Analyzing Circadian Expression Data by Harmonic Regression Based on Autoregressive Spectral Estimation

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ISMB, 2010

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Outline



Motivation

- The Basic Problem That We Studied
- Previous Work

2 ARSER Algorithm

- Basic Principle
- Application for Large-scale Temporal Datasets

3 Our Results

- Results of Our Synthetic Data
- Results of Public Synthetic Data
- Results on Public Microarray Data

The Basic Problem That We Studied Previous Work

Outline



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The Basic Problem That We Studied Previous Work

Circadian Rhythm: Concept and Description

Definition

A biological rhythm with a periodicity of approximate 24 hours that persists in constant conditions.

Description



- Period [20h, 28h]
- Phase timing of peak expression
- Amplitude half the range of oscillation
- Mean level average value

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Detecting rhythmic gene expression

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Detecting rhythmic gene expression

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Circadian Clock: How Many Genes Involved?



Nature Reviews | Genetics 🚽 🚊 🕨

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Microarray and Circadian Rhythm

Design of Circadian Microarray Experiment



Computational Challenges

- Extremely sparse determination
- Extremely high dimensionality
- Low replicate numbers

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The Basic Problem That We Studied Previous Work

Statistical Assessment of Circadian Rhythms in Microarray Data

Categories of Prior methods

Time-domain algorithms (Such as COSOPT)

- Pros: Efficient for short time-series
- Cons: Model dependent, Predefine wavelength

Frequency-domain methods (Such as Fisher's G-test)

- Pros: Model independent
- Cons: Low resolution for short time-series

Our Solution

Combine both time-domain and frequency-domain analyses.

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Basic Principle Application for Large-scale Temporal Datasets

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Results on Public Microarray Data

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Frequency Domain: Period Detection

Autoregressive Spectral Estimation

Input

An evenly spaced time-series $\{x_t : t = 1, \dots, n\}$

Algorithm

Apply the autoregressive(AR) model of order p, noted as AR(p), to fit {x_t} by:

$$x_t = \sum_{i=1}^{p} \alpha_i x_{t-i} + \varepsilon_t \tag{1}$$

2 Estimate the frequency spectrum from AR coefficients α_i by:

$$p_x(f) = \frac{\sigma_{\varepsilon}^2}{|1 + \sum_{k=1}^{p} \alpha_k e^{-ifk}|^2} \quad 0 \le f < 0.5$$

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Time Domain: Rhythm Modeling Harmonic Regression

Input

 $\{x_t\}$ and frequency f_i (derived in Eq. (2))

Algorithm

Harmonic Regression models the rhythmic components of $\{x_t\}$ by

$$x_t = \mu + \sum_{i=1}^n \beta_i \cos(2\pi f_i t + \phi_i) + \varepsilon_t$$
(3)

then Eq. (3) can be reduced to a simple linear regression form:

$$x_t = \mu + \sum_{i=1}^n \{ p_i \cos(2\pi f_i t) + q_i \sin(2\pi f_i t) \} + \varepsilon_t$$
(4)

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ARSER in Action

a synthetic time-series

Generated by $f(t) = 500e^{-0.01 \cdot t} + 140e^{-0.01 \cdot t} \cdot \cos(\frac{2\pi}{24}t) + \varepsilon$, where $t \in [0, 96]$ with 4h intervals



The diagram of ARSER and a case study

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Multiple Testing Corrections

ARSER

False discovery rate *q*-value (Storey et al. 2003)

Prior methods

- COSOPT
 - pMMC- β value to correct for multiple comparisons
- Fisher's G-test
 - false discovery rate method

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Testing Datasets in Our Study

- Dataset 1: Our generated synthetic data
 - periodic time-series
 - Stationary cosine wave with *constant* amplitude and mean level
 - Nonstationary cosine wave with exponentially damped
 amplitude and mean level
 - random time-series
 - white noise following ($\mu = 0, \sigma = 1$) normal distribution
 - AR(1) process
 - time-series sampled every 4h over 48hrs
- Dataset 2: Public synthetic data
 - 120 time-series containing five circadian rhythmic patterns (Michael *et al.* 2008)
 - time-series sampled every 4h over 48hrs
- Dataset 3: Public microarray data
 - Arabidopsis circadian expression data (Edwards et al. 2006)
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Results of Our Synthetic Data Results of Public Synthetic Data Results on Public Microarray Data

Outline



Results on Public Microarray Data

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Results of Our Synthetic Data Results of Public Synthetic Data Results on Public Microarray Data

Periodicity Detection with Random Background Models



- 10 000 stationary periodic signals and 10 000 white noise signals
- 10 000 non-stationary periodic signals and 10 000 white noise signals
- I0 000 stationary periodic signals and 10 000 AR(1) signals
- 10 000 non-stationary periodic signals and 10 000 AR(1) signals

Performance measurement

 binary classification: periodic and non-periodic

ROC curve < D > < = > < =</p>

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Robustness to Noise and Wavelength



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Identifying (A) stationary and (B) non-stationary periodic signals under decreasing signal-to-noise ratio (SNR)

Distribution of differences between predicted wavelength and the actual wavelength for each periodic signals (wavelength \in [20h, 28h) with 0.1-h spaced)

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Detection of Non-sinusoidal Periodic Waveforms



120 time-series

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- 5 circadian rhythmic patterns, 24 samples for each
- ARSER identified 87% (104/120) periodic signals

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Data downloaded from http://haystack.cgrb.oregonstate.edu/

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Analysis of Arabidopsis Circadian Expression Data



Comparison of three algorithms for identifying *Arabidopsis* circadian-regulated genes

Original Report

- COSOPT algorithm by setting pMMC-β < 0.05
- 3505 genes, 16% of Arabidopsis whole genome are rhythmically expressed

ARSER identified

- 4929 genes rhythmically expressed (q-value<0.05)
- covering 96% of genes identified by COSOPT

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Newly identified *Arabidopsis* Rhythmic Transcripts by ARSER



Computational Validation

- PCA analysis
- first two components show rhythmic pattern

Biological Validation

 find 2 core clock genes from 27 known Arabidopsis clock genes.

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CRY1 and PRR9

Principal component analysis of the 1549 newly-found rhythmic

transcripts in Arabidopsis identified by ARSER.

Summary

- ARSER combines the time-domain and frequency-domain analyses to efficiently identify sinusoidal and non-sinusoidal periodic patterns in short, noisy and non-stationary time-series.
- Tested on well defined simulation data, ARSER is superior to two former methods, COSOPT and Fisher's G-test.
- Analysis of Arabidopsis microarray data using ARSER led to identification of a novel set of periodic transcripts
- Outlook
 - ARSER can only used to analyze evenly spaced time-series. We are developing an algorithm for irregularly spaced samples

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BioClock: a platform for analyzing circadian expression data

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BioClock System	
Home Analysis Br	owse Jobs Search Download FAQ
News	Introduction and Motivation
2010/4/10: Analysis module available.	We would like BioClock to represent a platform for analysis of biological clock behaviour in living organisms. BioClock could analysis time-ocurse microarray data to find probe sets (genes) behaviour in circadian mode. A circadian <i>hythm is a</i> roughly 24-hour cycle in the biochemical, physiological, or behavioural processes of
Statistics	living entities (from Witepedia). In addition, genes involved in circadian rhythm process from published microarray experiments were collected and stored in
Jobs runned: 12	BioClock for users to browse.
	Citations
Related Links	BioClock System was supported by those references below:
ARSER	Rendong Yang and Zhen Su, Analyzing circadian expression data by harmonic regression based on autoregression spectral estimation Biomformatics. 2010 bm 152:e012614-74. [bg] Dodering Li, Rendong Yang, Zhennan Mao, Tao Wang and Zhen Su, Biotodot : web server and database almod for interpreting circadian rhythm 2010 1948 (Posters).
Cyclebase	
CIRCA	
Diumal	
CCDB	Abilities
	Fuctions of pages listed below:
	In terms: this pape, A kerl introduction of this fact-) Interms: an advanced and advanced for a start of the advanced

Website

http://bioinfo.cau.edu.cn/BioClock

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Poster

Poster Section E34

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Detecting rhythmic gene expression

Acknowledgement

- Prof. John Hogenesch for sharing COSOPT software
- Daofeng Li for developing the interface of BioClock
- Ms. Wenying Xu and our colleagues in the Lab for helpful discussions
- Funding
 - Ministry of Science and Technology of China (2008AA02Z312, 2006CB100105)
 - ISCB, DOE and NSF for travel fellowship award to support my presentation

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Thank you!



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