INFORMATION COMPRESSION IN BIOLOGICAL RHYTHM BY WAVELET ANALYSIS

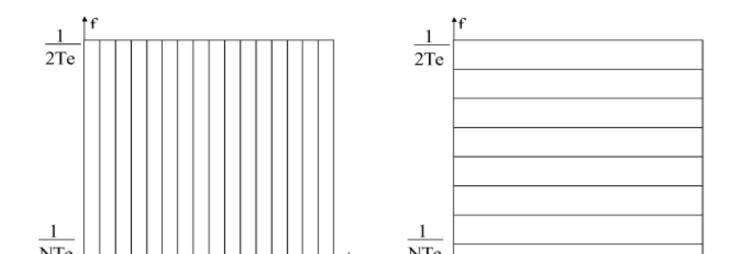
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WAVELET TRANSFORM WAVELET ANALYSIS APPLIED TO BIOLOGICAL RHYTHMS

Time/frequency domains

Representation of rhythms in time/frequency (t/f) domain is linked to data processing.

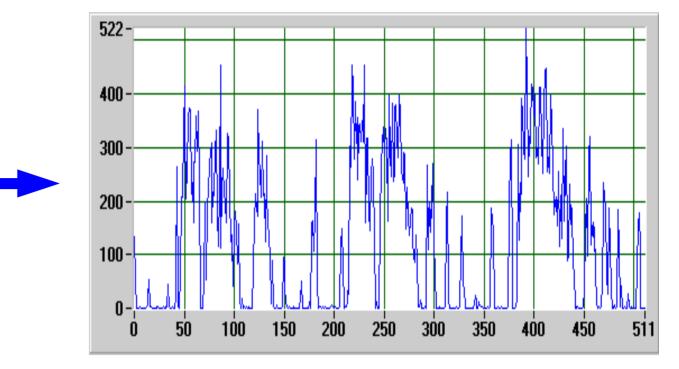


Biological rhythm analysis and reconstruction

Examples from rhythm activity of inbred strains of mice (in L:D 12:12) defined with 512 samples in a 3 day window.

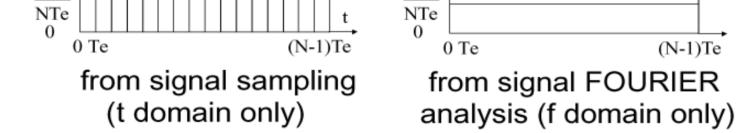
7-6-5-4-3-2-1reconstructions

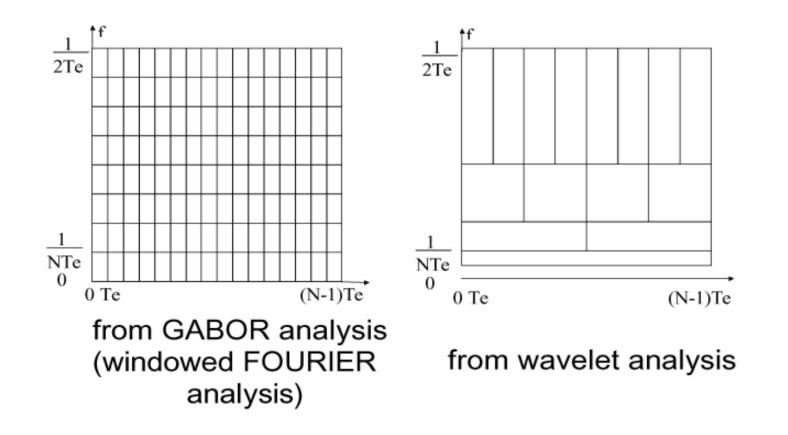
Exact : L=100%; r=1, τ=0



temporal original signal

wavelet transform





Only the last two cases allow simultaneous time and frequency study; but wavelet transform optimises t/f domain.

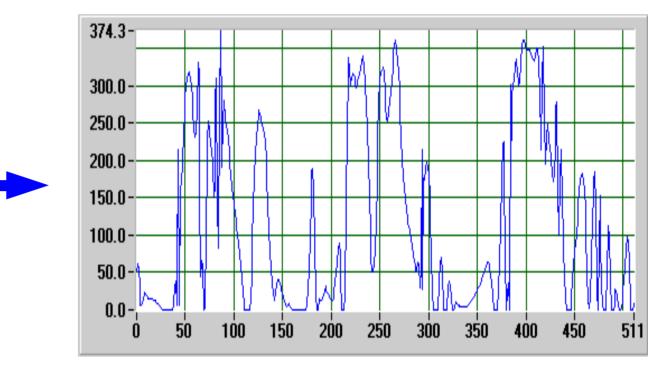
Continuous case

From the wavelet analysing Ψ defined with the conditions :

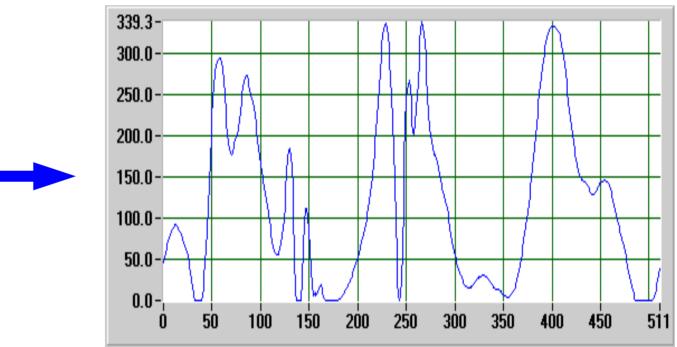
Reconstruction efficiency is measured by correlation between original and reconstructed signals. - r is the maximum normalised correlation

- τ the shift of this maximum (in samples)

reduce data quantity more than 90% without information loss in order jto simplify comparison between rhythms to characterize genetic or interindividual differences L=10%; r=0.95, τ=0



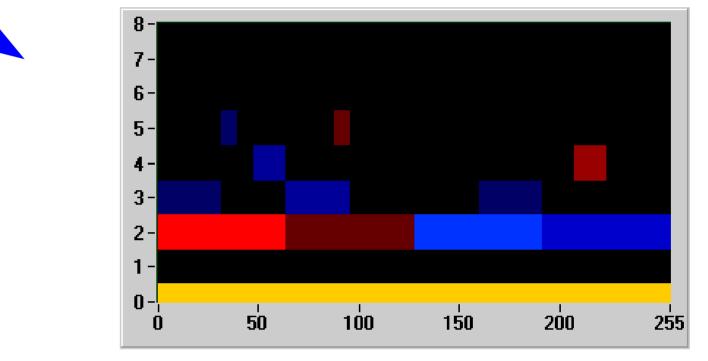
L=2.5%; r=0.88, τ=-1



Directly on WT graph we can observe : - at very low frequency (at the bottom) the stationarity - at frequency corresponding to 1 day, the intensity of circadian component - at medium frequency a pulsatile activity phased with light/dark synchronizer



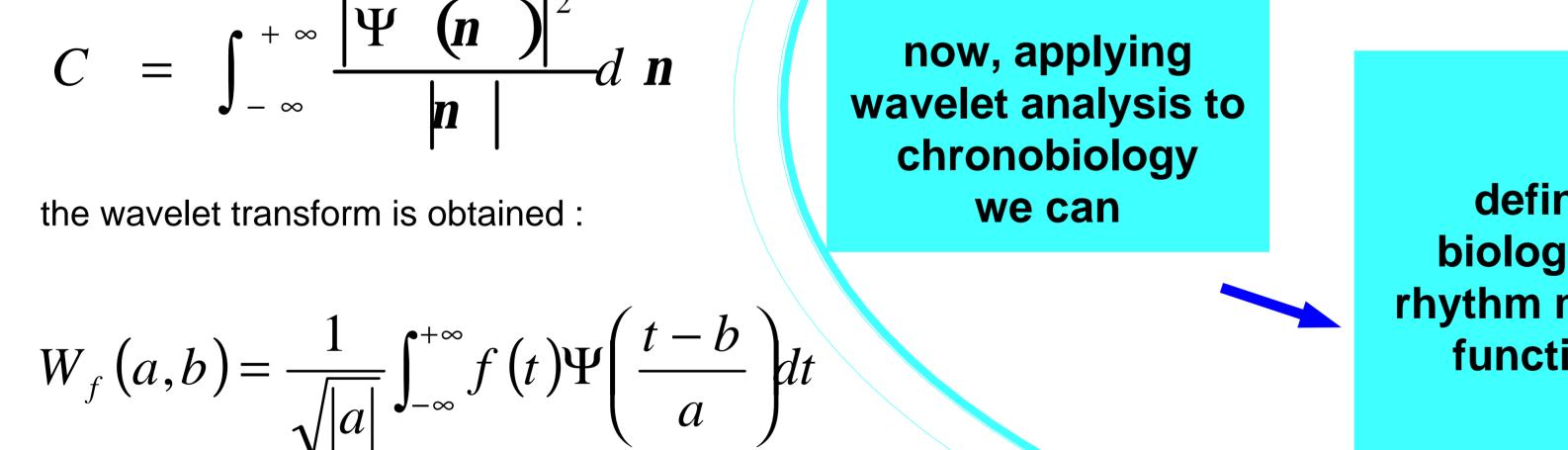
Threshold criterion here is obtained by suppression of coefficients smaller than L in % of the greater coefficient.



thresholded WTs



SM



 $f(t) = \frac{1}{C} \int_{-\infty}^{+\infty} \int_{-\infty}^{+\infty} \Psi(a,b) W_f(a,b) \frac{da}{a^2} db$

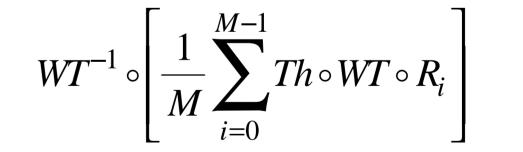
where *a* is a dilatation coefficient (f domain) *b* a time translation coefficient (t domain)

define biological rhythm model function

in order to study evolution of rhythm to characterize behavioural deregulations induced by environment or age or pharmacology

in order to associate a prototype rhythm to a population Method :

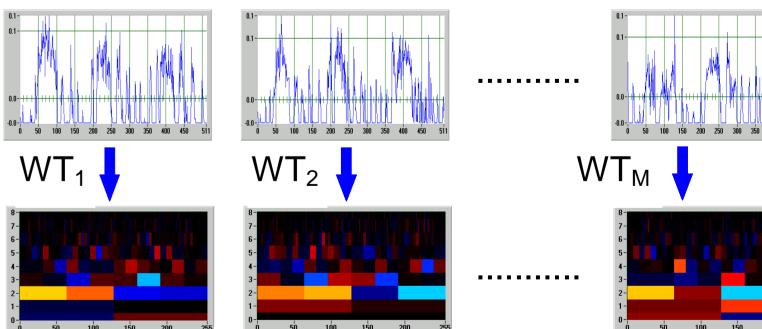
in a population each subject rhythm S_i is analysed
 on each WT_i an identical Th function is applied
 the WT model function is the mean of these WT_i
 Inverse wavelet transform leads to the model function.



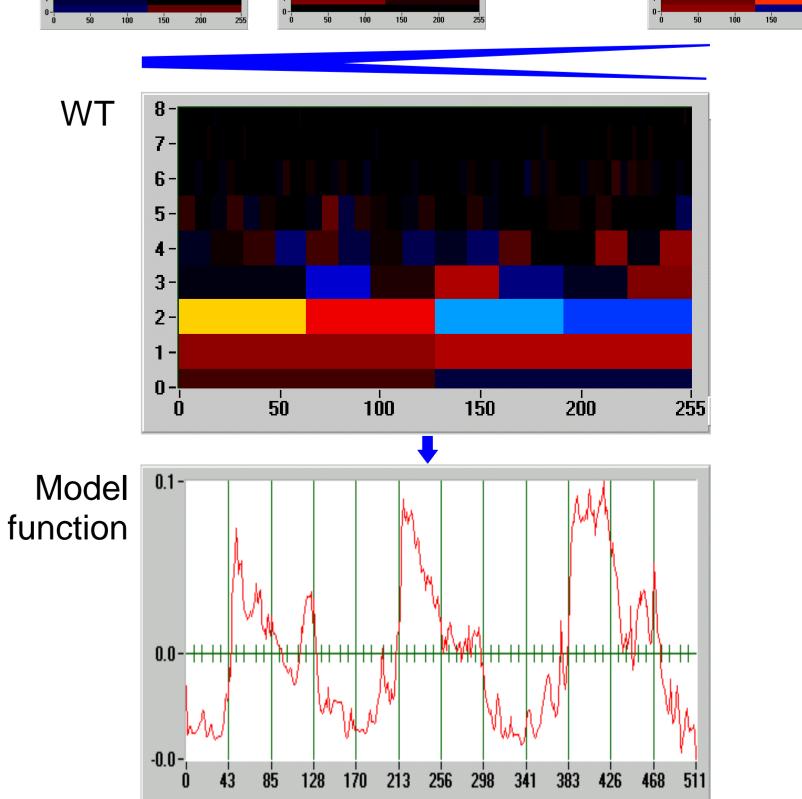
NB : this operation is fundamentally different from a simple averaging by introduction of the non-linearity of thresholding.

S₁

Using model function in order to evaluate rhythm variations



 S_2



Discrete case

Rather than integral calculus, discrete case uses matrix



Model function validation

Correlation (r and τ) between each subject and model function evaluate the quality of the model function. Calculus are performed on a 16 subject population.

	Correlation r	Shift t
Mean	0.66	0.44
Standard devia-	0.08	1.75

where Pi is a permutation matrix and Ti a transform matrix defined with known DAUBECHIES coefficients.

This WT algorithm is extremely fast like FFT but must also use 2^p samples.

Compression method operator:

 $WT^{-1} \circ Th \circ WT$

On the reconstruction the Th operator is defined by a specifically threshold criterion.

 F1 comparisons

 B6 : C57/BI6 strain

 C : Balb/C strain

 CB and BC : reciprocal F1

 F1 comparisons are measured by the correlation coefficient r.

 Here, reciprocal F1 are identical what verify non maternal effect.

