### The USA algorithm

#### (a) Compendium data

**TF**
- Gene1
- Gene2
- Gene3
- Gene4
- Gene5
- Gene6
- Gene7
- Gene8
- GeneY
- GeneZ

**All genes**

#### (b) Experimental conditions

For a TF target gene pair (e.g. TF → Gene2)

i) all the known genes regulated by this TF (e.g. Gene2, 4, 6)

ii) the TF target gene pair

#### (c) Invert normalized expression profiles of input genes with inhibitory relationship to the TF

<table>
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<th>Input target</th>
<th>Other known input target</th>
<th>Putative target</th>
</tr>
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<tbody>
<tr>
<td>1</td>
<td>TF → Gene2</td>
<td>TF → Gene4, 6</td>
<td>TF → Gene1, 3, 7, 8</td>
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#### (d) Calculate the genes weighted row average across the selected conditions c

\[
S_g = \frac{\sum c (S_c E_{gc})}{\#\text{genes}}
\]

**TF**
- Gene1
- Gene2
- Gene3
- Gene4
- Gene5
- Gene6
- Gene7
- Gene8
- GeneY
- GeneZ

**All genes**

#### (e) Select the genes whose weighted row average across the selected conditions c satisfies \(|S_g - \text{mean}(S_g)| > threshold_{row}\)

- Gene1
- Gene2
- Gene3
- Gene4
- Gene5
- Gene6
- Gene7
- Gene8

#### (f) Correlate the expression profile of the input target Gene2 (across the UTM conditions) with each of the other gene profiles in the UTM. Retain genes whose correlation coefficient R satisfies \(|R| > \alpha = threshold_{correlation}\)

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**UTM**

**Conditions**
- 3
- 5
- 7
- 9
- 11
- 13
- 14
- 15