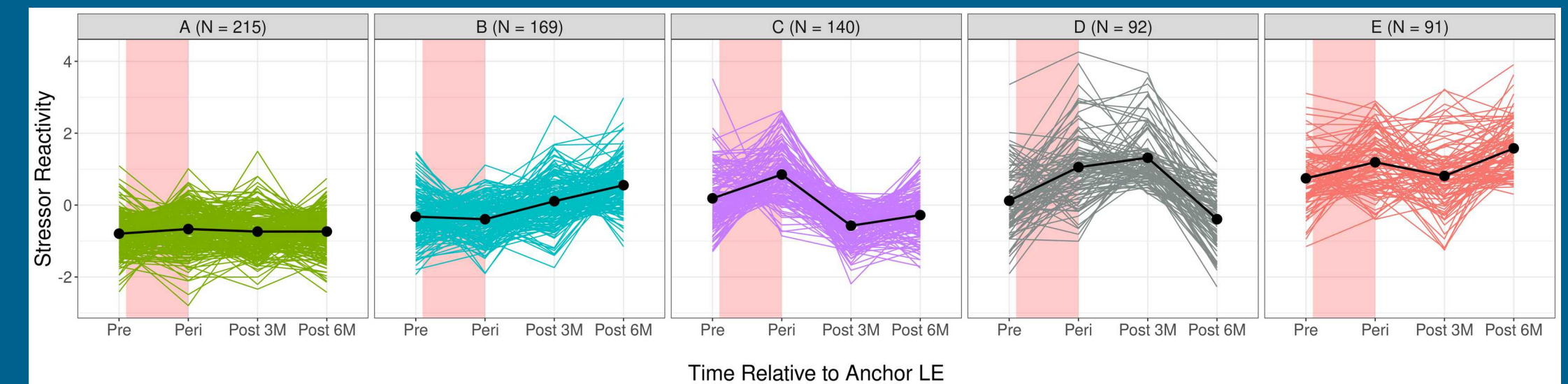
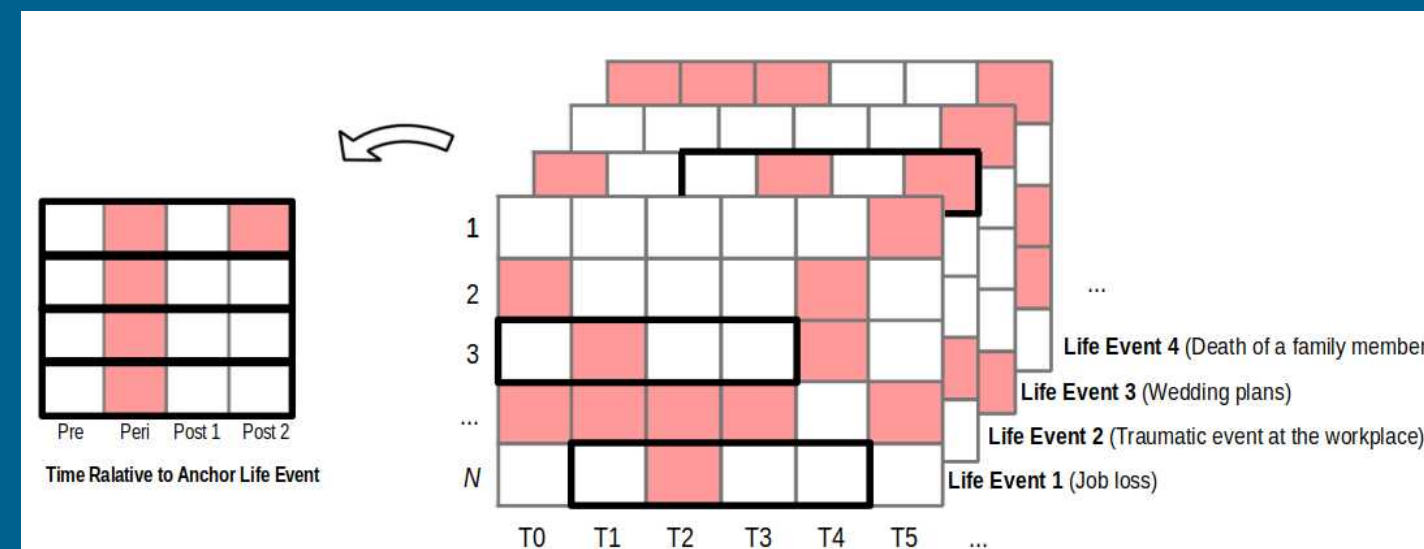
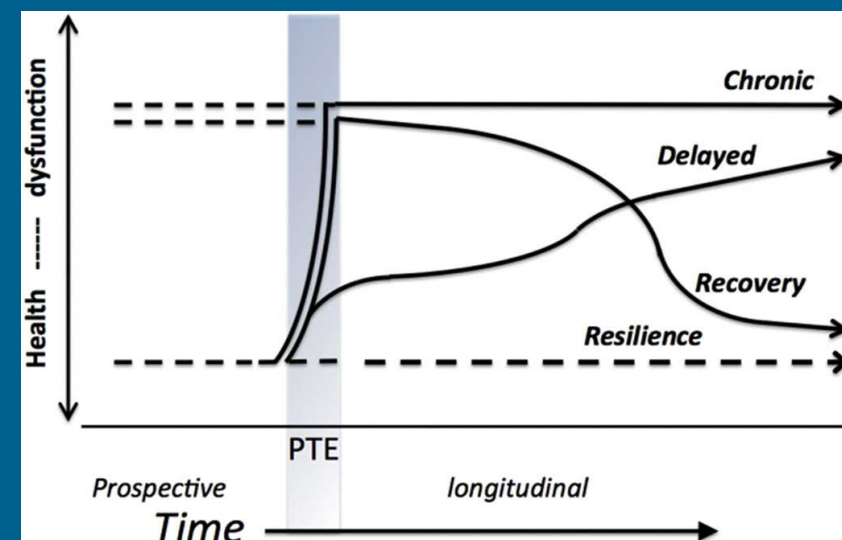


Trajectories

Charlotte Schenk, M.Sc. Psychology; c.schenk@med.uni-frankfurt.de

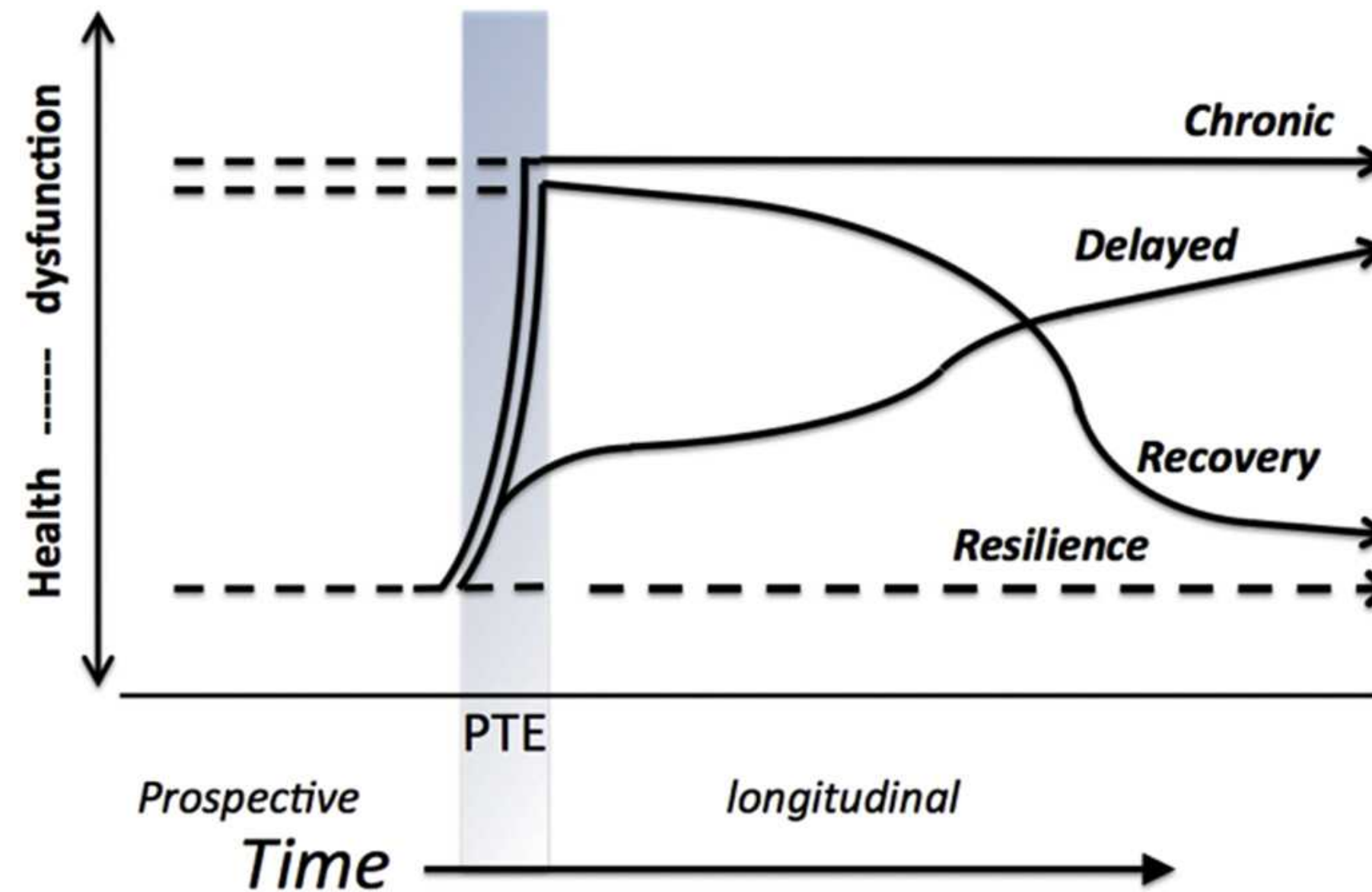
Dept. of Psychiatry, Psychosomatic Medicine and Psychotherapy, University Medical Centre Frankfurt



Resilience: Maintenance or quick recovery of mental health during or after stressor exposure.^[1, 2, 3]

Figure 1

Commonly observed longitudinal trajectories of response to potential trauma.



Note. Sourced from Galatzer-Levy et al. (2018).^[4, 5]

[1] Kalisch, R., Müller, M. B., & Tüscher, O. (2015). A conceptual framework for the neurobiological study of resilience. *Behavioral and brain sciences*, 38, e92.

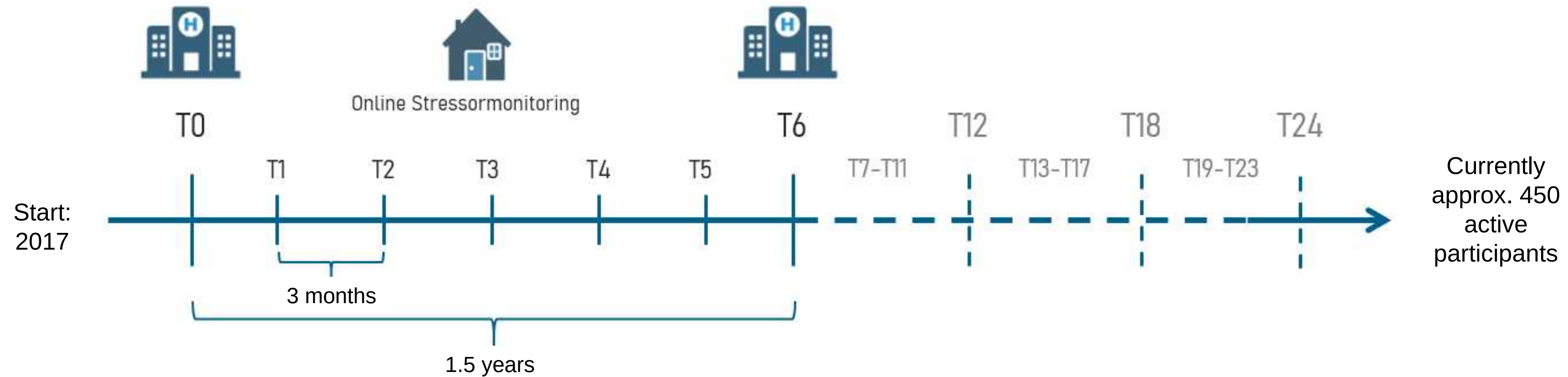
[2] Luthar, S. S., Cicchetti, D., & Becker, B. (2000). The construct of resilience: A critical evaluation and guidelines for future work. *Child development*, 71(3), 543-562.

[3] Masten, A. S. (2001). Ordinary magic: Resilience processes in development. *American psychologist*, 56(3), 227.

[4] Bonanno, G. A., Westphal, M., & Mancini, A. D. (2011). Resilience to loss and potential trauma. *Annual review of clinical psychology*, 7(1), 511-535.

[5] Galatzer-Levy, I. R., Huang, S. H., & Bonanno, G. A. (2018). Trajectories of resilience and dysfunction following potential trauma: A review and statistical evaluation. *Clinical psychology review*, 63, 41-55.

$N = 1.191$,
Initially healthy participants,
Sex: 35% male, 65% female,
Age: $M = 28.59$, $SD = 7.96$



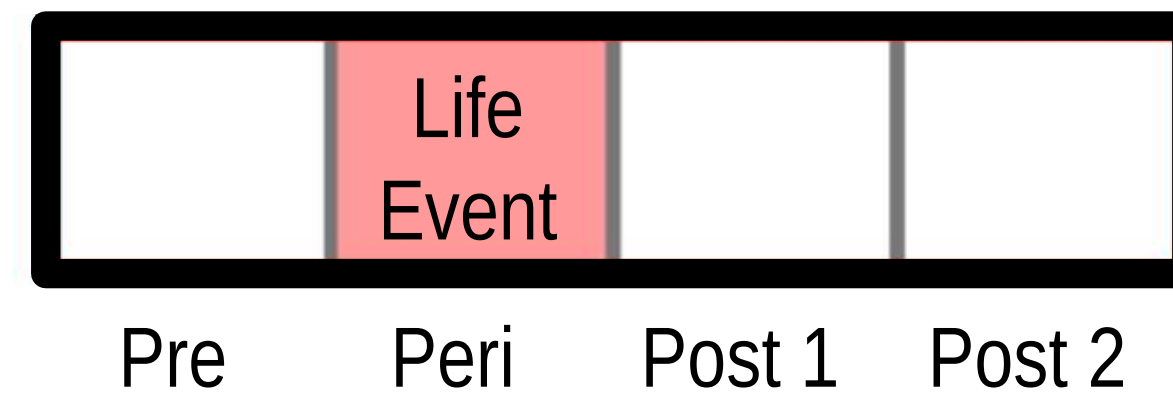
Online Stressormonitoring

Mental Health Problems

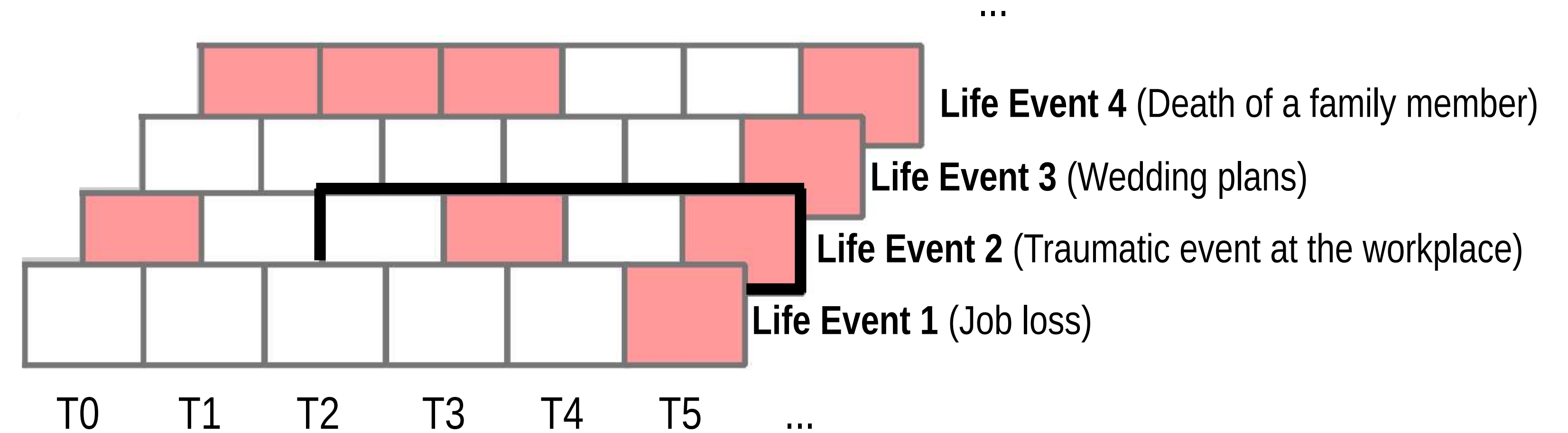
Critical life events in the past 3 months

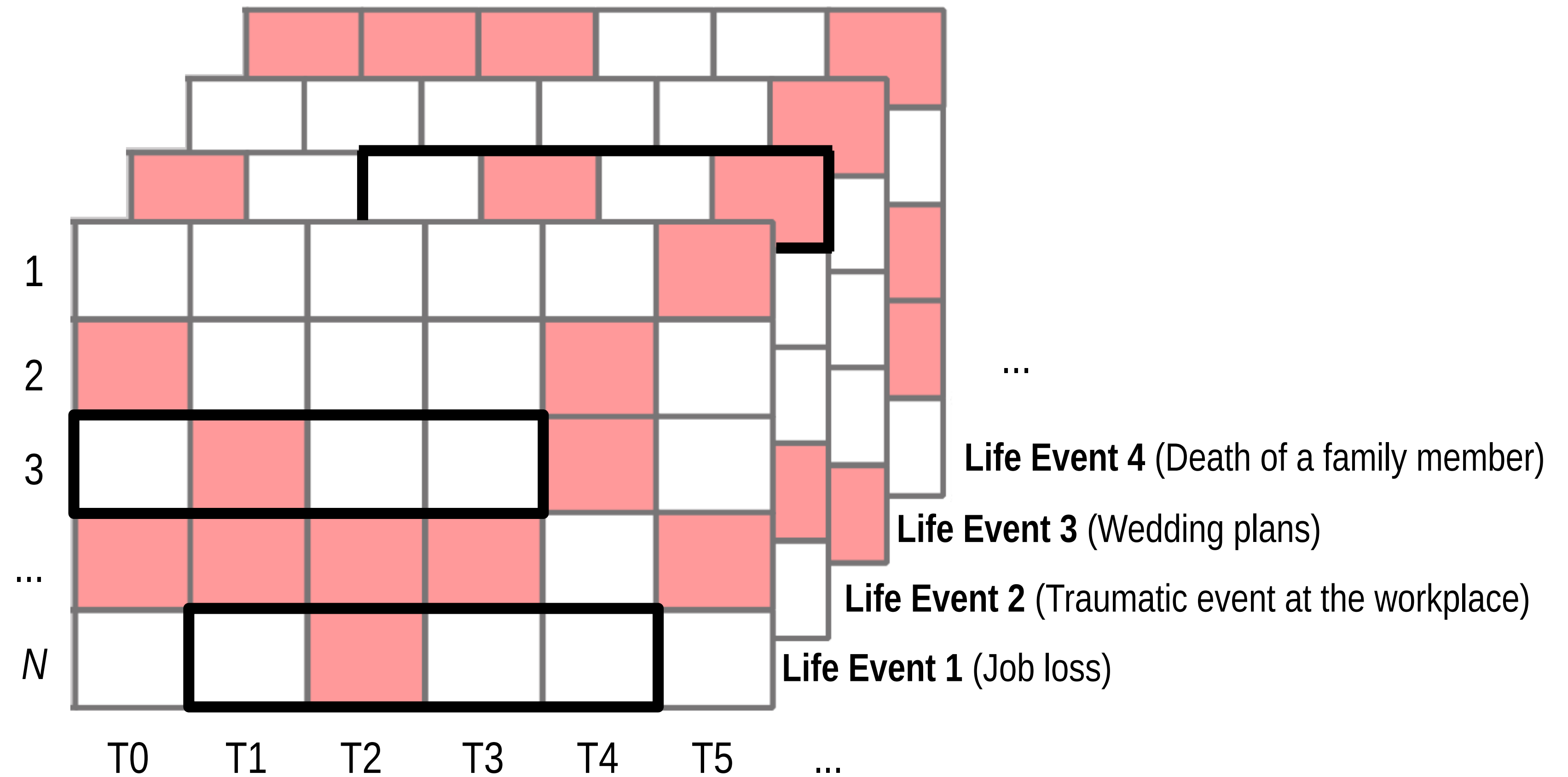
Daily hassles in the past 7 days at the end of each 3-month period

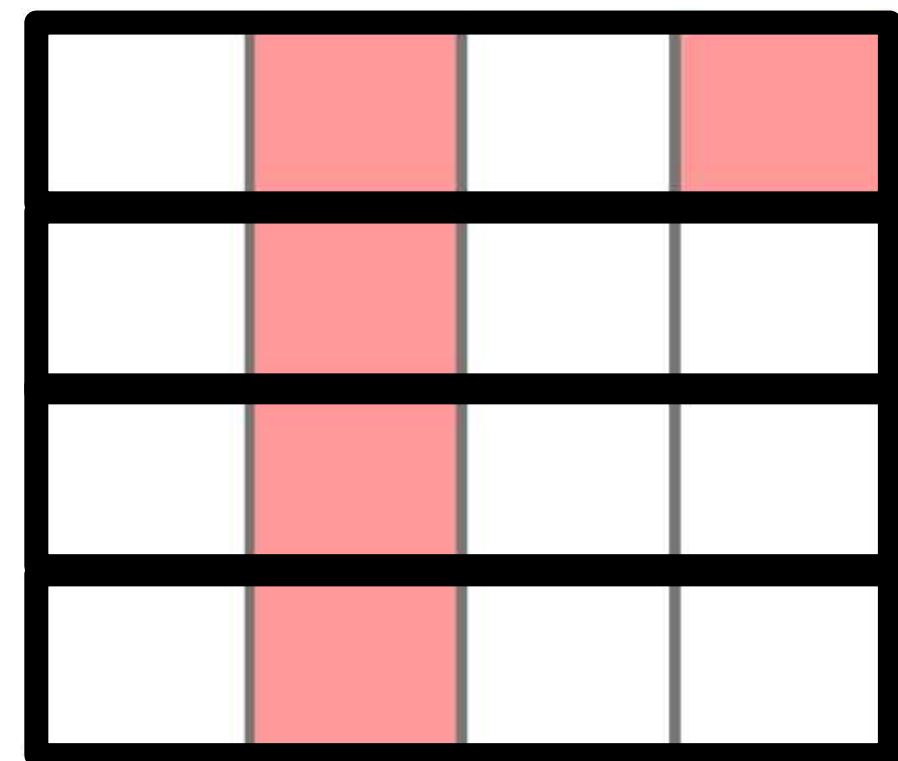
Hair cortisol
Microbiome



Time Relative to Anchor Life Event

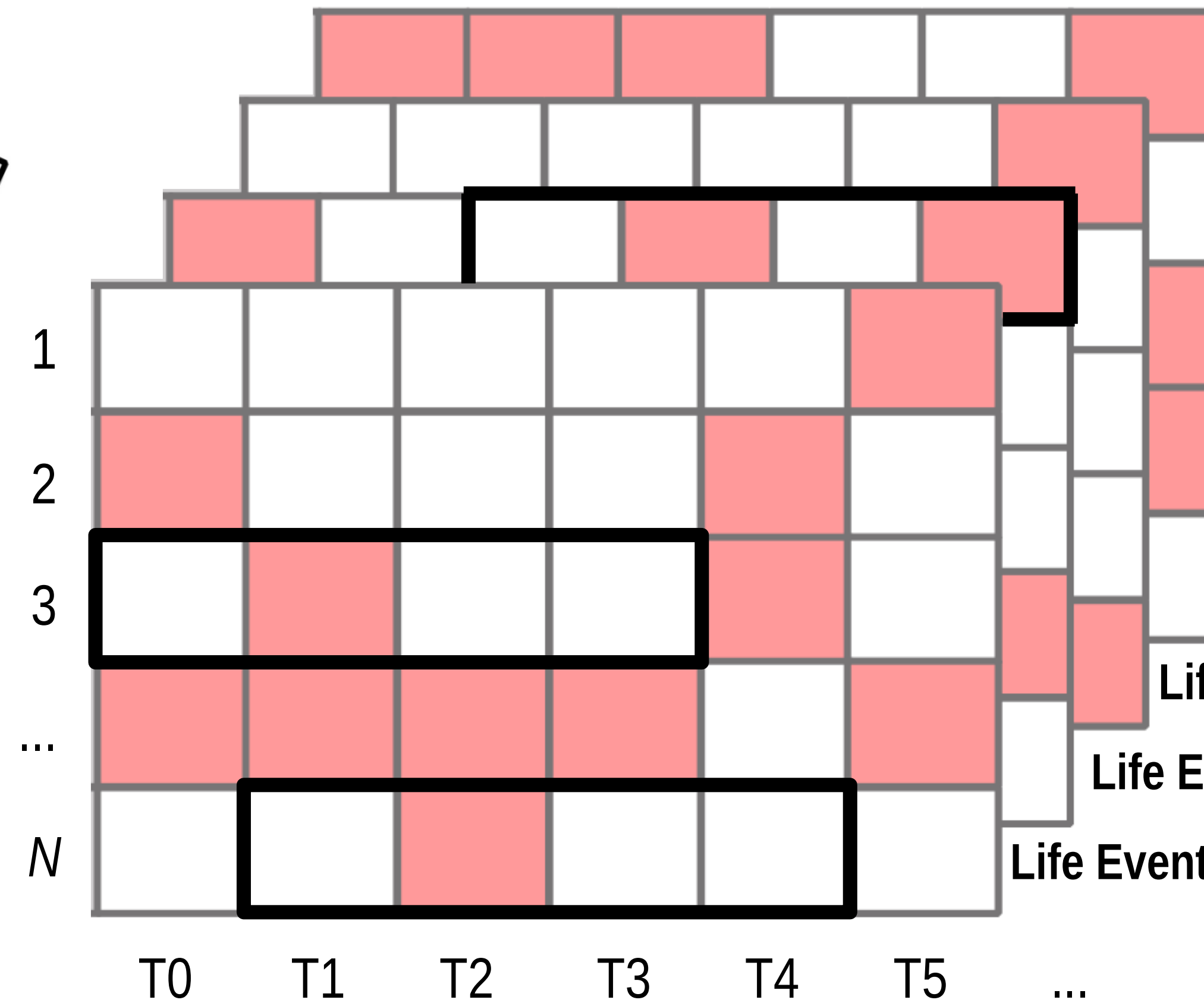






Pre Peri Post 1 Post 2

Time Relative to Anchor Life Event

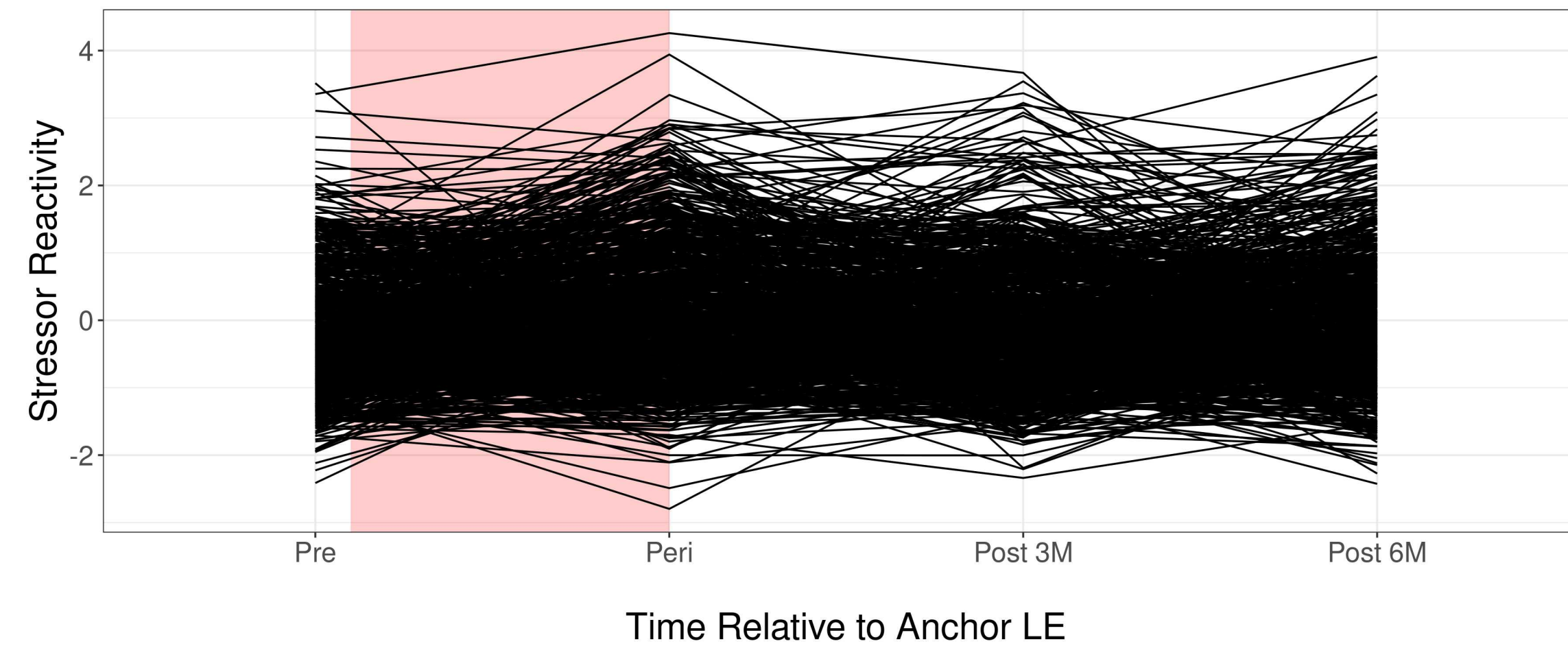


Life Event 1 (Job loss)

Life Event 2 (Traumatic event at the workplace)

Life Event 3 (Wedding plans)

Life Event 4 (Death of a family member)





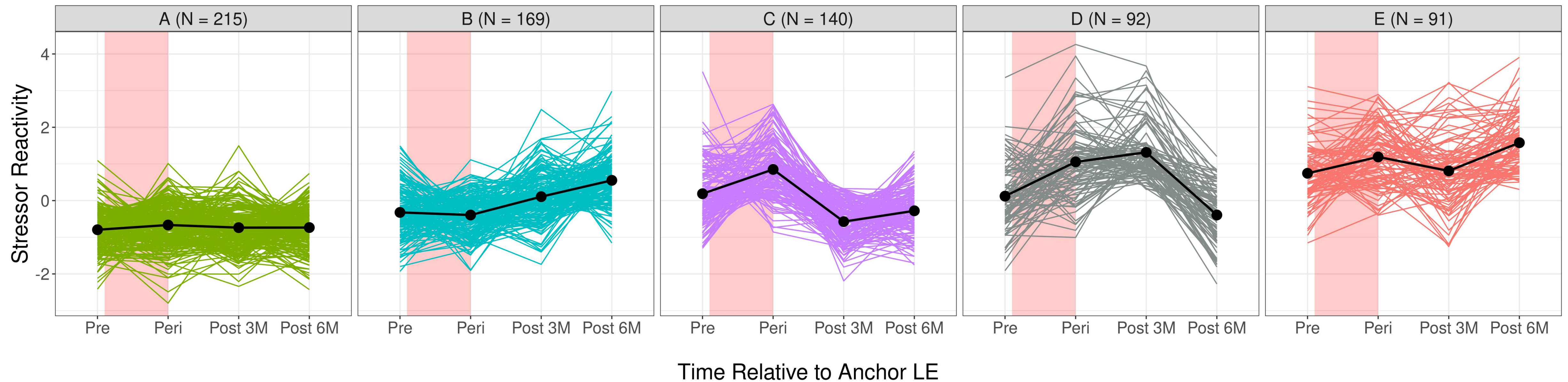
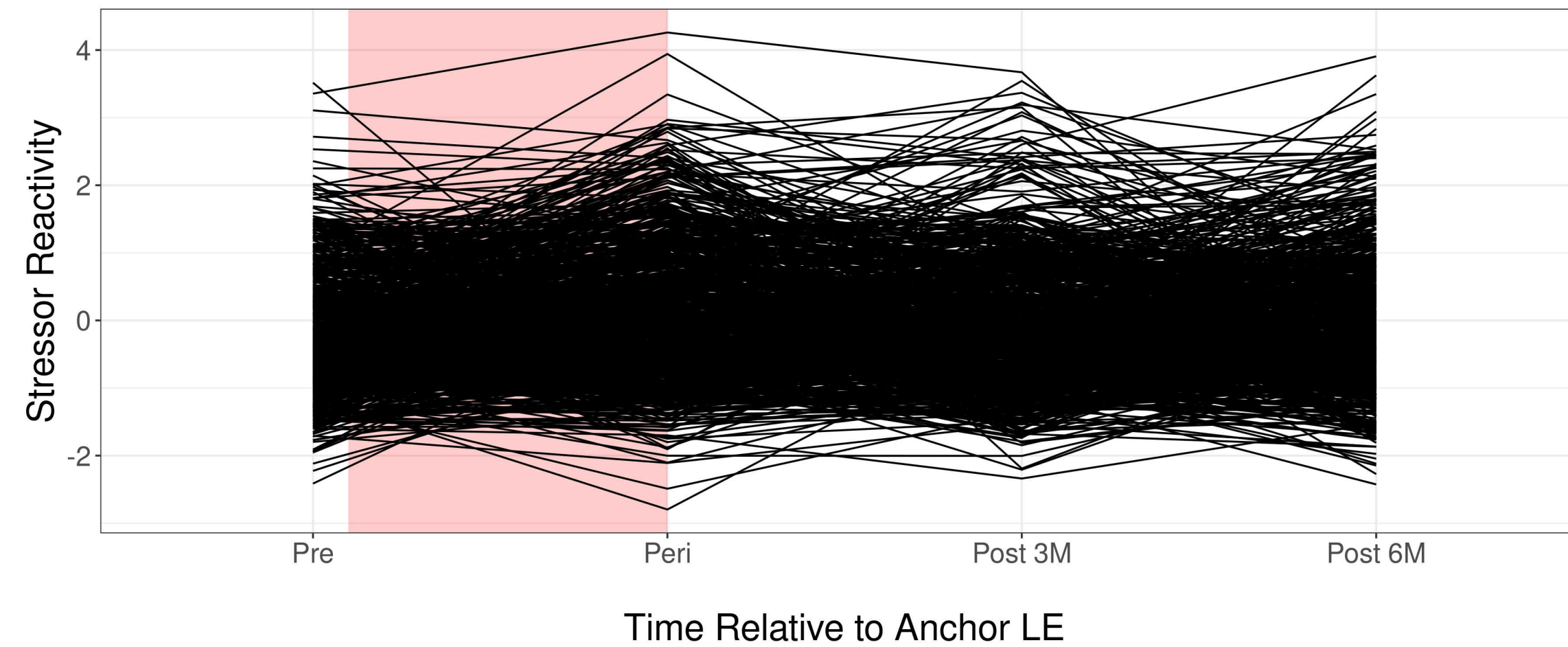
Dr. Kira
Ahrens

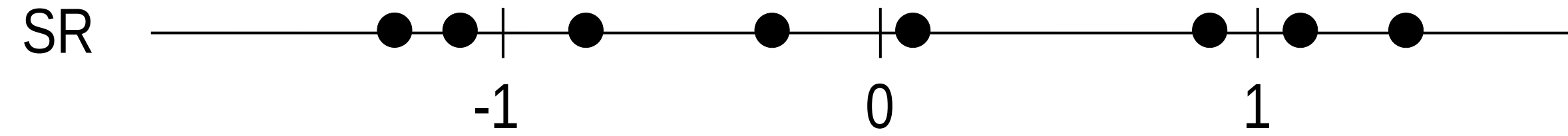


Prof. Dr. Raffael
Kalisch

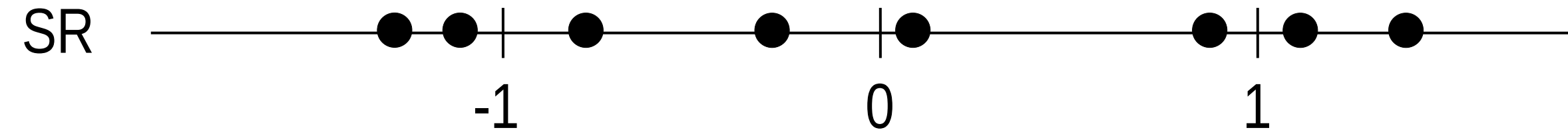


Prof. Dr. Michael
Plichta

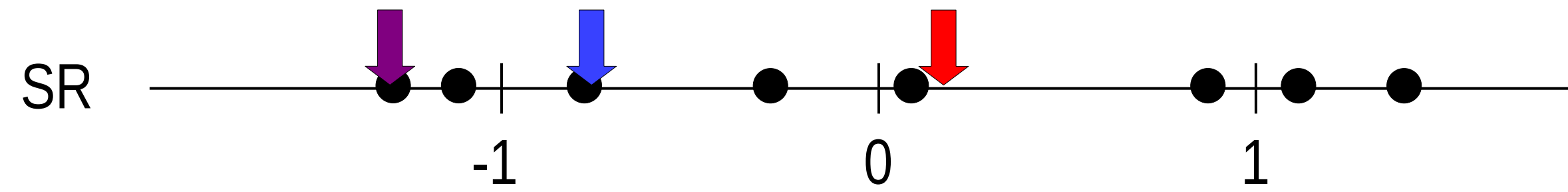




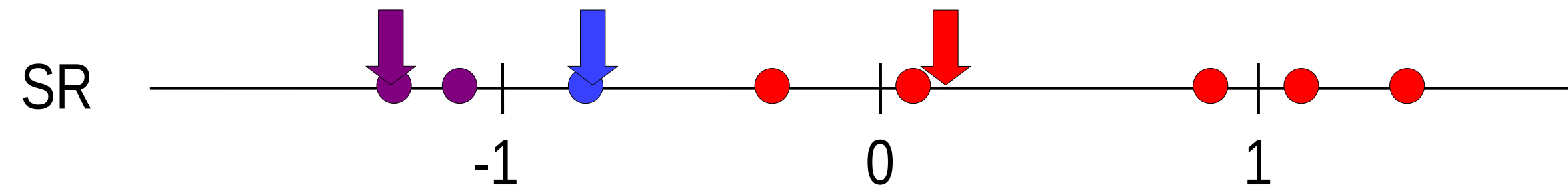
1. Choosing the number of clusters: $k = 3$



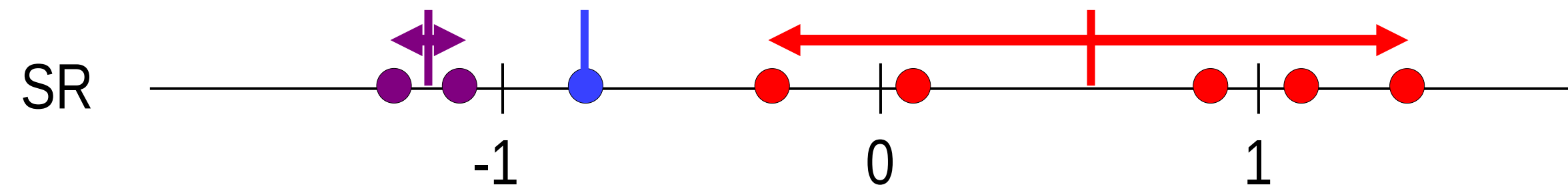
1. Choosing the number of clusters: $k = 3$
2. Select cluster centers



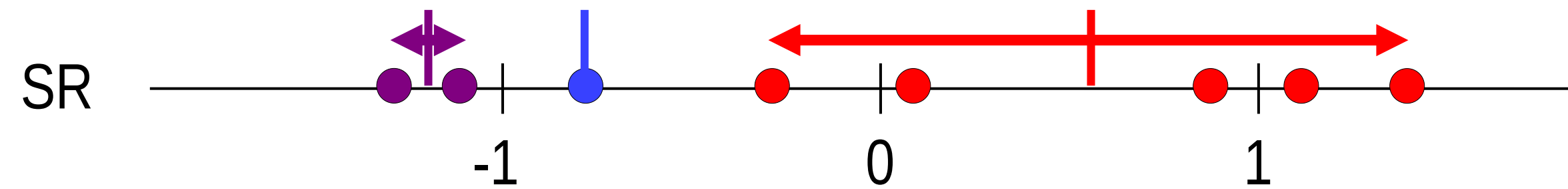
1. Choosing the number of clusters: $k = 3$
2. Select cluster centers
3. Assign data points to the nearest cluster



1. Choosing the number of clusters: $k = 3$
2. Select cluster centers
3. Assign data points to the nearest cluster
4. **Re-initialize centroids**



1. Choosing the number of clusters: $k = 3$
2. Select cluster centers
3. Assign data points to the nearest cluster
4. Re-initialize centroids

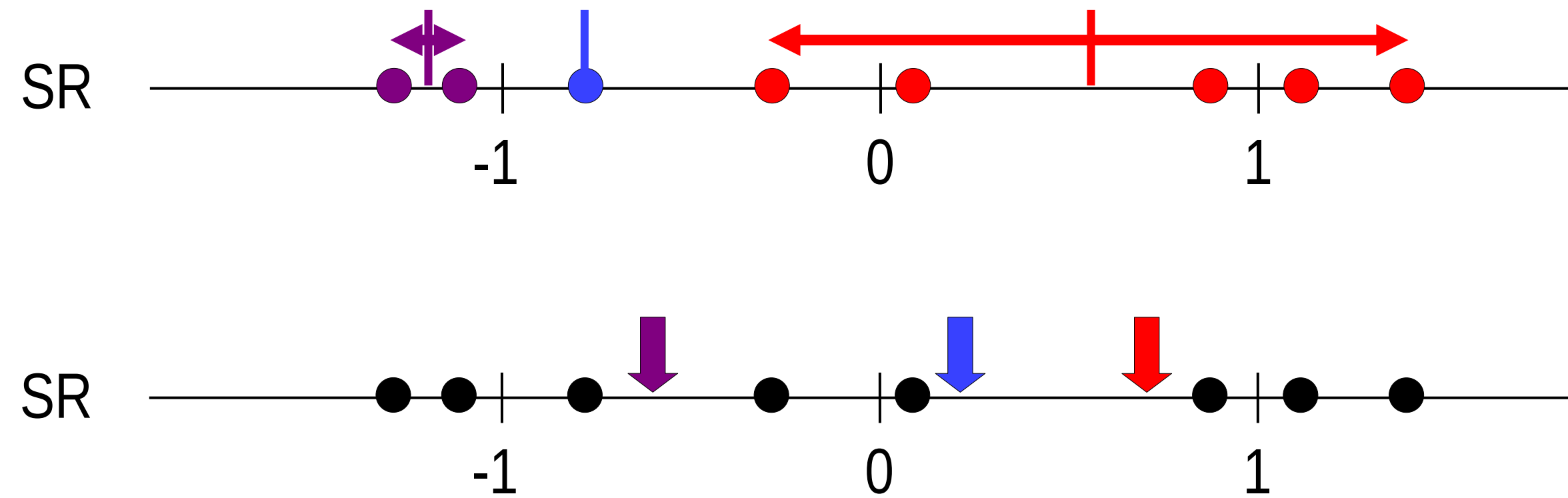


1st run:

Total within-cluster variance:



1. Choosing the number of clusters: $k = 3$
2. Select cluster centers
3. Assign data points to the nearest cluster
4. Re-initialize centroids

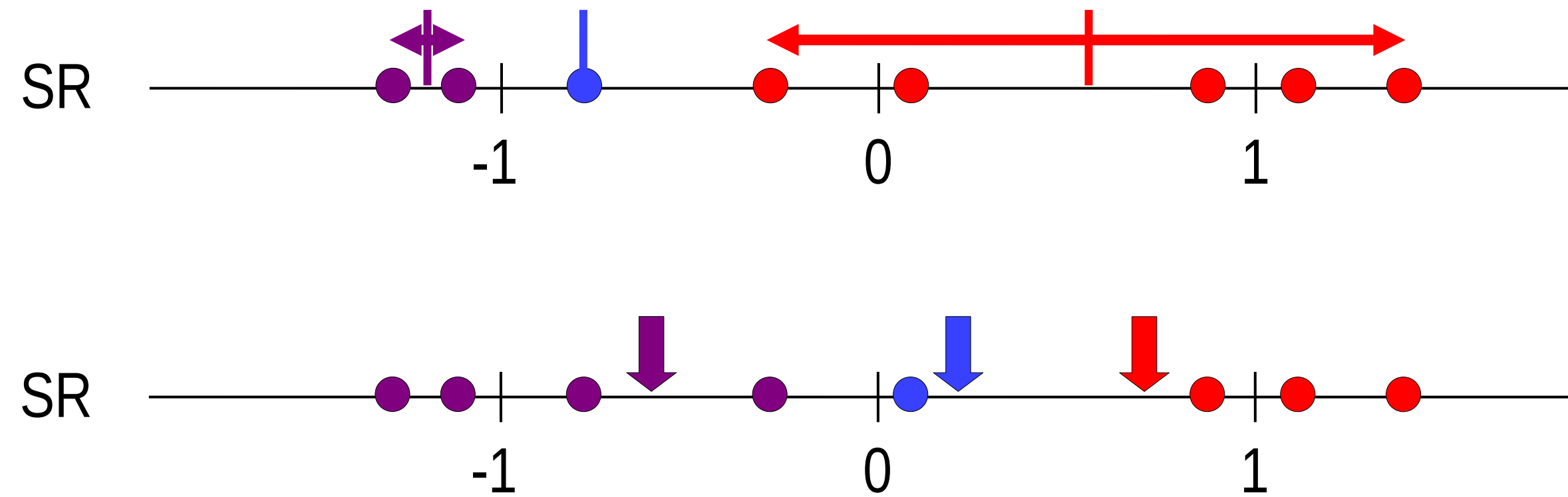


1st run:

Total within-cluster variance:



1. Choosing the number of clusters: $k = 3$
2. Select cluster centers
3. Assign data points to the nearest cluster
4. Re-initialize centroids

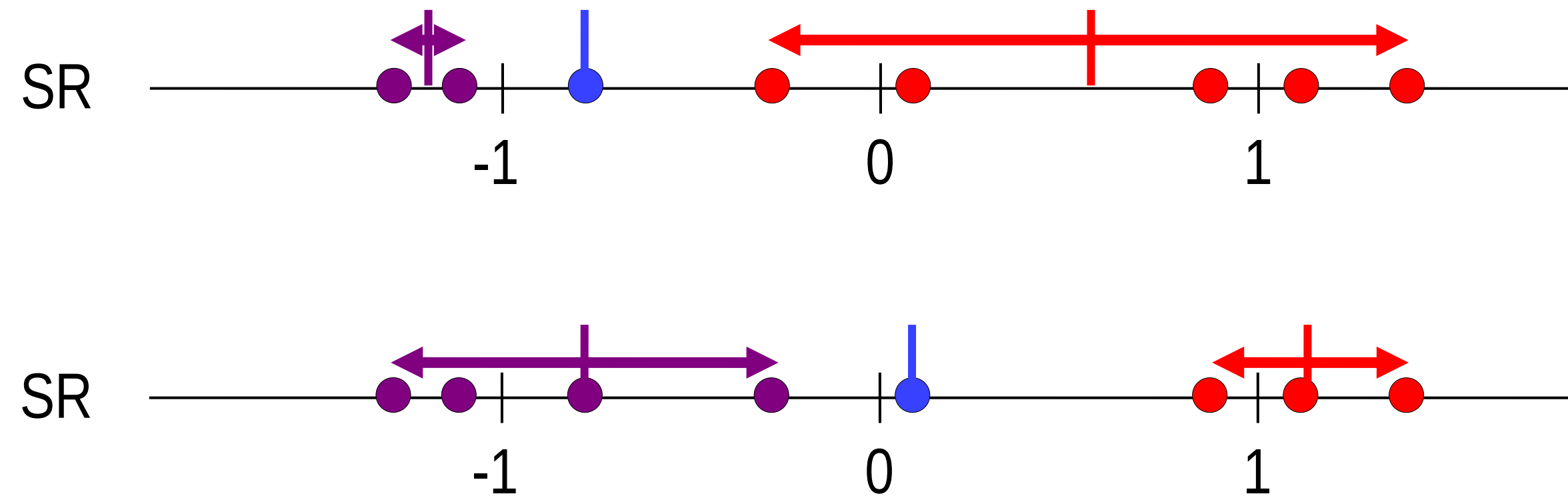


1st run:

Total within-cluster variance:



1. Choosing the number of clusters: $k = 3$
2. Select cluster centers
3. Assign data points to the nearest cluster
4. Re-initialize centroids

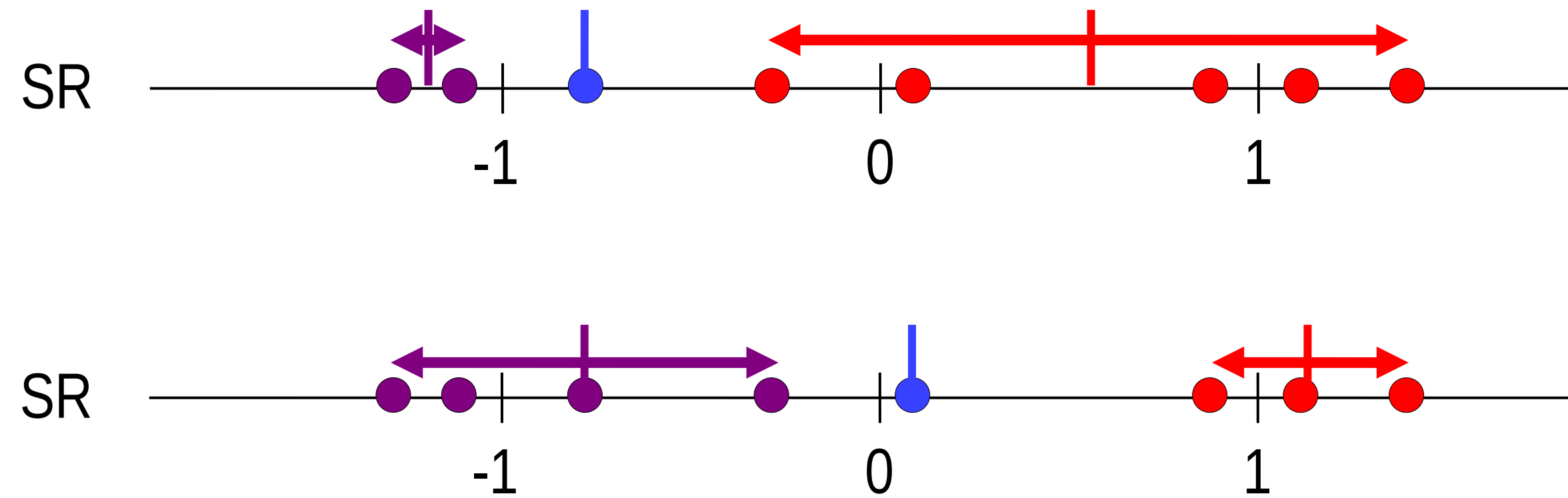


1st run:

Total within-cluster variance:



1. Choosing the number of clusters: $k = 3$
2. Select cluster centers
3. Assign data points to the nearest cluster
4. Re-initialize centroids



Total within-cluster variance:

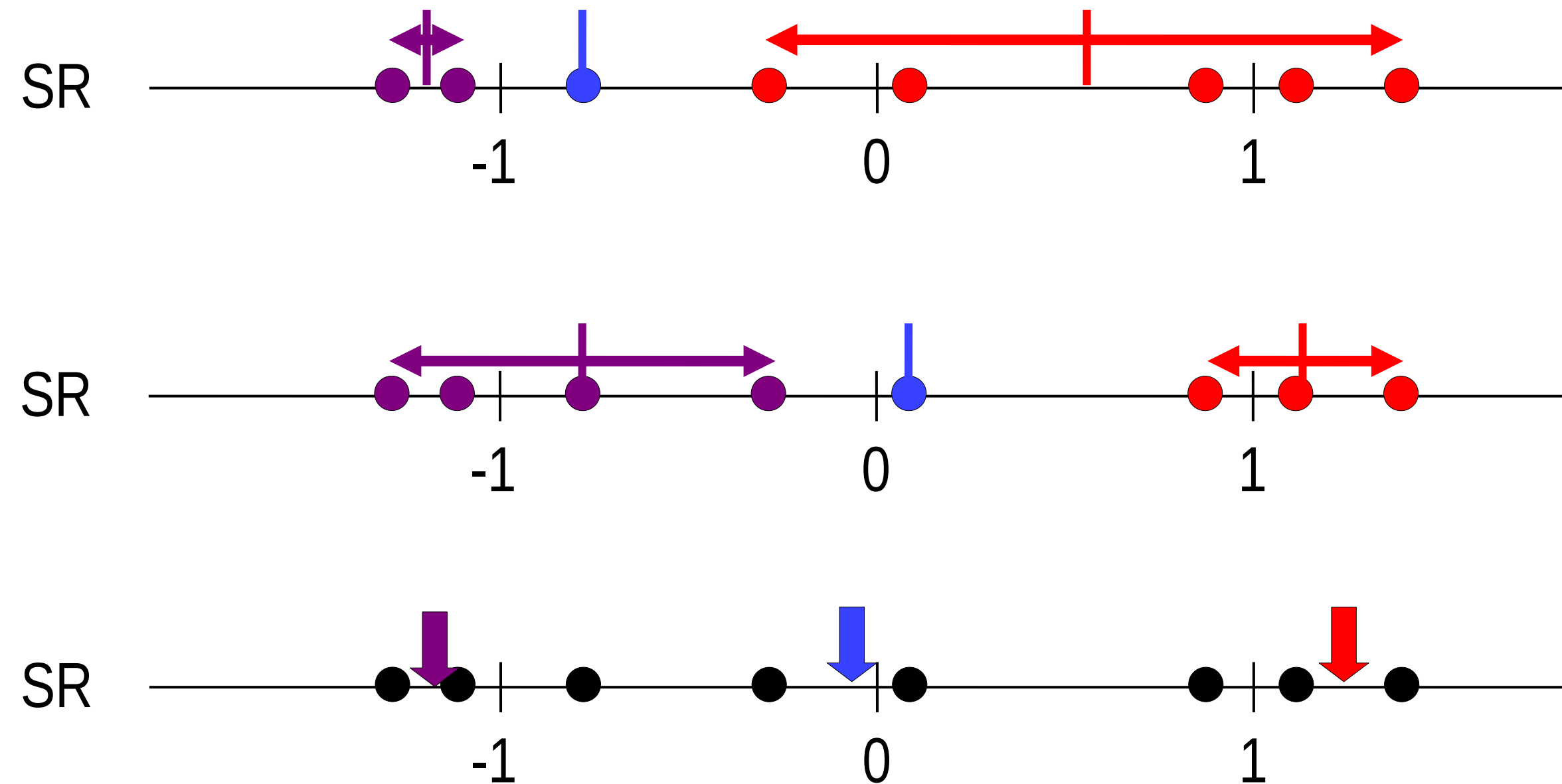
1st run:



2nd run:



1. Choosing the number of clusters: $k = 3$
2. Select cluster centers
3. Assign data points to the nearest cluster
4. Re-initialize centroids



Total within-cluster variance:

1st run:



2nd run:

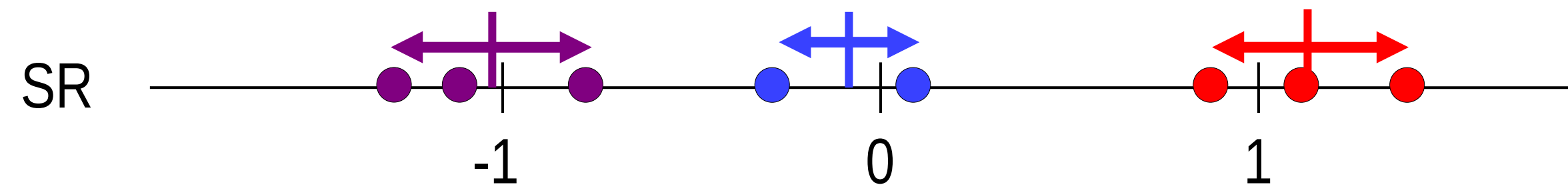
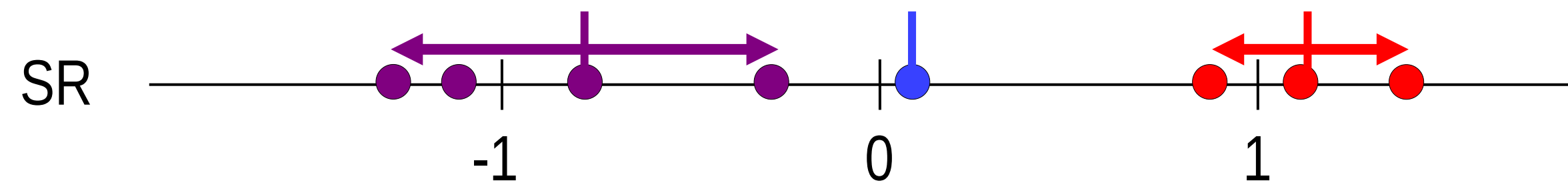
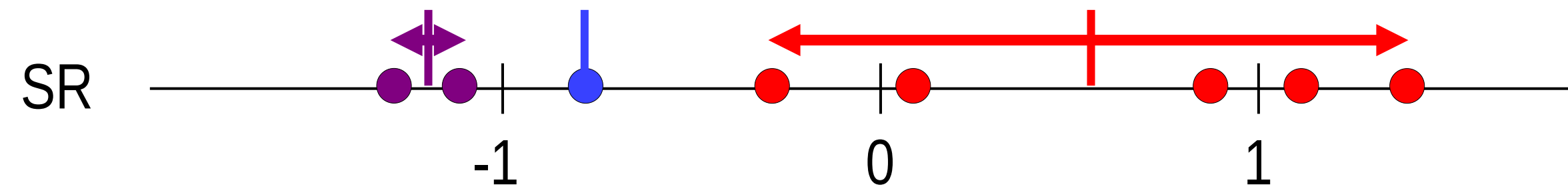


1. Choosing the number of clusters: $k = 3$

2. Select cluster centers

3. Assign data points to the nearest cluster

4. Re-initialize centroids



Total within-cluster variance:

1st run:



2nd run:

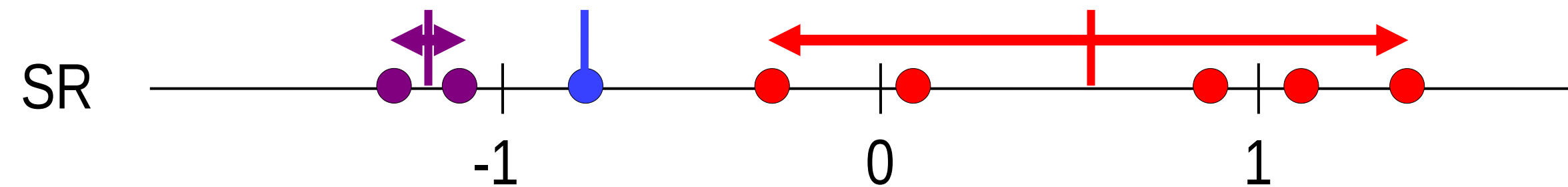


3rd run:

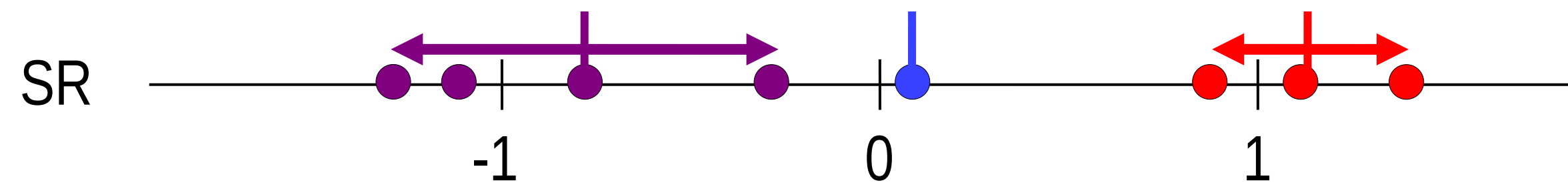


1. Choosing the number of clusters: $k = 3$
2. Select cluster centers
3. Assign data points to the nearest cluster
4. Re-initialize centroids

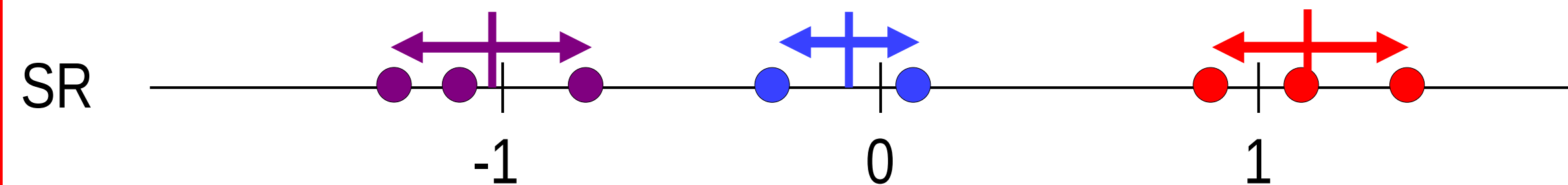
Total within-cluster variance:



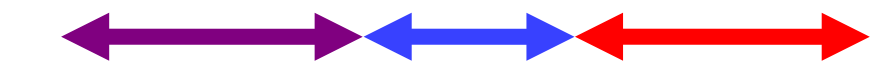
1st run:



2nd run:

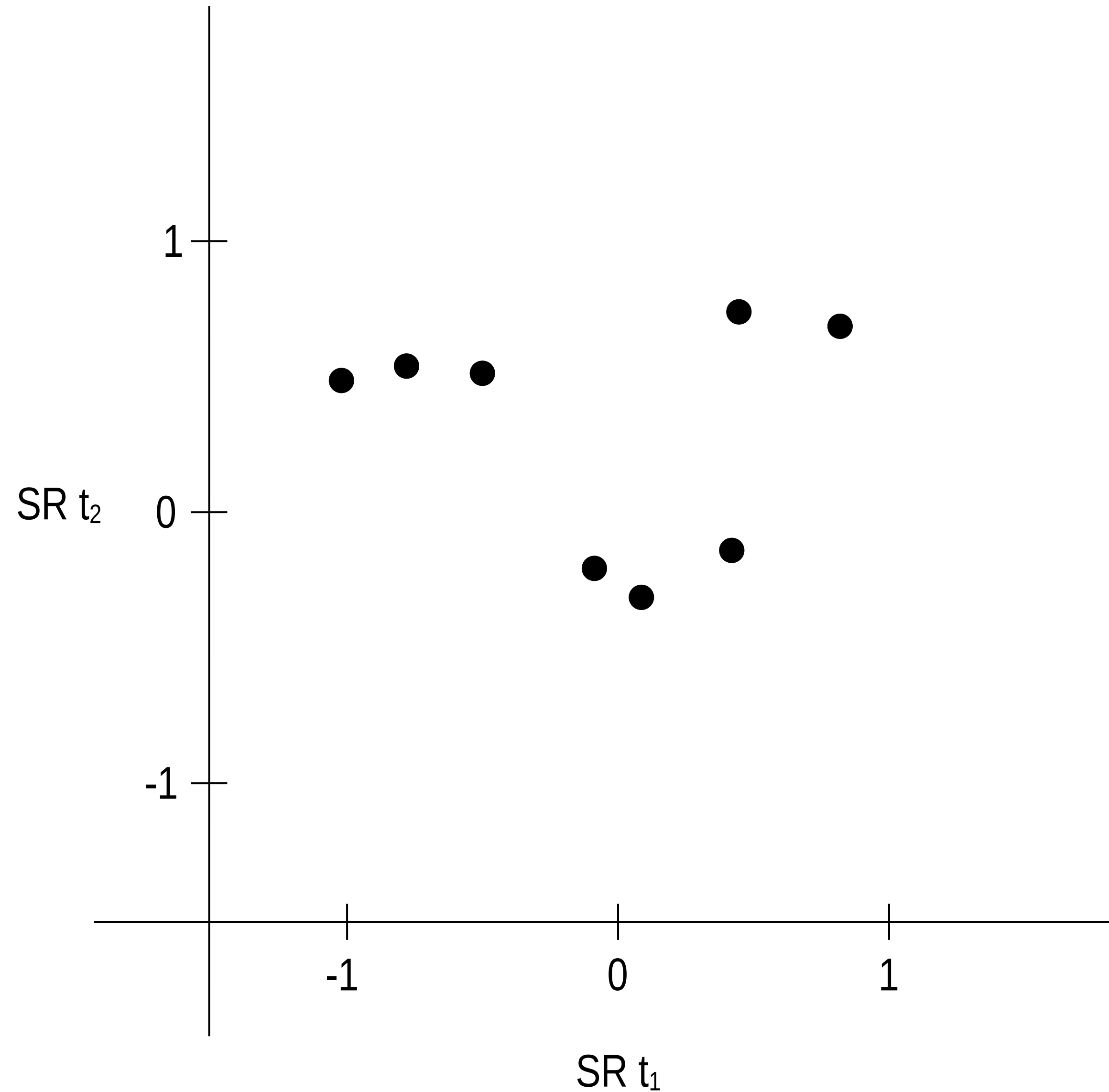


3rd run:

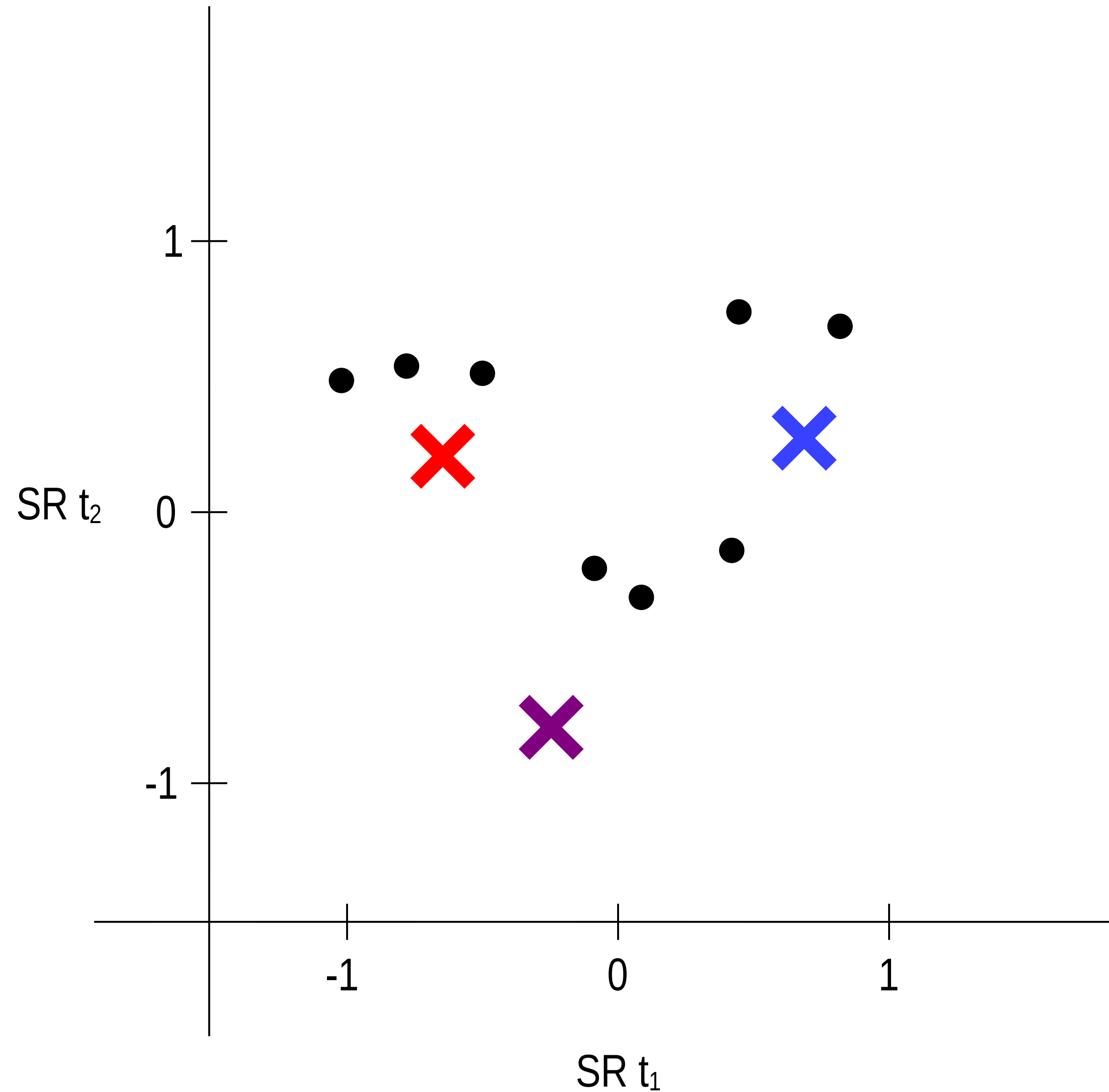


...

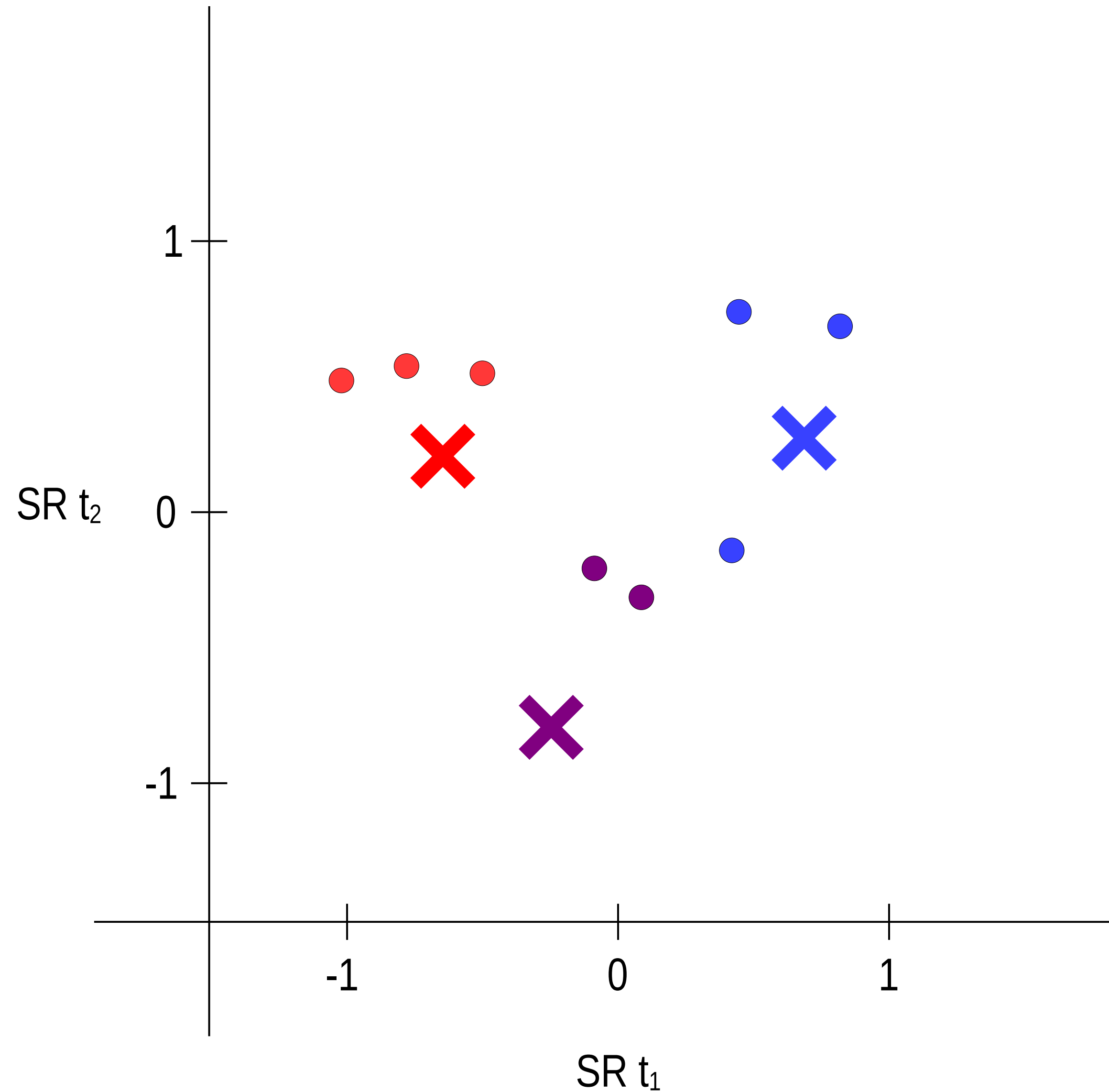
1. Choosing the number of clusters: $k = 3$
2. Initializing centroids
3. Assign data points to the nearest cluster
4. Re-initialize centroids



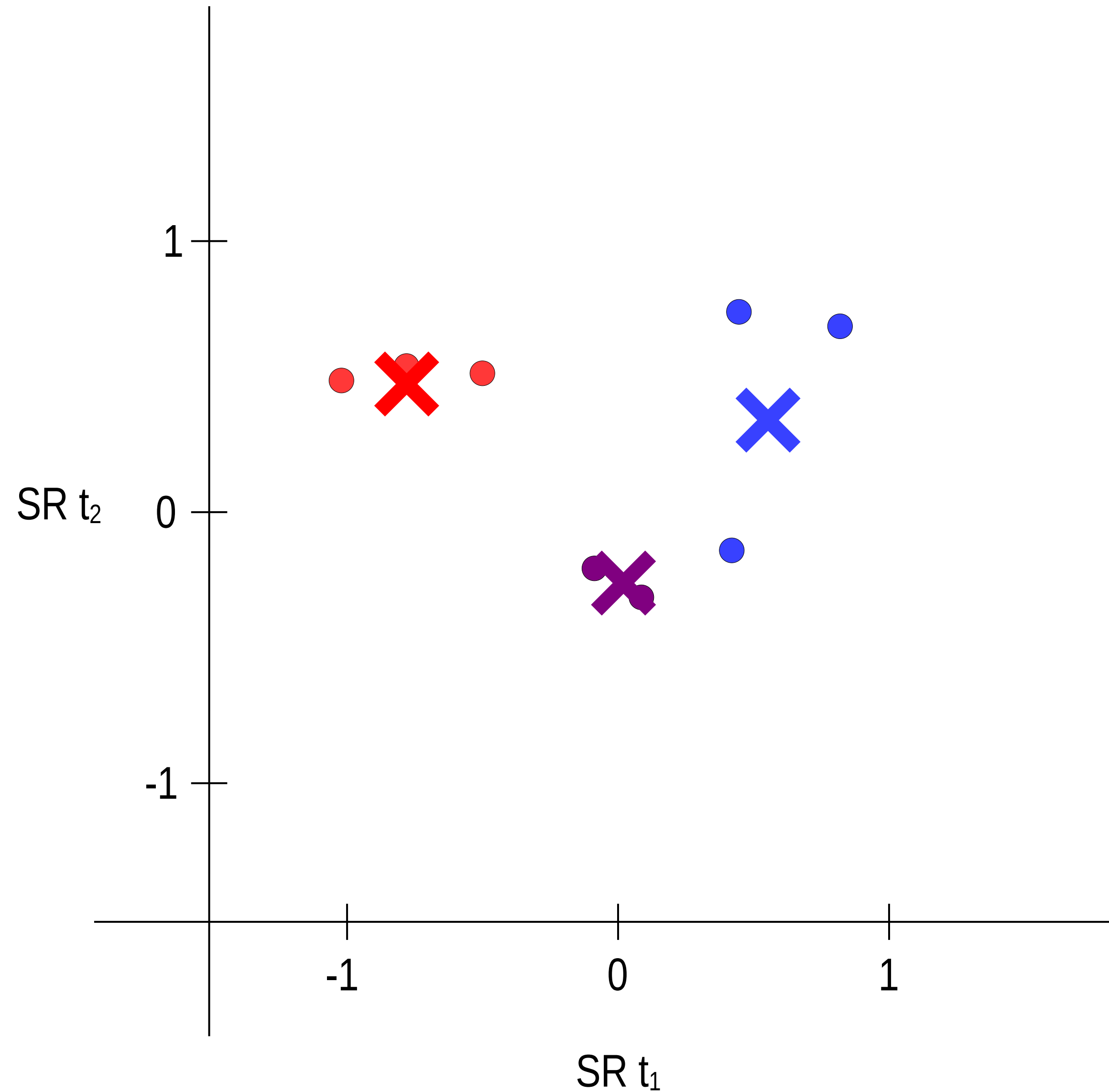
1. Choosing the number of clusters: $k = 3$
2. Initializing centroids
3. Assign data points to the nearest cluster
4. Re-initialize centroids



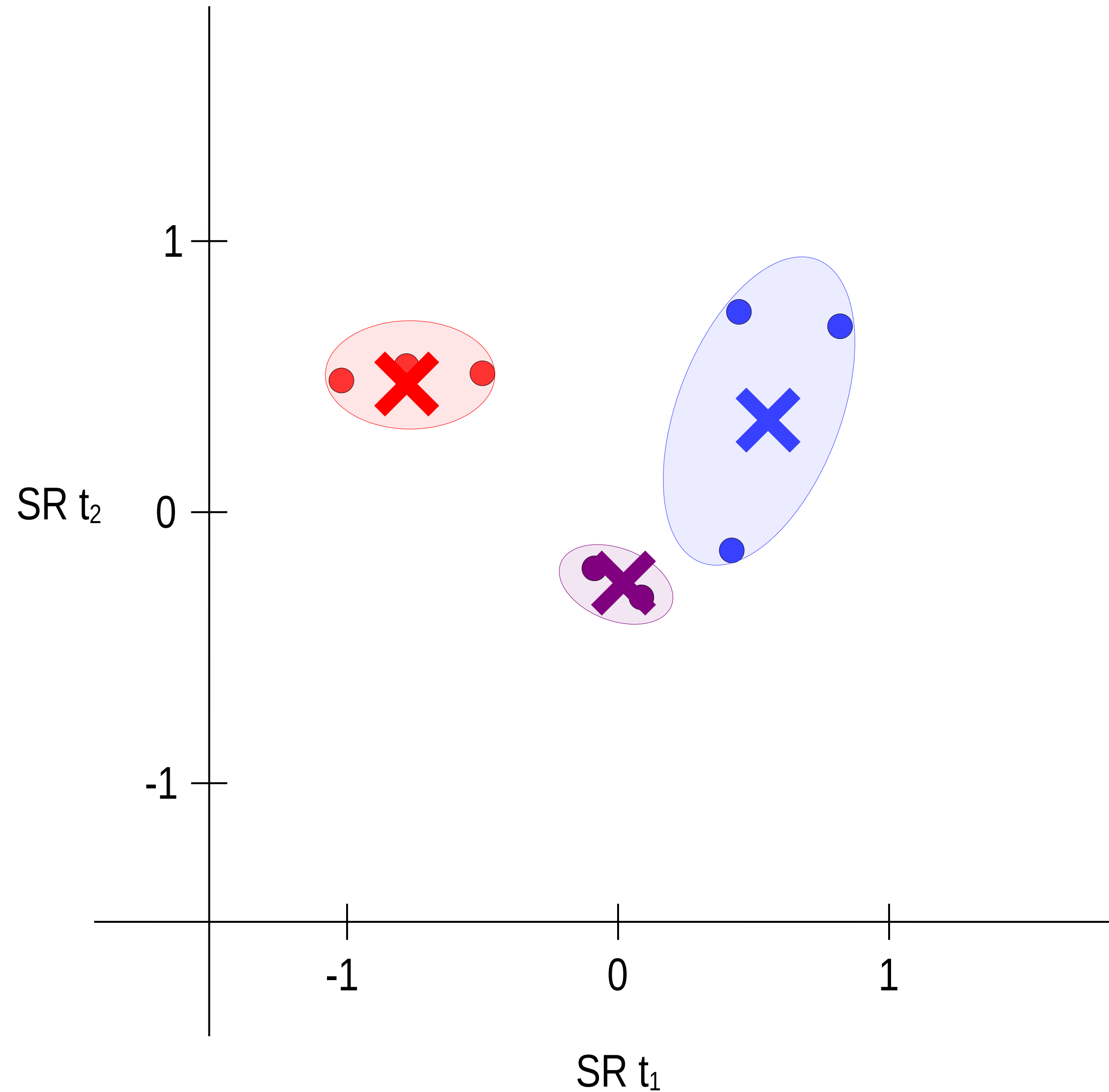
1. Choosing the number of clusters: $k = 3$
2. Initializing centroids
3. Assign data points to the nearest cluster
4. Re-initialize centroids



1. Choosing the number of clusters: $k = 3$
2. Initializing centroids
3. Assign data points to the nearest cluster
4. Re-initialize centroids



1. Choosing the number of clusters: $k = 3$
2. Initializing centroids
3. Assign data points to the nearest cluster
4. Re-initialize centroids



Data Preparation

`clusterLongData` (or `cld` in short) is the constructor for a object of class `ClusterLongData`.

Arguments:

- `traj` [`matrix(numeric)`] or [`data.frame`]: structure containning the trajectories. Each line is the trajectory of an individual. The columns refer to the time during which measures were made.
- `idAll` [`vector(character)`]: single identifier for each trajectory (ie each 'individual').
- `timeInData` [`vector(numeric)`]: precise the column containing the trajectories.

```
cldSDQ <- cld(traj      = data_wide_SR[, c("SR_pre", "SR_peri",  
                                           "SR_post1", "SR_post2")],  
              idAll     = data_wide_SR$subject.ID,  
              timeInData = 1:4)
```


Building partition with kml

kml is a implementation of k-means for longitudinal data (or trajectories).

Arguments:

- `object` [ClusterLongData] (see above)
- `nbClusters` [vector(numeric)]: Vector containing the number of clusters with which kml must work. (Default is 2:6 and maximum number of cluster is 26)
- `nbRedrawing` [numeric] Sets the number of time that k-means must be re-run (with different starting conditions) for each number of clusters.
- `toPlot` [character]: either 'traj' for plotting trajectories alone, 'criterion' for plotting criterion alone, 'both' for plotting both or 'none' for not display anything

```
kml(object      = cldSDQ,  
     nbClusters  = 2:5,  
     nbRedrawing = 100,  
     toPlot      = "none")
```

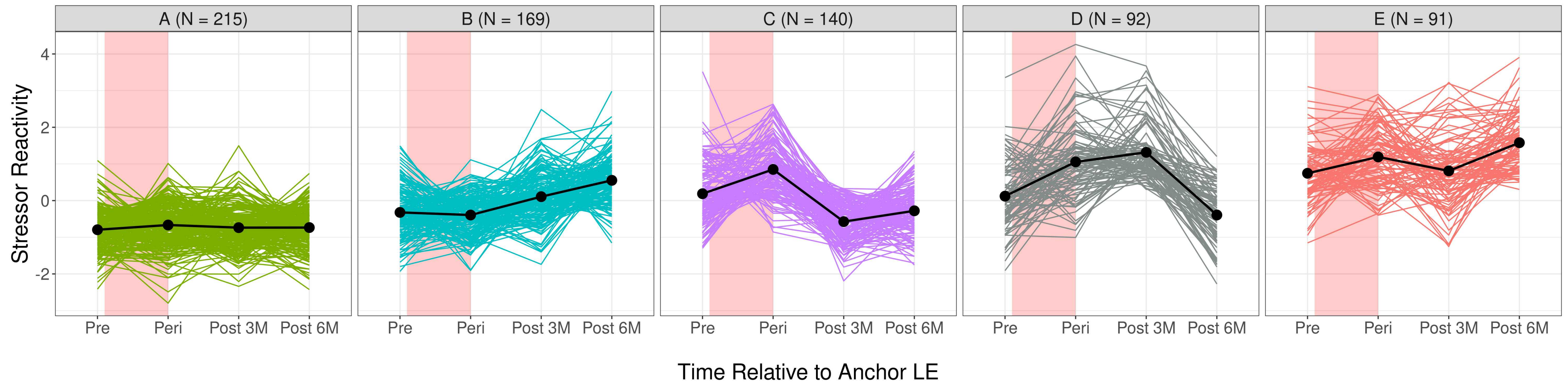
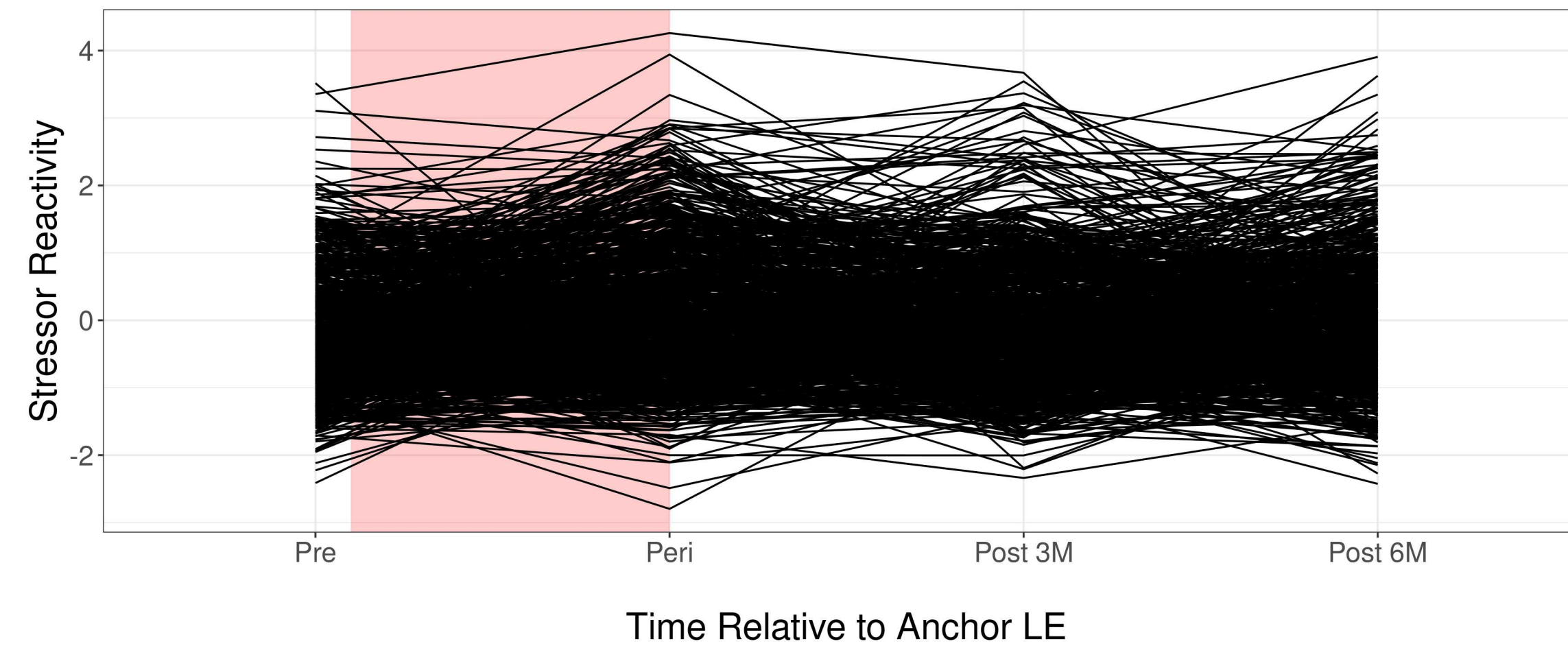
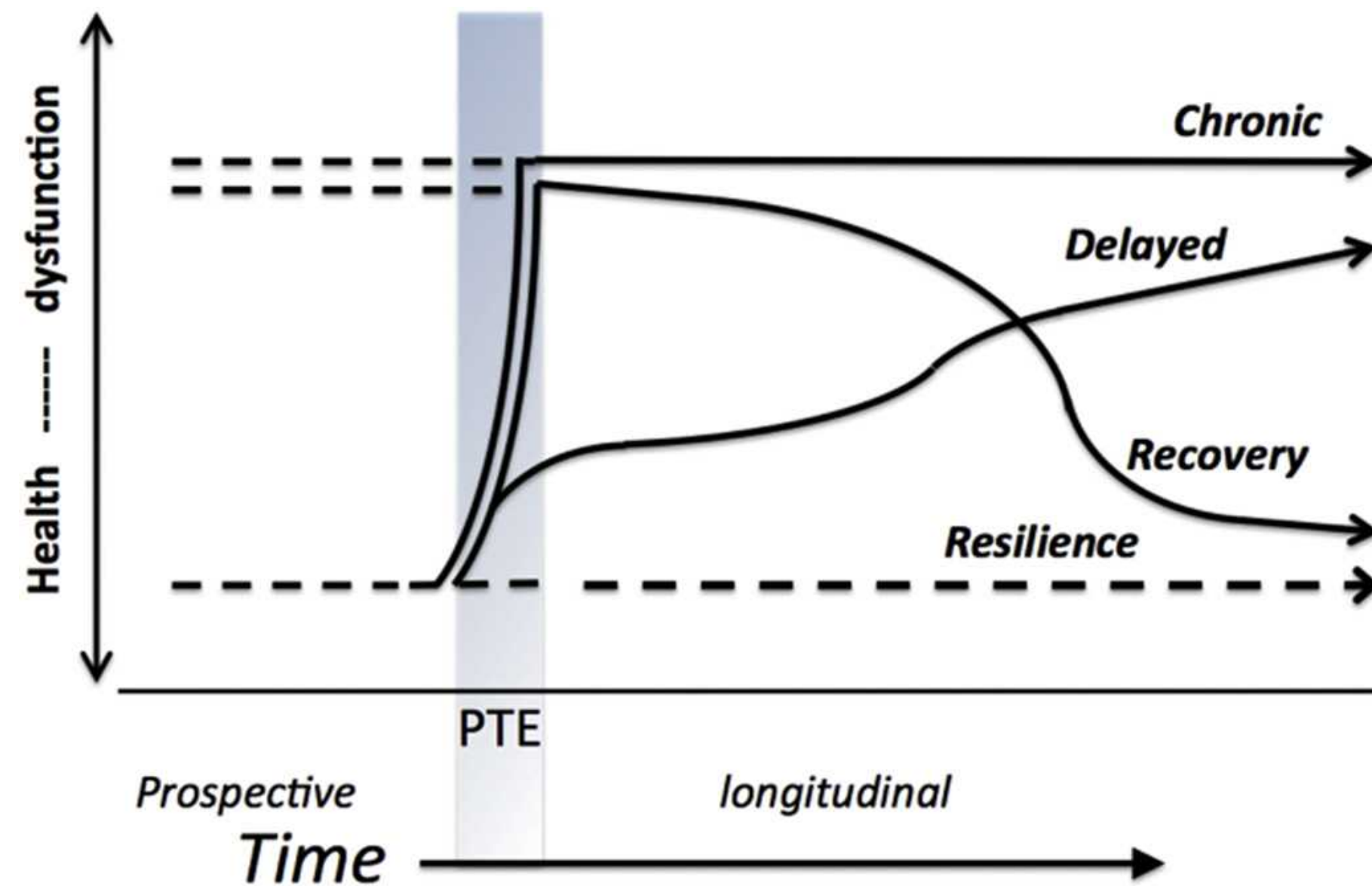
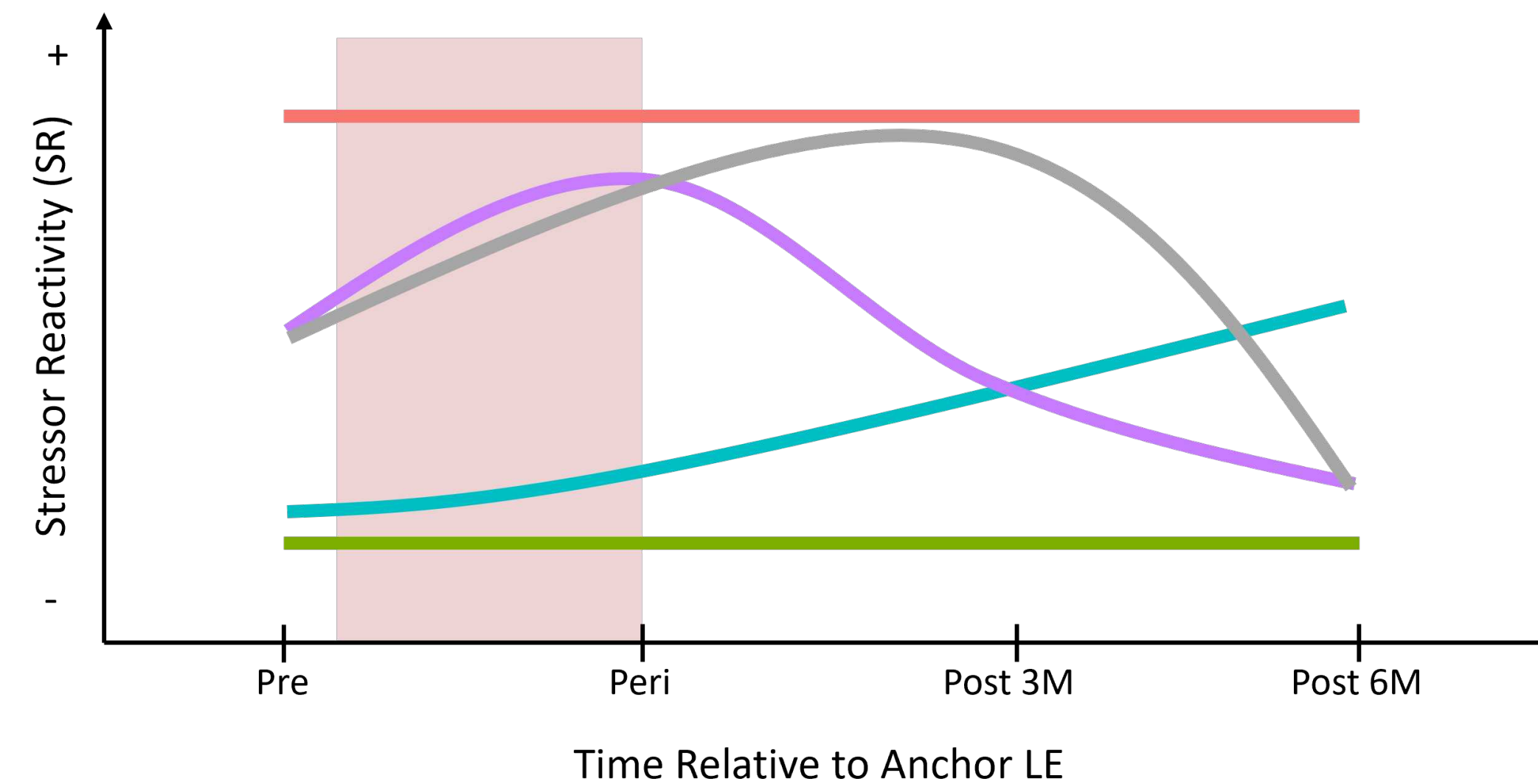



Figure 4.
Commonly observed longitudinal trajectories of response to potential trauma.

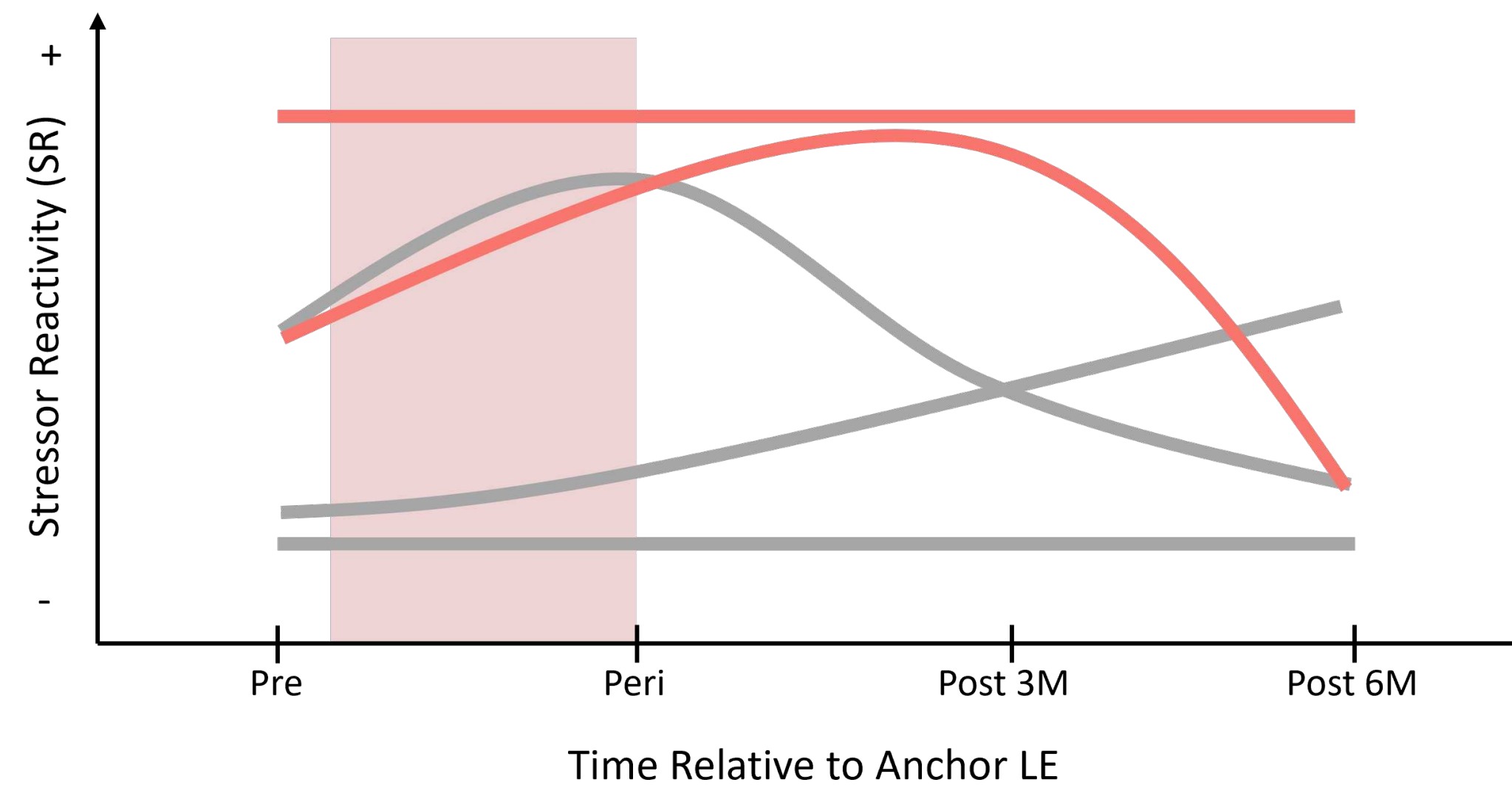


Note. Sourced from Galatzer-Levy et al. (2018).^[1]

Figure 5.
Schematically illustrated trajectories of the presented study.



Note. In order to cluster the trajectories, not the raw mental health scores but the stressor reactivity was used to consider the background stressors.



Predictive validity:
Cluster membership significantly predicts mental disorders.

Thank you for your attention! Are there any questions?