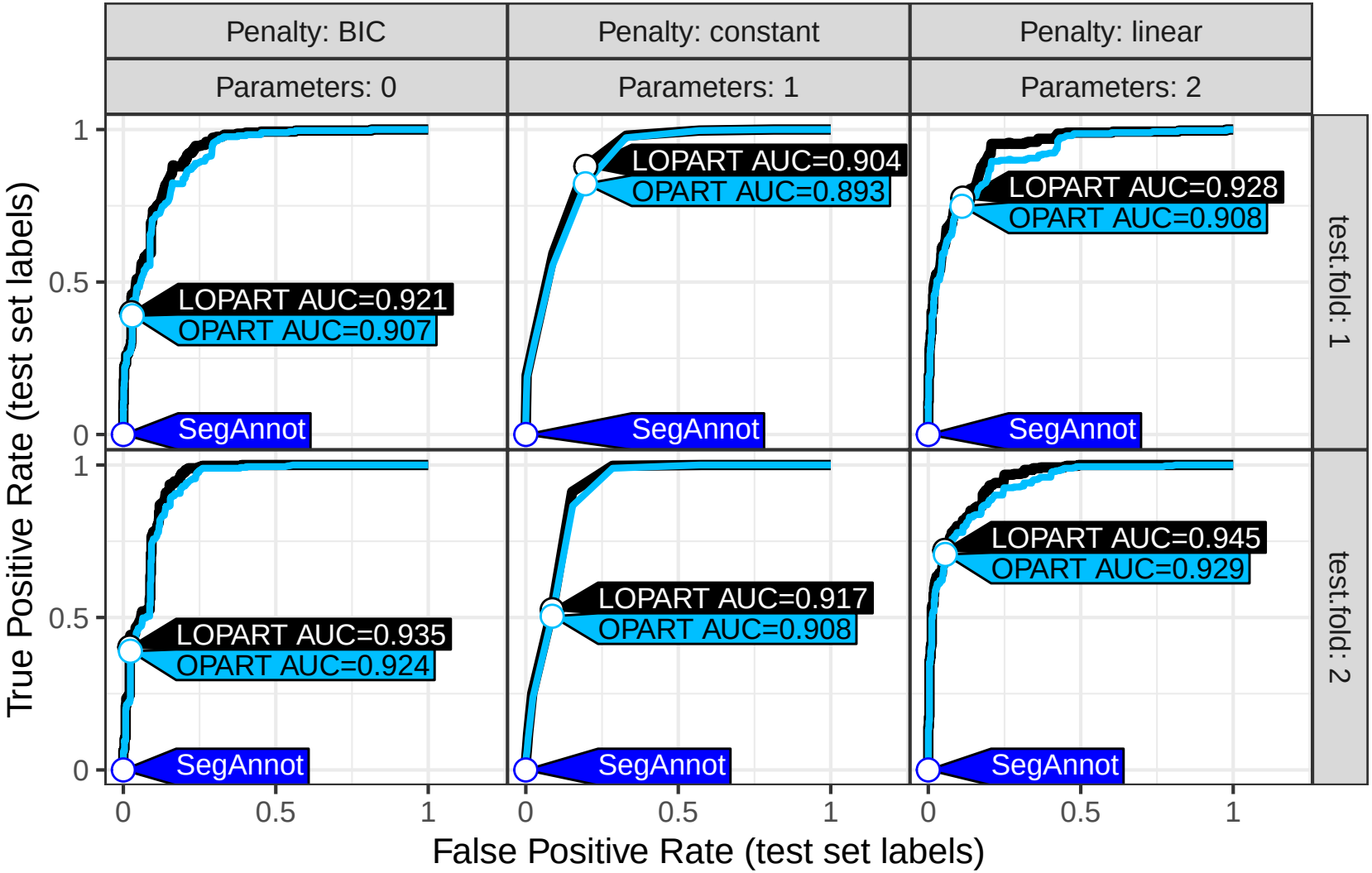

Best case comparison with OPART
Test label error difference (OPART−LOPART)
2
1
0
5
1
29
9
2
685
81
14
0
1
2
OPART train label errors (LOPART is always=0)
log10(seqs)
2
1
0


Best case comparison with SegAnnot
Number of LOPART false positive labels (SegAnnot always has false positives=0)
2
1
0
2
40
15
5
4
282
419
38
15
5
1
0
2
4
Number of LOPART true positive labels (SegAnnot always has true positives=0)
log10(seqs)
2.5
2.0
1.5
1.0
0.5
0.0

Test accuracy in cross-validation experiments



Test ROC curves in cross-validation experiments



Summary and Discussion

- Proposed algo fixes issues with two previous algorithms (better train AND test accuracy).
- Results demonstrate improved speed and accuracy.
- R package on CRAN and `https://github.com/tdhock/LOPART`
- Figure/slide code on `https://github.com/tdhock/LOPART-paper`
- Future work: functional pruning algorithm, which can solve more complex constrained changepoint problems (e.g. change must be non-decreasing), and should be faster (log-linear instead of quadratic).