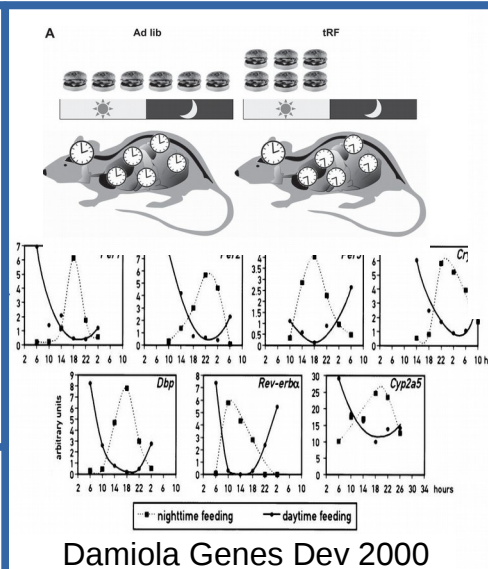
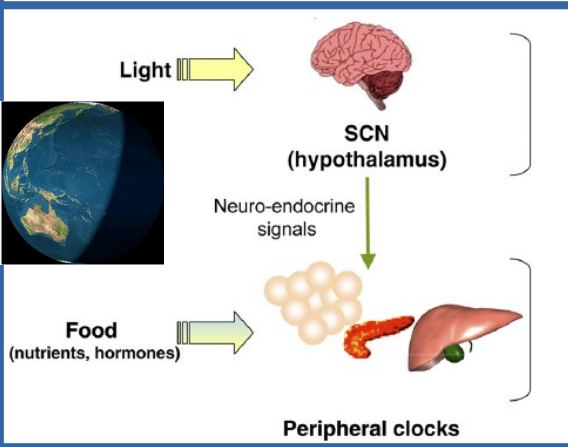
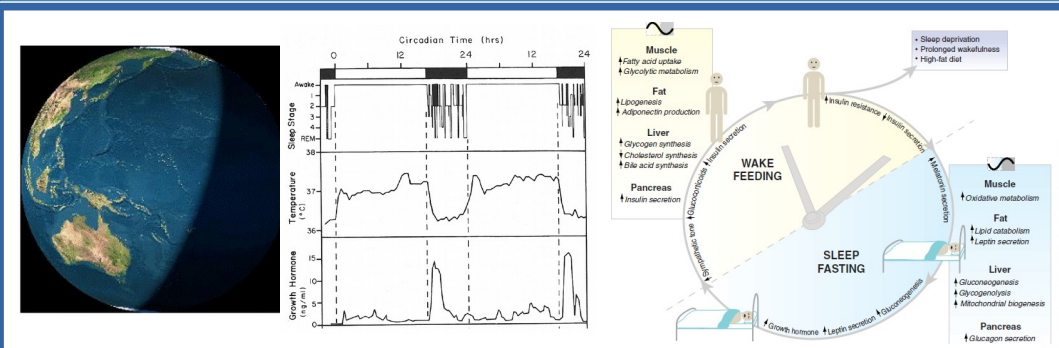


Modeling the entrainment of liver clock by feeding/fasting cycles

A. Woller, H. Duez, B. Staels & M. Lefranc (Université de Lille)



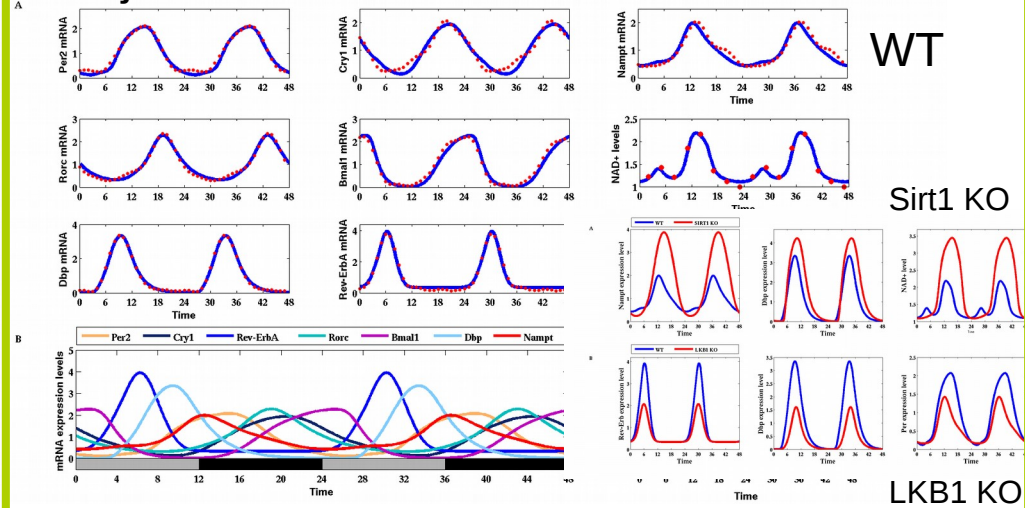
Damiola Genes Dev 2000

Build a mathematical model of clock network...

$$\text{basal_mper} \left(1 + \text{fold_per} \left(\frac{[\text{CB}]}{\text{thr_perc} \cdot (1 + \text{c_srt} \cdot [\text{Sirt1}])} \right)^{\text{hill_percb}} \right)$$

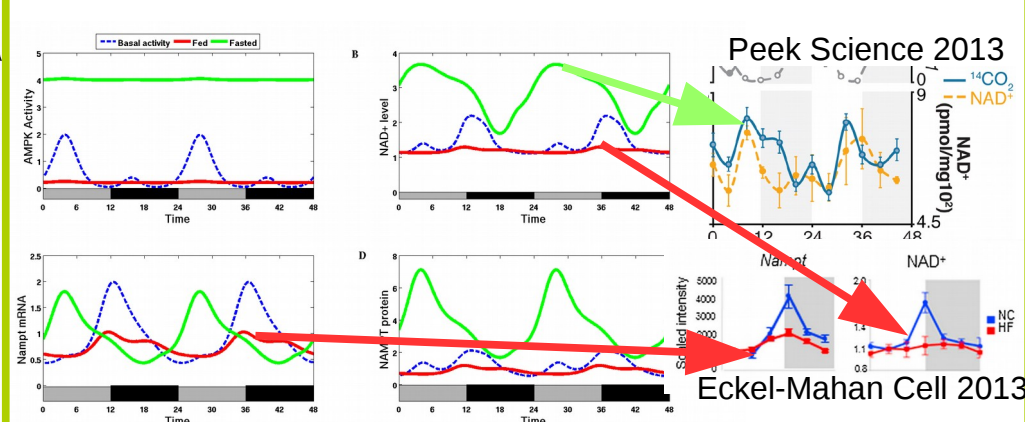
$$1 + \left(1 + \left(\frac{[\text{PC}]}{\text{thr_perpc}} \right)^{\text{hill_perpc}} \right) \left(\frac{[\text{CB}]}{\text{thr_perc} \cdot (1 + \text{c_srt} \cdot [\text{Sirt1}])} \right)^{\text{hill_percb}}$$

Adjustment of the mathematical model



Clock gene data: Hughes et al. Plos Genet. 2012 (Hogenesch gr.), NAD+ data: Hatori et al. Cell Metab 2012 (Panda group).

Simulate various diets by different AMPK profiles



Our minimal mathematical model reproduces the loss of amplitude in clock gene expression and NAD+ levels under high-fat diet as well as phase shift under fasting. Can we design a pharmacological approach to rescue clock profiles? => see poster

Food is the primary zeitgeber for liver clock

Metab. gauges: AMP/ATP, NAD+/NADH

Sensors: AMPK (AMP), SIRT1 (NAD+)

Clock network incorporating the sensors SIRT1 and AMPK ----->

