SUPPLEMENTARY MATERIALS for the paper

Alain B. Tchagang, Kevin V. Bui, Thomas McGinnis, Panayiotis V. Benos,
"***Extracting biologically significant patterns from short time series gene expression data***"

ASTRO pseudo code

```
Input
    - $A_0$ = raw gene expression data,
    - $G$ = set of genes
    - $T$ = set of sample time points
    - $\varepsilon$ = filtering threshold
Output
    - C{k} = coherent clusters
    - I{k} = set of genes in clusters
    - J{k} = set of time points in clusters
Begin
    A = filter(A_0, ε); [N,M] = size(A); % remove constant genes.
    R = rank(A); [N_R,M_R] = size(R); % rank matrix construction.
    U = union(R,R,'rows'); [N_U,M_U] = size(U); % identify sets of distinct patterns.
        For k = 1:N_U
            For n = 1:N_R
                If R(n,:) == U(k,:)
                    C{k} = [C{k};A(n,:)]
                    I{k} = [I{k};G(n)];
                End If
            End For; J{k} = T;
        End For
End begin
```

MiMeSR pseudo code

```
Input
    - $A_0$ = raw gene expression data,
    - $G$ = set of genes
    - $T$ = set of sample time points
    - $\varepsilon$ = filtering threshold
    - $I_0$ = minimum number of genes in a cluster
Output
    - $C\{k\}$ = minimum mean squared residue clusters
    - $I\{k\}$ = set of genes in clusters
    - $J\{k\}$ = set of time points in clusters
Begin
    $A$ = filter($A_0$, $\varepsilon$);  $[N,M]$ = size($A$); $k = 0$; $X = [0]$;
    For $n = 1:N$
        If $n \notin X$
            o Construct $Z_1$, using row $n$ of $A$.
            o $Z_2 = A - Z_1$
            o $Index$ = find(max($Z_2$')-min($Z_2$') < $\varepsilon$)
            o If $Index \geq I_0$
                ▪ $k = k+1$;
                ▪ $C\{k\} = A(Index,:)$;
                ▪ $I\{k\} = G(Index)$;
                ▪ $J[k\} = T$;
            o End If
            o $X$ = union($X$,$Index$)
        End If
    End For
End begin
```