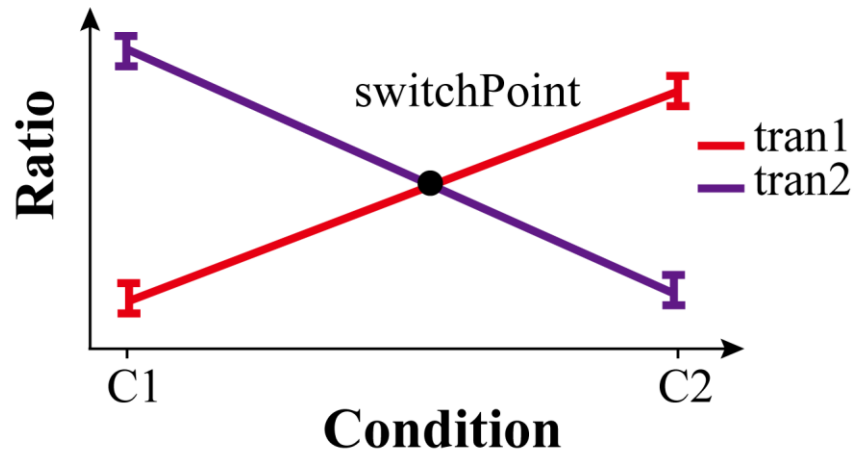


Pairwise TS events



The schematic displays a pairwise TS event intuitively, C1 and C2 represent two different conditions, respectively. The y-axis (**Ratio**) in Figure S1 represents relative abundance of a transcript in the specific condition (e.g. the expression of transcript A divided by the sum of all transcript expression in a gene).

To help users to select TS events with specific patterns, deepTS provided five parameters which are described as below:

meanRa represents the average **Ratio** of a transcript across N_c biological replicates under condition C,

$$meanRa = \frac{sum(Ratio_{tran}|C)}{N_c}$$

Where **Ratio_{tran}C** represents **Ratios** of N biological replicates under condition C, N_c is the number of biological replicates under condition C.

meanExp is similar to **meanRa**, which represents the average expression abundance of a transcript across N_c biological replicates under condition C, the formula is as follows:

$$meanExp = \frac{sum(Exp_{tran}|C)}{N_c}$$

Here, **Exp_{tran}|C** is the expression abundance of the transcript “tran” in N_C biological replicates under condition C. TS events can be further filtered using the following four parameters.

Filtered parameters

- 1) **switchPoint**: a logic value indicating whether there is a cross point between the paired ratio curves in a TS event (default: TRUE).

$$\begin{aligned} &sign (meanRatio_{tran1}|C1 - meanRatio_{tran2}|C1) \\ &\neq sign (meanRatio_{tran1}|C2 - meanRatio_{tran2}|C2) \end{aligned}$$

- 2) **max_Exp**: a numerical vector describing the maximum **meanExp** of two transcripts in a TS events (default: (1, 1)).

$$\{max (meanExp_{tran1}|C1, meanExp_{tran1}|C2), max (meanExp_{tran2}|C1, meanExp_{tran2}|C2)\}$$

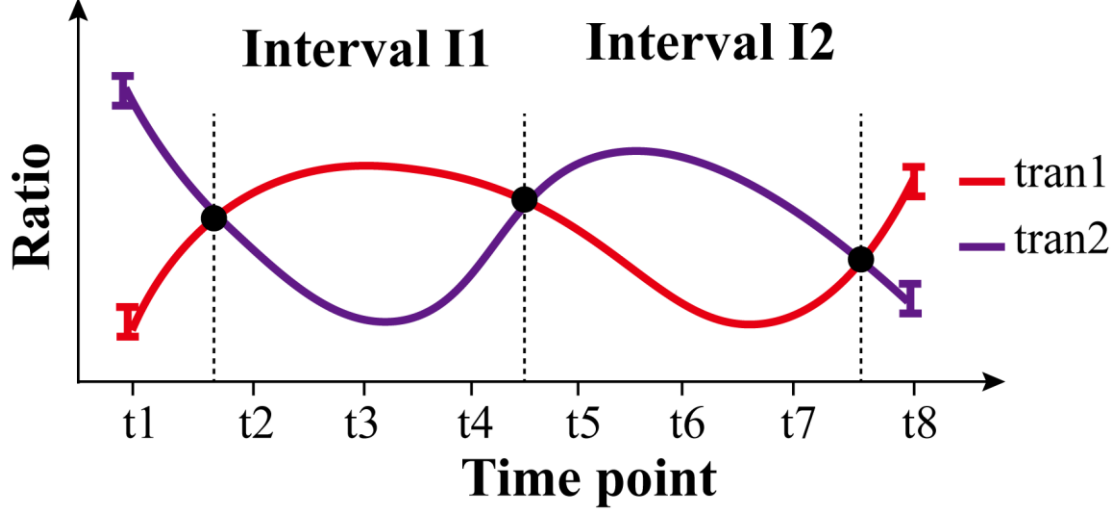
- 3) **max_FC**: a numerical parameter presenting the log₂ of maximum fold change of transcripts under two conditions (default: 2).

$$max (\log_2 \frac{meanExp_{tran1}|C2}{meanExp_{tran1}|C1}, \log_2 \frac{meanExp_{tran2}|C2}{meanExp_{tran2}|C1})$$

- 4) **min_Ratiodiff**: a numerical parameter specifying the minimum **Ratio** difference of two transcripts under two conditions (default: 0.15).

$$\begin{aligned} &min (|meanRa_{tran1}|C1 - meanRatio_{tran2}|C1|, |meanRa_{tran1}|C2 \\ &\quad - meanRa_{tran2}|C2|) \end{aligned}$$

Time-series TS events



The schematic shows a time-series TS event between transcript “tran1” and “tran2”, where **Ratio** represents relative abundance for a transcript at a time point. The time series with eight time points are divided into four intervals by the intersection points of average expression. For each switch point, a series of scores are calculated and used to construct filtered metrics. For example, I₁ and I₂ are before and after time interval of a switch point, each contains three consecutive time points.

$$I1: \{t2, t3, t4\} \quad I2: \{t5, t6, t7\}$$

meanExp is similar to **meanRa**, which represents the average Ratio of a transcript at time interval I,

$$meanRa = \frac{\sum(Ratio_m_{tran}|I)}{N_I}$$

Where **Ratio_m_{tran}|I** represents the average **Ratio** of biological replicates at each time point in interval I, **N_I** is the number of time points at time interval I. Similarly,

meanExp represents the average expression abundance of a transcript at time interval I,

$$meanExp = \frac{sum(Exp_{m_{tran}}|I)}{N_I}$$

Where **Exp_m_{tran}|I** represents the average expression abundance of biological replicates at each time point in interval I TS events can be further filtered using the following eight parameters:

Filtered parameters

- 1) **num**: a numerical vector describes the least number of consecutive time points in interval I_1 and I_2 (default: (1,1));

$$(N_{I1}, N_{I2})$$

- 2) **cor**: the Pearson's correlation coefficient between the expression values of the paired transcripts across time courses in interval I_1 and I_2 (default: -0.2);

$$correlation(Ratio_{m_{tran1}}|(I1 + I2), Ratio_{m_{tran2}}|(I1 + I2))$$

- 3) **freq**: a numerical value in the range of 0–1, reflecting that the frequencies of samples of one transcript is greater than that of the other in interval I_1 and is less in interval I_2 (default: 0.5);

$$|P(Ratio_{m_{tran1}} > Ratio_{m_{tran2}}|I1) + P(Ratio_{m_{tran1}} < Ratio_{m_{tran2}}|I2) - 1|$$

- 4) **diff_ra**: a numerical vector describes the mean difference between two transcripts in terms of relative abundance in intervals I_1 and I_2 (default: (0.3, 0.3));

$$((meanRa_{tran1} - meanRa_{tran2})|I1, (meanRa_{tran1} - meanRa_{tran2})|I2))$$

5) **diff_pvalue**: a numerical vector describes the significance level of the difference between the relative abundances of two transcripts in intervals I_1 and I_2 (default: (0.05, 0.05));

$$(t.test(Ratio_{m_{tran1}}|I1, Ratio_{m_{tran2}}|I1), t.test(Ratio_{m_{tran1}}|I2, Ratio_{m_{tran2}}|I2))$$

6) **change_ra**: a numerical vector describes the difference in relative abundance of each transcript between interval I_1 and I_2 (default: (0.2,0.2));

$$((meanRa_{tran1}|I1 - meanRa_{tran1}|I2), (meanRa_{tran2}|I1 - meanRa_{tran2}|I2))$$

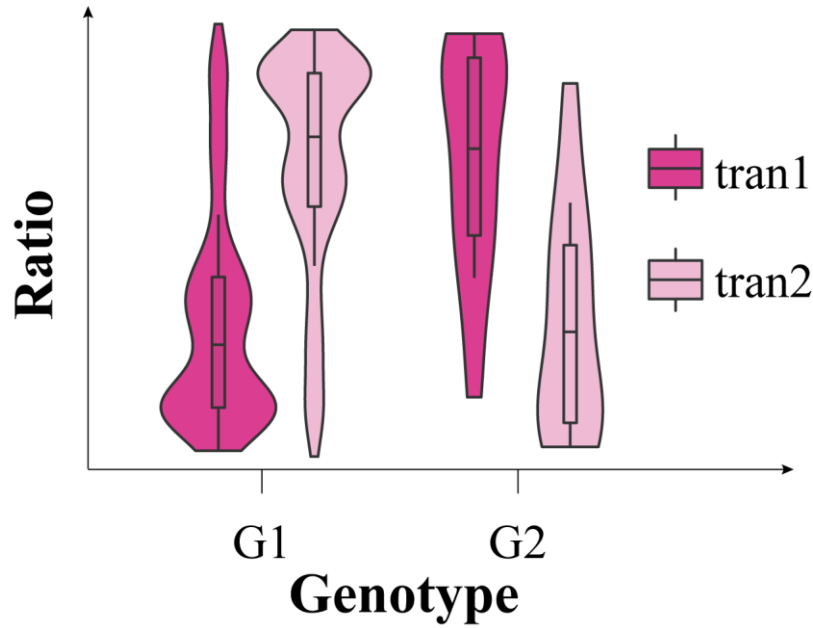
7) **diff_exp**: a numerical vector describes the mean difference between two transcripts in terms of expression values in intervals I_1 and I_2 (default: (3, 3));

$$((meanExp_{tran1} - meanExp_{tran2})|I1, (meanExp_{tran1} - meanExp_{tran2})|I2)$$

8) **change_exp**: a numerical vector describes the difference in average expression value of each transcript between interval I_1 and I_2 (default: (3,3)).

$$((meanExp_{tran1}|I1 - meanExp_{tran1}|I2), (meanExp_{tran2}|I1 - meanExp_{tran2}|I2))$$

Population TS events



The schematic shows a sQTL associated TS event, **Ratio** represents the relative abundance of a transcript in a genotype, G1 and G2 are two different genotypes. Several parameters are defined to filter population transcriptome derived TS events. **meanRa** represents the average **Ratio** of transcript “tran with genotype G,

$$meanRa = \frac{\sum(Ratio_{tran}|G)}{N_G} \quad G: \{G1, G2\}$$

Where **Ratio_{tran}|G** is the **Ratio** of transcript “tran” in population samples with genotype G; **N_G** is the number of population samples with genotype G. TS events can be further filtered using parameter **diff_Ratio**, which is the relative difference of two transcripts between two genotypes.

$$(meanRa_{tran1} - meanRa_{tran2})|G1 - (meanRa_{tran1} - meanRa_{tran2})|G2$$