```
      ┌─────────────┐
      │    Start    │
      └─────────────┘
             │
             ▼
```

Dataset $\mathcal{D}$
It is a 3D-array of dimentions $(V \times T \times S)$. Here, $V =$ number of genes, $T =$ number of time points in each time series, $S =$ number of time series.

```
             │
             ▼
```

Compute the Mutual Information (MI) matrix, denoted by $\mathcal{M}$. It is a $(V \times V)$ matrix. The $(v_i, v_j)^{th}$ cell of $\mathcal{M}$, denoted by $\mathcal{M}(v_i, v_j)$, represents the estimated MI value between v_i and v_j.

```
             │
             ▼
```

Initialize $\mathcal{G} \leftarrow$ a null graph over $(V \times T)$ nodes.

```
             │
             ▼
```

$\mathcal{G}_{\mathrm{CLR}} \leftarrow \mathrm{CLR}(\mathcal{D}, \mathcal{M})$ (Algorithm 2, main paper).

```
             │
             ▼
```

Set $p \leftarrow 1$

```
             │
             ▼
```