A MORE EFFICIENT WAY
TO DETECT DNB IN A LARGE NETWORK

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STEPS

01

PART1

The theory of DNB

02

PART2

The time is limit

03

PART3

The parallel computing to detect DNB

04

PART4

The next work

PART 1

My understanding of DNB theory

Fewer datas

Merely requires a few samples in each sampling period, in stark contrast to the consecutive time-series data over the entire period required by the traditional methods

Important significance

Early-warning signal which indicating an imminent bifurcation

or sudden deterioration before the critical transition occurs

Model-free

This **model-free method based on measured individual data**, can detect specific signals for each individual or potentially apply this method to personalized medicine

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The core of detecting DNB

$$CI = \frac{SD \cdot PCC_{inner}}{PCC_{outer}}$$

PART2

Algorithm complexity

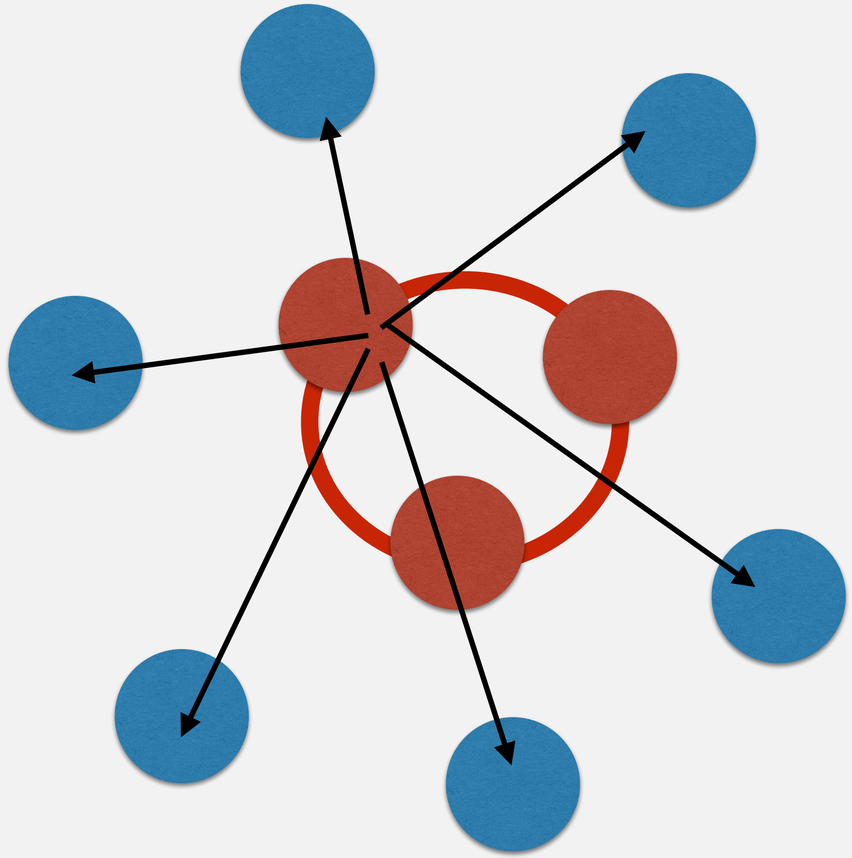
$$CI = \frac{SD \uparrow \cdot PCC_{inner} \uparrow}{PCC_{outer} \downarrow}$$

1. suppose n is the number of nodes

2. **SD: O(n)**
   The average standard deviations (SDs) of molecules in this group drastically increase.

3. **PCC(inner): $O(n^2)$**
   A group of molecules's average Pearson's correlation coefficients

4. **PCC(outer): $O(n^2)$**
   The average PCCs of molecules between this group and any others

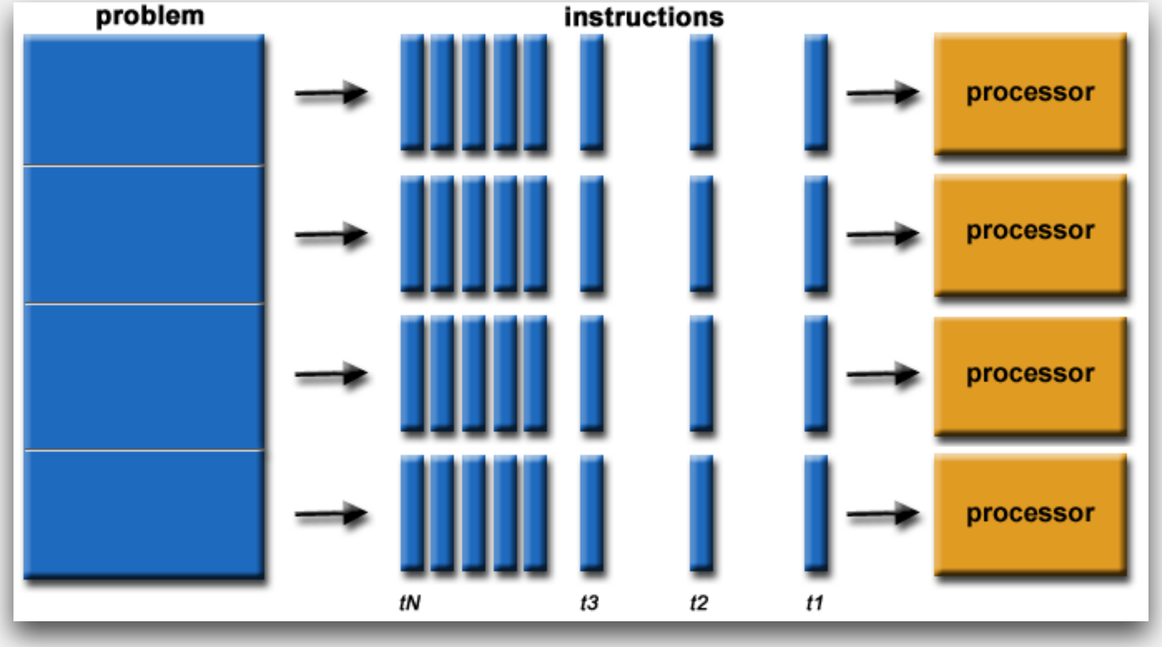


PART2

Our solution for this problem

Time complexity is a limit for us to find a DNB in a large network

Parallel Computing



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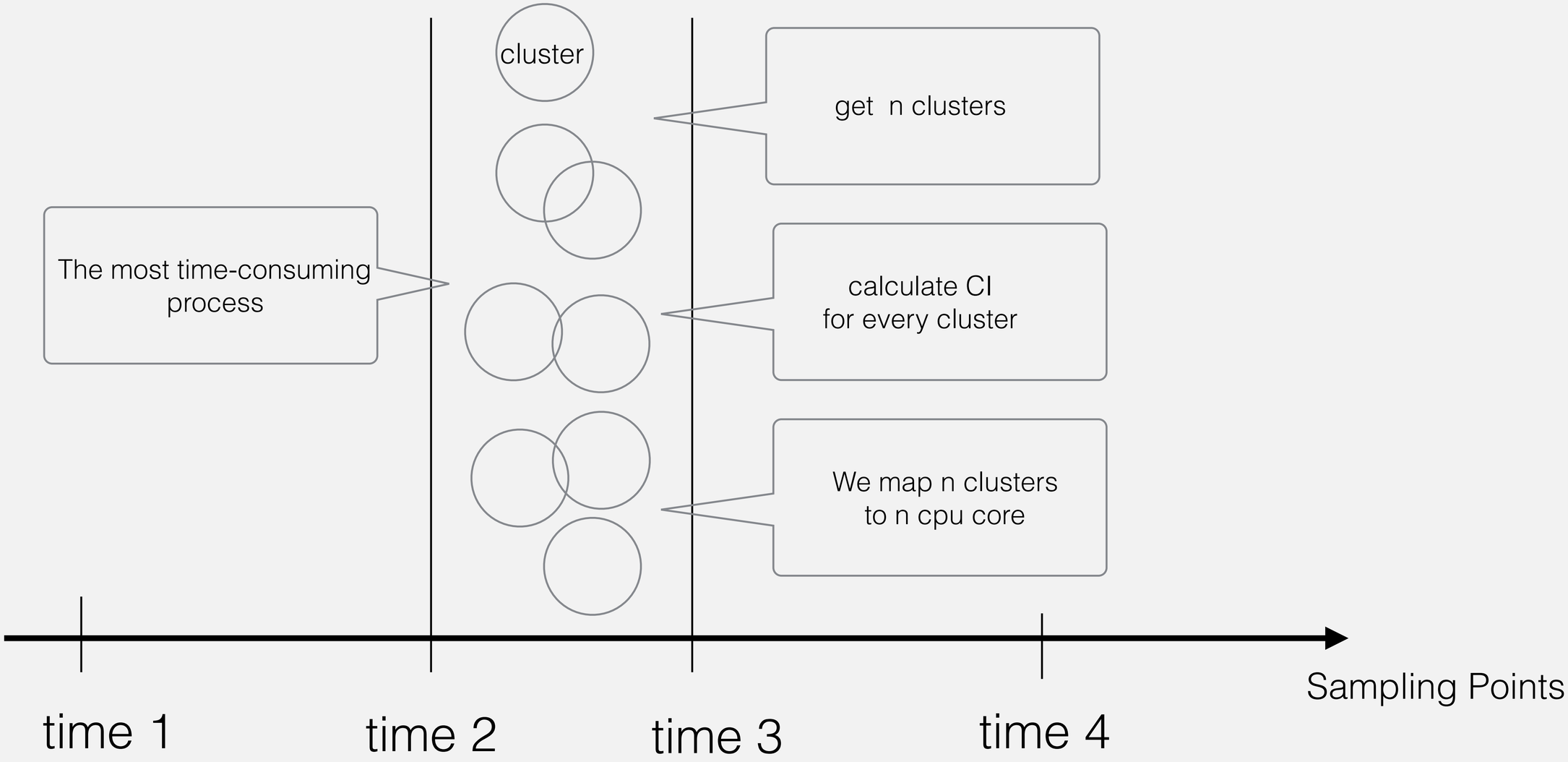
Design idea of Parallel Algorithm



PART3

Performance Comparison

RAW DATA OF LIVE CANCER

10729 nodes

5 samples

5 Sampling points

AFTER VAR AND T-TEST FILTER

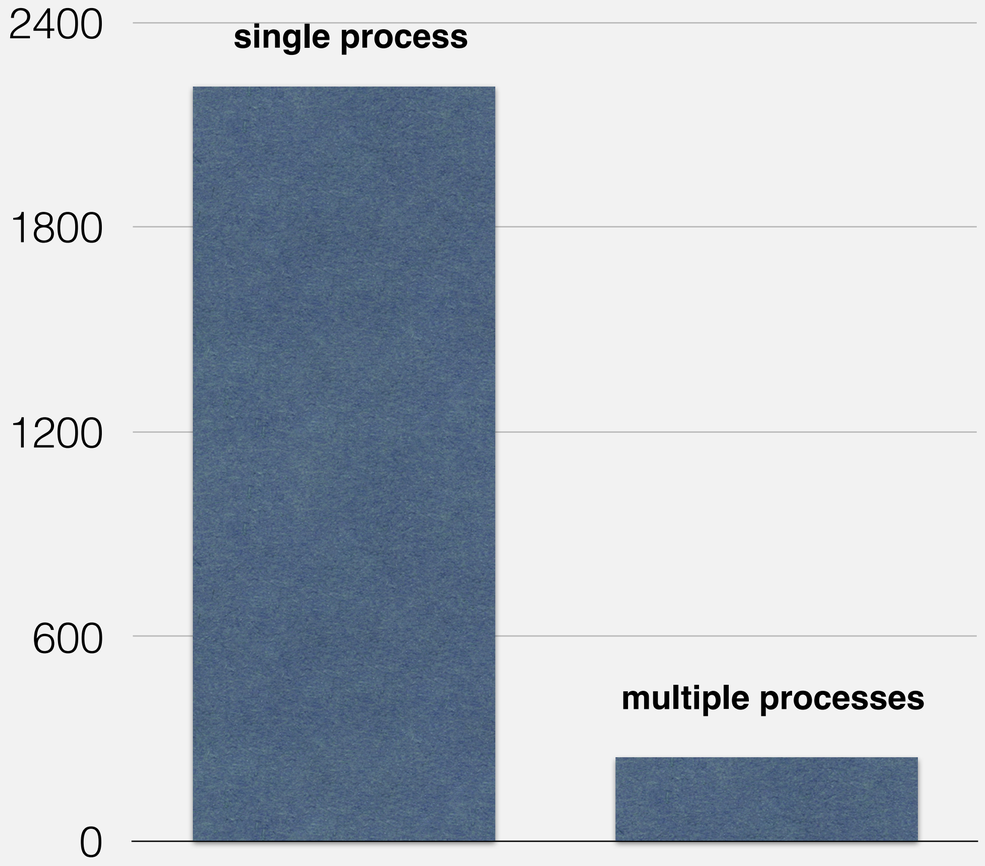
Period 1:	1242 nodes
Period 2:	953 nodes
Period 3:	962 nodes
Period 4:	919 nodes
Period 5:	845 nodes

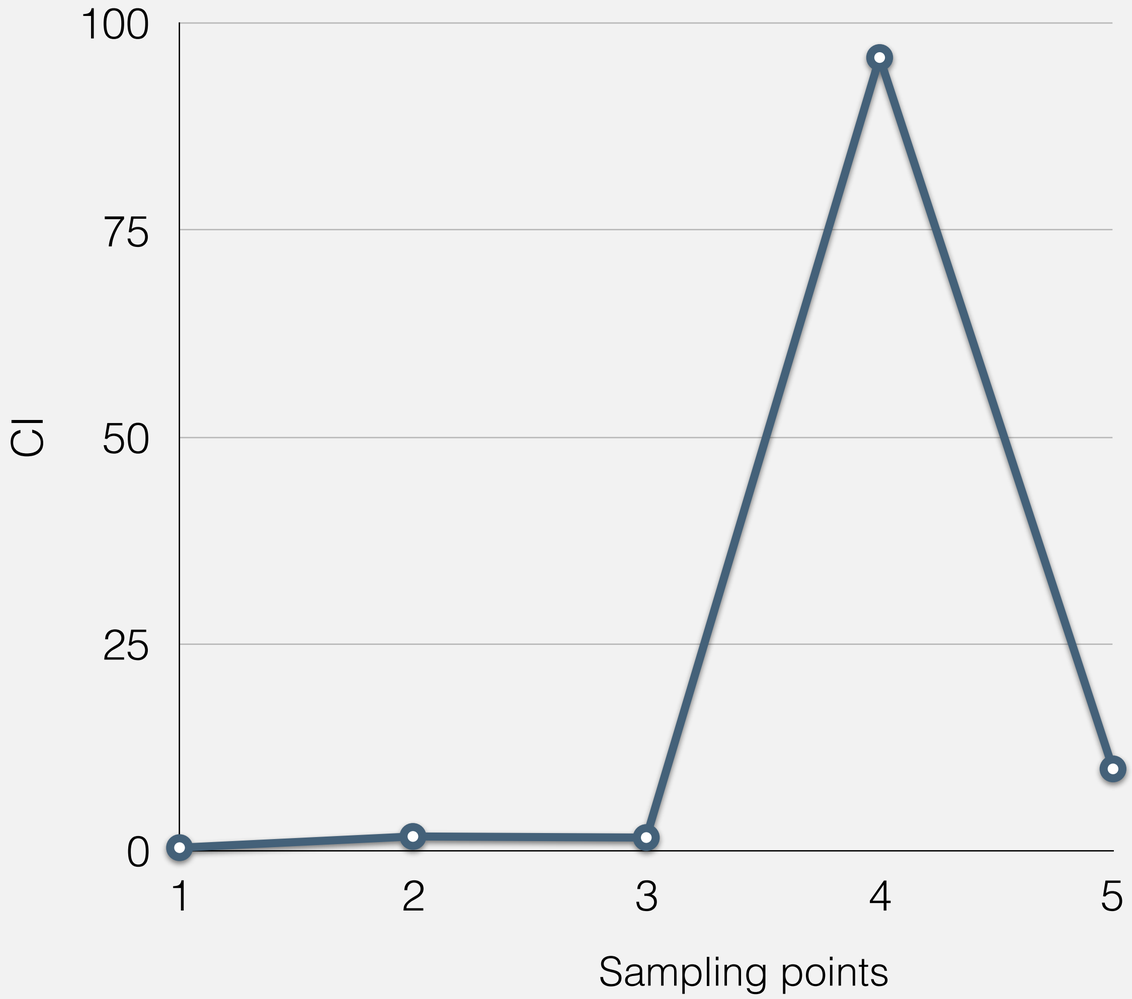
CLUSTERS OF EACH SAMPLING POINT

Period 1:	35 clusters
Period 2:	35 clusters
Period 3:	38 clusters
Period 4:	34 clusters
Period 5:	37 clusters

PART3

Performance Comparison

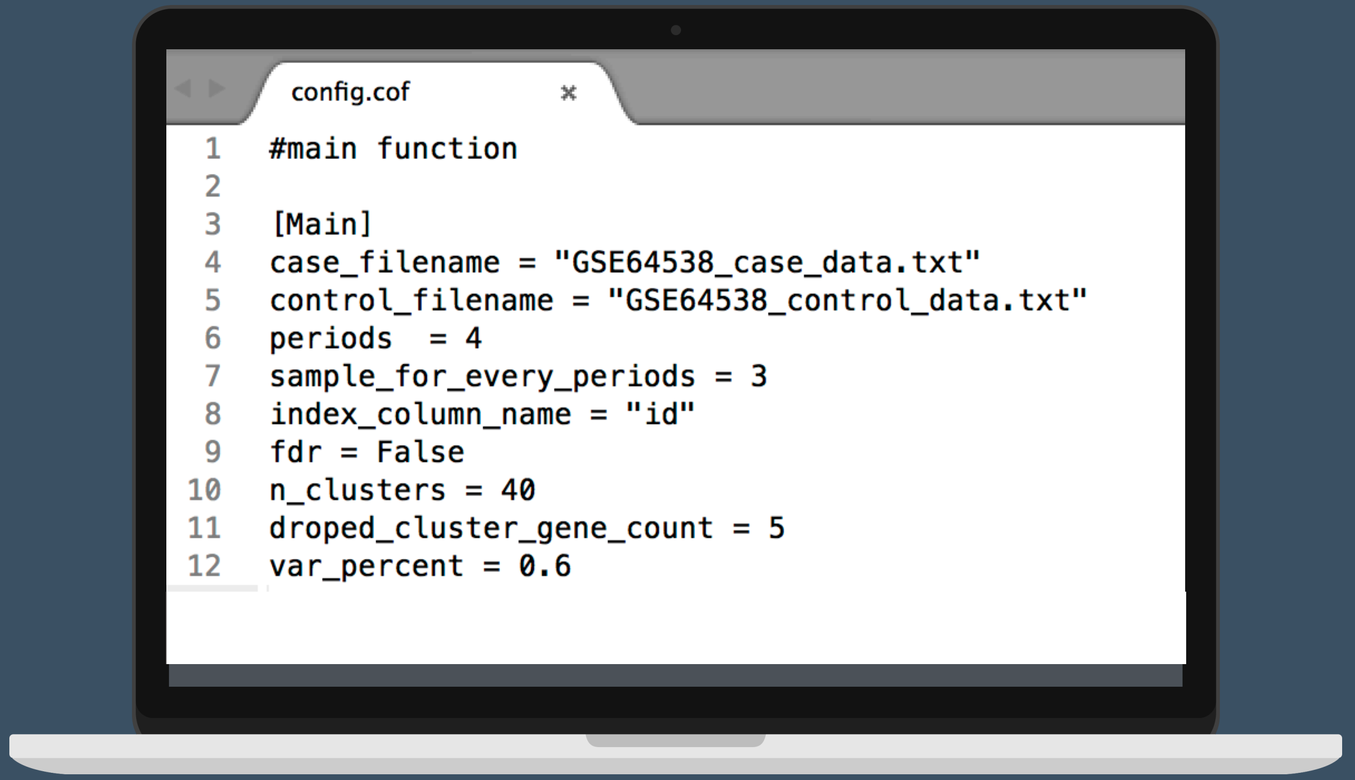




PART3

We hava made the detecting algorithm a software

Just need to modify the configure file，then click run



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A GUI Software

Test the dataset of human group coming from different altitude

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- From GSE73996
- 651 samples from 40 populations has been genotyped using the Affymetrix platform Axiom_GW_Hu_SNP.r2