**Method section:**

**1.1** **Clock-controlled expression simulation based on peak phase**

Using the peak phase data, we simulated expression of each clock-controlled mRNA and protein over a 24 hour period starting at DD. Expression is simulated using arbitrary amplitude units that vary between 0 and 2, with 2 being the "peak phase" (θ) according to the following function:

  {Latendresse, 2011 #2}

Where the period T=24, the amplitude A and the offset D both equal 1. Time *t* is simulated every 2 hours from DD at 0h, to 22h.

**1.2 Metabolic overview posters1**

* Clock-controlled mRNA peak phase
* Clock-controlled protein peak phase
* Number of hours the protein peak lags the mRNA peak

**1.3** **Metabolic overview animation2**

* mRNA - Using the PwyRNAOscillations dataset, we overlaid a 24-hour time series of clock-controlled mRNA simulated expression onto the cellular overview.

**1.3.1****Clock-controlled mRNA expression simulation**

* + RNAOscillations.tsv contains expression data for all clock-controlled mRNA. This dataset is used to generate the mRNA Omics Dashboard char
  + PwyRNAOscillations.tsv contains expression data for only clock-controlled mRNA whose product is an enzyme in a known pathway. This dataset is used to generate the mRNA cellular overview animation.
* Protein - Using the PwyProteinOscillations dataset we generated an animation of the proteins using the NeurosporaCyc Omics Viewer

**1.3.2** **Clock-controlled protein expression simulation**

* ProteinOscillations.tsv contains expression data for all clock-controlled proteins. This dataset is used to generate the protein Omics Dashboard charts
* PwyProteinOscillations.tsv contains expression data for only clock-controlled proteins that are enzymes in a known pathway. This dataset is used to generate the protein cellular overview animation.

**1.4****Omics dashboard3**

For the omics dashboard,

* Black color represents mRNA expression
* Red color represents protein expression
* Each small dot represents the expression of a single gene in the pathway class (Amino Acid synthesis, for example) at a specific time point.
* The large dot represents the average amplitude across all genes in that pathway class for that time point.
* The line connecting the dots represents the "spread" of different expression levels for the genes in the pathway.
* RNAandProteinOscillations12.pdf displays 12 data points per clock-controlled gene, where simulated mRNA and Protein expression is alternated every 2 hours: 0h\_mRNA, 2h\_protein, 4h\_mRNA, 6h\_protein, 20h\_mRNA, 22h\_protein.
* RNAandProteinOscillations24.pdf displays 24 data points per gene, where simulated mRNA and Protein expression is interleaved: 0h\_mRNA, 0h\_protein, 2h\_mRNA, 2h\_protein, 22h\_mRNA, 22h\_protein

### **1.4.1****Interleaving Protein and RNA Oscillations for the Omics Dashboard charts**

RNAandProteinOscillations24.tsv contains 24 data points per gene, where simulated mRNA and Protein expression is interleaved: 0h\_mRNA, 0h\_protein, 2h\_mRNA, 2h\_protein, 22h\_mRNA, 22h\_protein

### **1.4.2****Alternating Protein and RNA Oscillations for the Omics Dashboard charts**

RNAandProteinOscillations12.tsv contains 12 data points per clock-controlled gene, where simulated mRNA and Protein expression is alternated every 2 hours: 0h\_mRNA, 2h\_protein, 4h\_mRNA, 6h\_protein, 20h\_mRNA, 22h\_protein

**1.5****SmartTables4**

* Hours the Protein peak lags behind the RNA peak.
* Clock-controlled mRNA and Protein Peak Phases for Neurospora
* 24-hour simulated expression based on peak phase:
  + All clock-controlled mRNA's in *N. crassa*
  + All clock-controlled proteins in *N. crassa*
  + Clock-controlled protein that are enzymes in a known *N. crassa* pathway
  + Clock-controlled mRNA whose product is an enzyme in a known *N. crassa* pathway
  + RNAandProteinOscillations12 contains 12 data points per clock-controlled gene, where simulated mRNA and Protein expression is alternated every 2 hours: 0h\_mRNA, 2h\_protein, 4h\_mRNA, 6h\_protein,20h\_mRNA, 22h\_protein
  + RNAandProteinOscillations24 contains 24 data points per gene, where simulated mRNA and Protein expression is interleaved: 0h\_mRNA, 0h\_protein, 2h\_mRNA, 2h\_protein, 22h\_mRNA, 22h\_protein

**References:**

1. S. M. Paley, P. D. Karp, The Pathway Tools cellular overview diagram and Omics Viewer. *Nucleic Acids Research* **34**, 3771-3778 (2006).
2. M. Latendresse, P. D. Karp, Web-based metabolic network visualization with a zooming user interface. *BMC Bioinformatics* **12**, 176-176 (2011).
3. S. Paley *et al.*, The Omics Dashboard for interactive exploration of gene-expression data. *Nucleic Acids Research*, gkx910-gkx910 (2017).
4. M. Travers, S. M. Paley, J. Shrager, T. A. Holland, P. D. Karp, Groups: knowledge spreadsheets for symbolic biocomputing. *Database: The Journal of Biological Databases and Curation* **2013**, bat061 (2013)