

About Group Testing

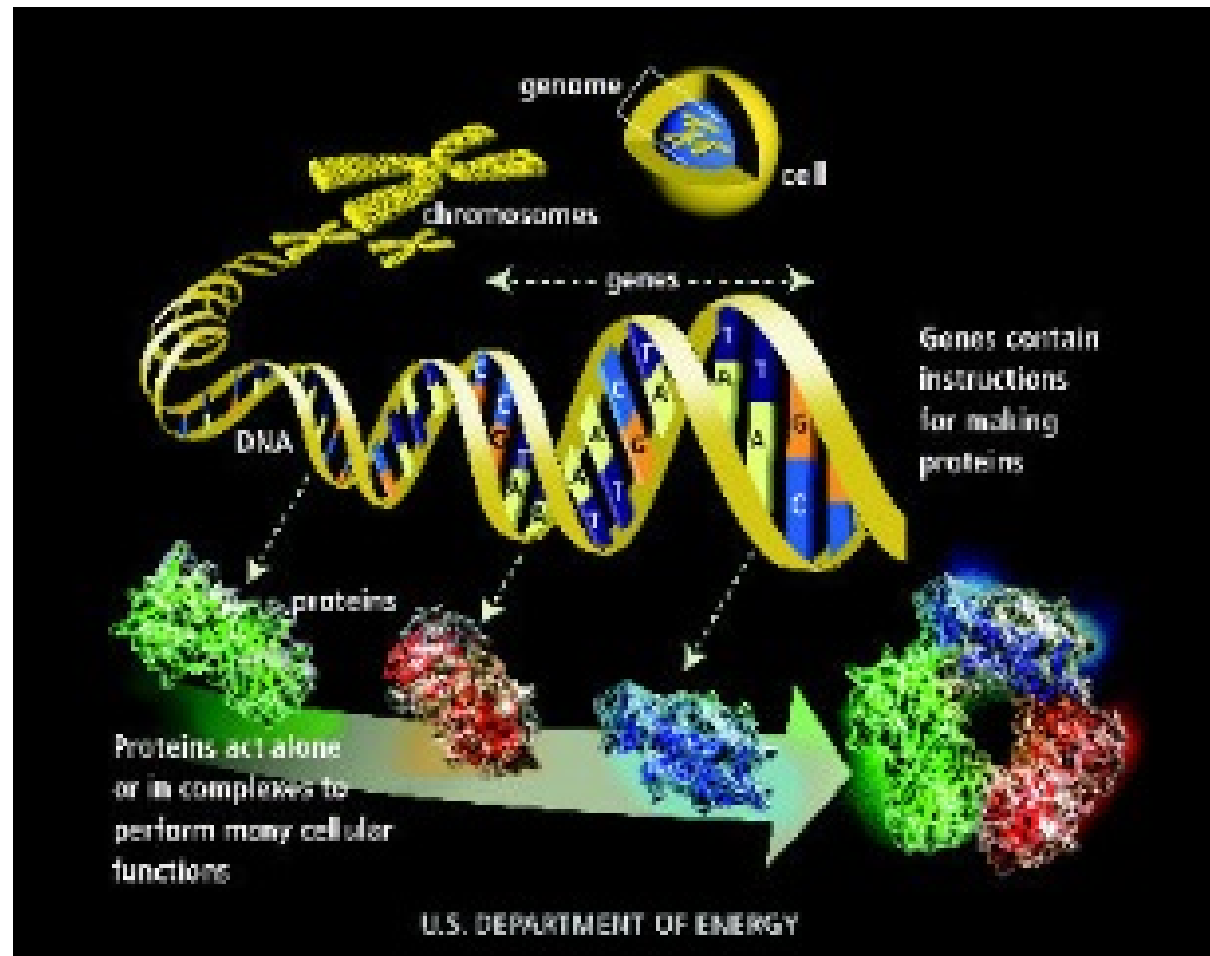
- We can approach this study via different topics such as *combinatorial design, algebraic combinatorics, coding theory and graph theory*.
- Group testing does play an important role in applications such as *computational molecular biology, network security, image compression, ..., etc.*

Human Genome Project



How does the human genome stack up?

Organism	Genome Size (Bases)	Estimated Genes
Human (人類)	3 billion	30,000
Laboratory mouse (白老鼠)	2.6 billion	30,000
Mustard weed (<i>A. thaliana</i>)	100 million	25,000
Roundworm (<i>C. elegans</i>)	97 million	19,000
Fruit fly (果蠅)	137 million	13,000
Yeast (酵母菌)	12.1 million	6,000
Bacterium (大腸桿菌)	4.6 million	3,200
Human immunodeficiency virus (HIV)	9700	9



- DNA: Deoxyribonucleic Acid
- Nucleotide (核苷酸)
 - Adenine (A)
 - Thymine (T)
 - Guanine (G)
 - Cytosine (C)

Computational Molecular Biology

- DNA解序後，需分析訊息，但資料量30億對。
 - 需要現代科技輔助。

- 主要課題

- 序列組合
- 序列分析
- 基因認定
- 生物資訊資料庫、種族樹建構、蛋白質三維結構推測…。

序列比對探究

- 說明
 - 找序列中「相似」及「相異」的部份。
 - 為何要比對序列？
 - 為何要使用電腦比對？
 - 如何使用電腦比對？
 - 困難點：序列型態多樣、需建構不同的資料結構及**演算法** (*Algorithm*)。

Example of Group Testing

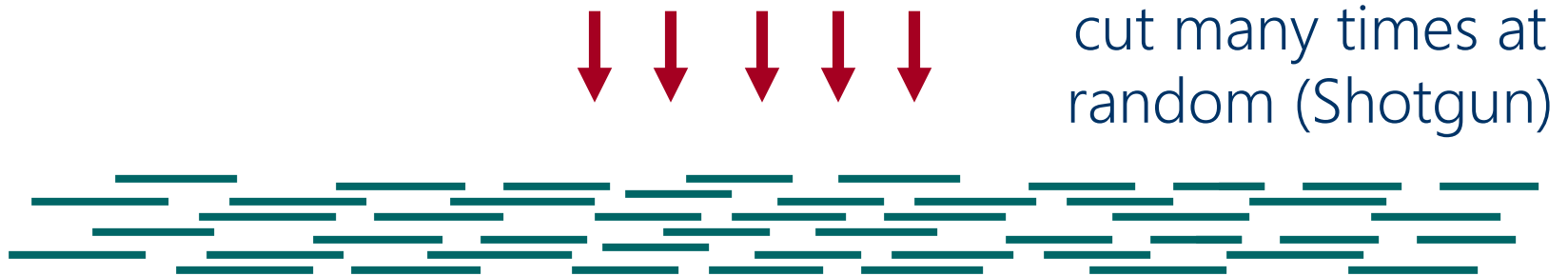
- In screening clone library the goal is to determine which clones in the clone library hybridize with a given probe in an efficient fashion. A clone is said to be **positive** if it hybridize with the **probe(探針)**, and **negative** otherwise.

Shotgun Sequencing

- Shotgun sequencing is a throughput technique resulting in the sequencing of a large number of bacterial genomes, mouse genomes and the celebrated human genomes. In all such projects, we are left with a collection of **contigs** that for special reasons cannot be assembled with general assembly algorithms. **Continued ...**

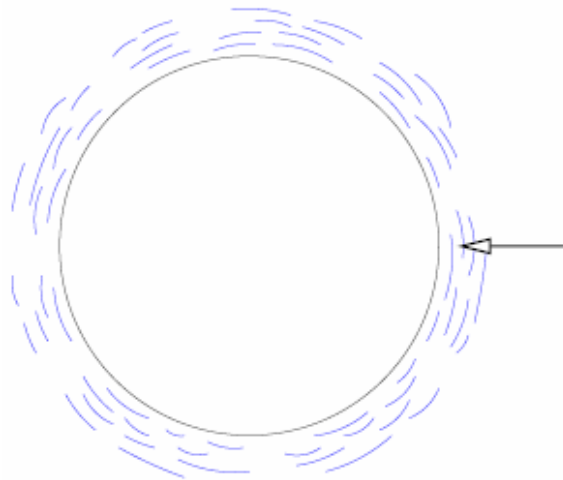
Random shotgun approach

genomic segment



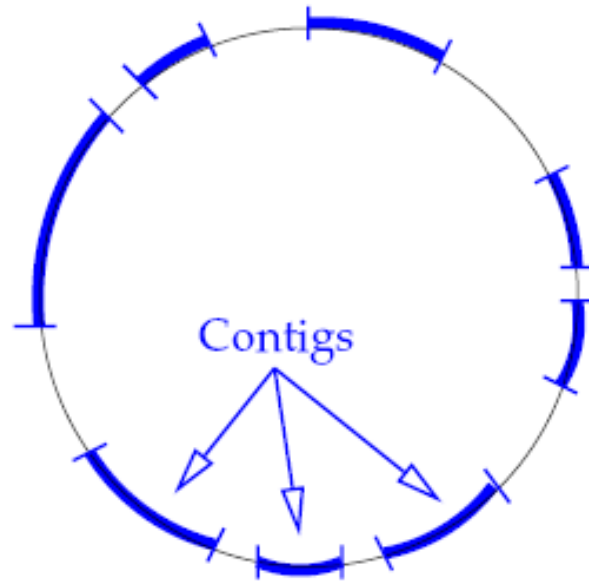
Whole-genome shotgun sequencing

- Short reads are obtained and covering the genome with redundancy and possible gaps.

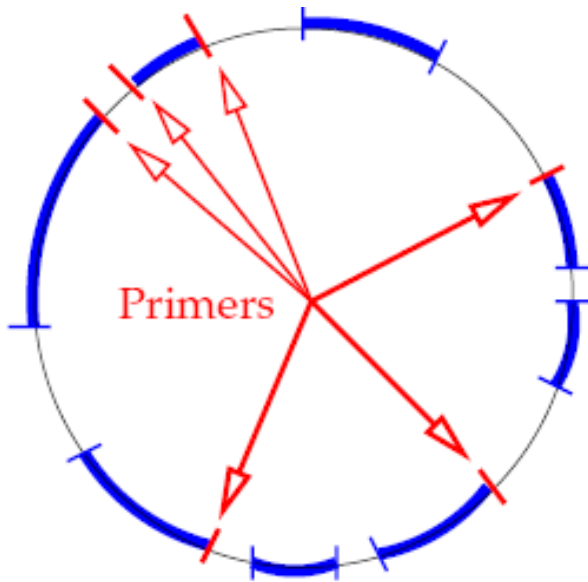


Circular genome

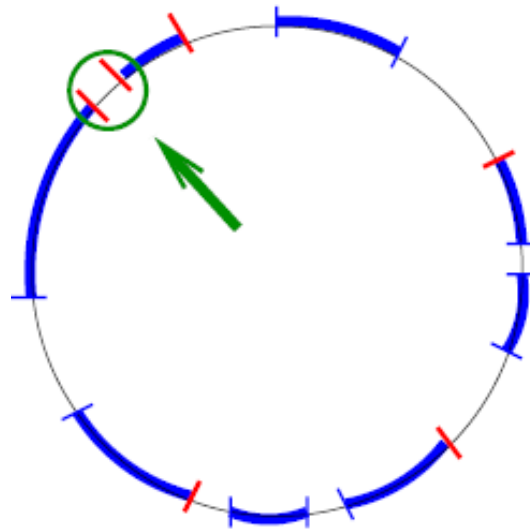
- Reads are assembled into contigs with unknown relative placement.

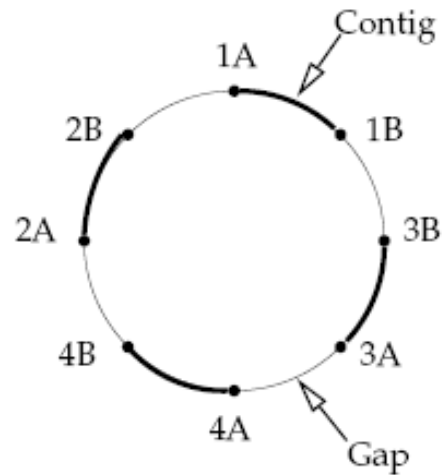


– **Primers** : (short) fragments of DNA characterizing ends of contigs.



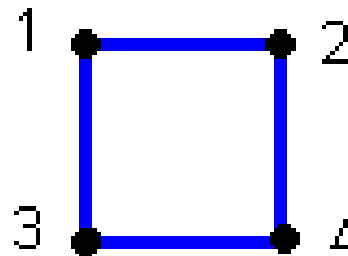
- A **PCR (Polymerase Chain Reaction)** reaction reveals if two primers are proximate (adjacent to the same gap).
- **Multiplex PCR** can treat multiple primers simultaneously and outputs if there is a pair of adjacent primers in the input set and even sometimes the number of such pairs.

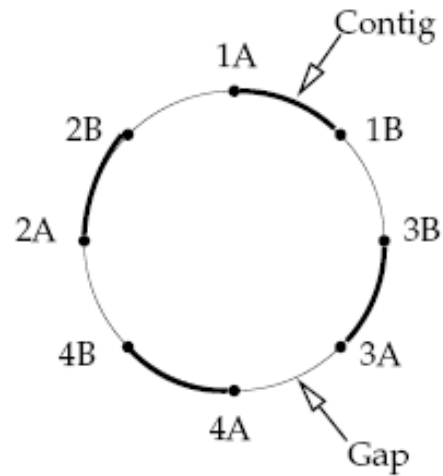




- Two primers of each contig are “mixed together”
 - Find a Hamiltonian cycle by PCRs!

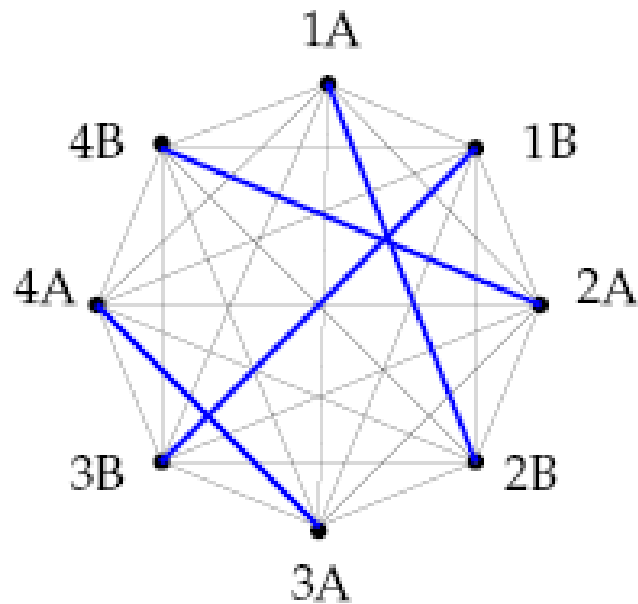
1A ——— 1B
 2A ——— 2B
 3A ——— 3B
 4A ——— 4B





1A ——— 1B
 2A ——— 2B
 3A ——— 3B
 4A ——— 4B

- Primers are treated independently.
 - Find a perfect matching by PCRs.



Goal

- Our goal is to provide an experimental protocol that identifies all pairs of adjacent primers with as few PCRs (queries) (or multiplex PCRs respectively) as possible.

Mathematical Models

Hidden Graphs ***(Reconstructed)***

- Topology-known graphs, e.g. Hamiltonian cycle, matching, star, clique, bipartite graph, ..., etc.
- Graphs of bounded degree
- Hypergraphs
- Graphs of known number of edges

Recent Result

- Theorem (Chang, Fu and Shih)

Let G be a graph with n vertices and m edges. Then we have an *adaptive algorithm* to reconstruct the hidden graph by using at most $m(2\log_2 n + 9)$ queries.

Compressed Sensing

- In compressed sensing (*CS*), we are given an n -dimensional sparse signal with support size K .
- *Random (?)* projections of the sparse signal are obtained. (We notice the projection if it is not orthogonal to the signal, i.e. the inner product of the two vectors is not equal to zero.)
- *The goal is to identify the support set while minimizing the number of projections.*

Have you seen “group testing”?

- We shall find a measurement *txn* matrix A with as less rows (minimizing t) as possible such that after t projections the support set of the sparse signal can be obtained.
- Here we only consider the Boolean version ($0, 1$) of *CS*.
- *Noticed that we use non-adaptive group testing algorithms for compressed sensing.*

Signal: 010000010000

Outcome vector: 010111100

1			1			1			1		
1				1			1			1	
1					1			1			1
	1		1					1		1	
	1			1		1					1
	1				1		1		1		
		1	1				1				1
		1		1				1	1		
		1			1	1				1	

The blanks
are zeros.

Network Security

無線感測網路 [編輯]

Wireless Sensor Network

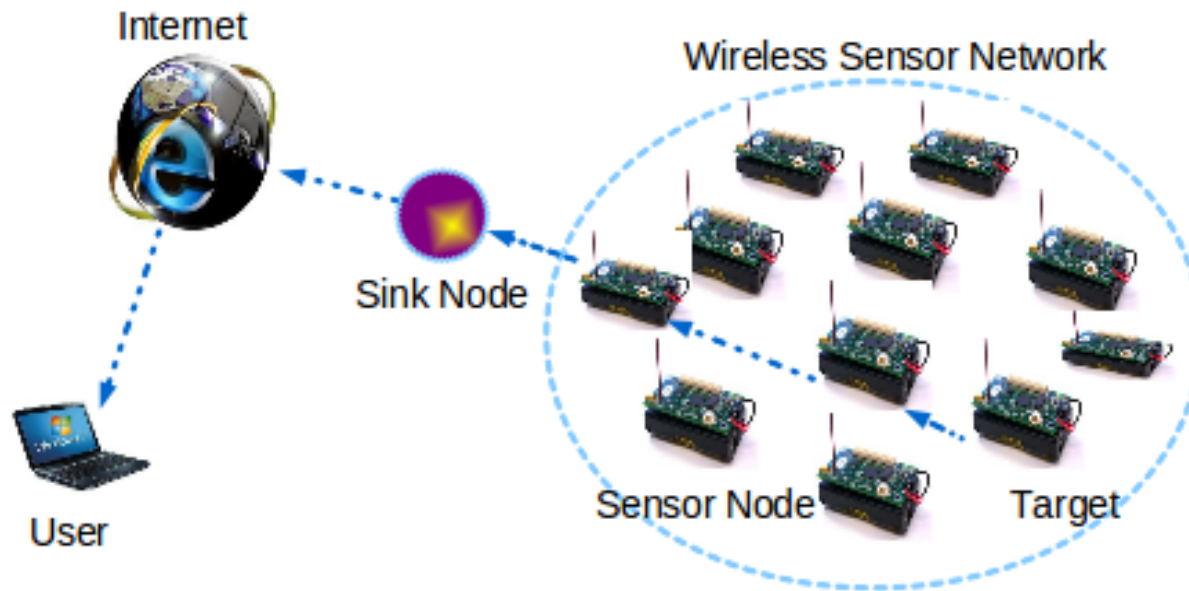
維基百科，自由的百科全書

無線感測網路（**Wireless sensor network**），或譯**無線感知網路**，是由許多在空間中分布的自動裝置組成的一種無線通訊**計算機網路**，這些裝置使用**感測器**協作地監控不同位置的物理或環境狀況（比如**溫度**、**聲音**、**振動**、**壓力**、**運動**或**污染物**）。無線感測器網路的發展最初起源於戰場監測等軍事應用。而現今無線感測器網路被應用於很多民用領域，如環境與生態監測、健康監護、**家居自動化**以及交通控制等。

無線感測網路的每個節點除配備了一個或多個感測器之外，還裝備了一個**無線電收發器**、一個很小的**微控制器**和一個能源（通常為**電池**）。單個感測器節點的尺寸大到一個太空梭，小到一粒塵埃。感測器節點的成本也是不定的，從幾百美元到幾美分，這取決於感測器網路的規模以及單個感測器節點所需的複雜度。感測器節點尺寸與複雜度的限制決定了能量、存儲、計算速度與頻寬的受限。

在**計算機科學**領域，無線感測網路是一個研究熱點，每年都會召開很多的研討會和國際會議。

Wireless Sensor Network



Jammer

- Constant jammer
- Deceptive jammer
- Random jammer
- Reactive jammer

Jammer

jammer

Dr.eye 譯典通

KK ['dʒæmə] DJ ['dʒæmə]  即時發音

【無】干擾發射機(臺)

相關詞

- cell phone jammer

» 查看全部

英文現學現辦：攻佔白宮！看電影準備多益

釋義

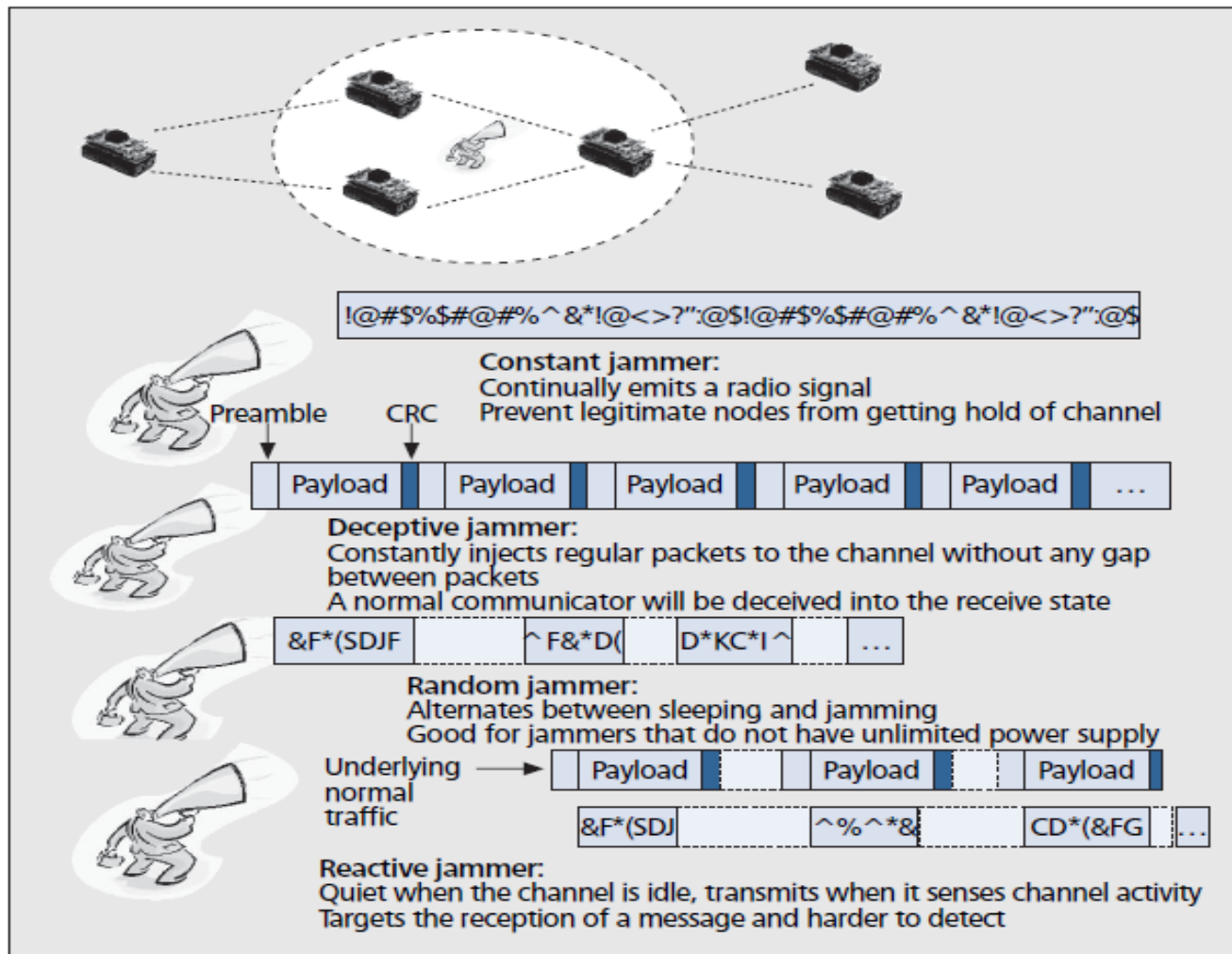
相關詞

鍵盤捷徑：按 A 可全選目前搜尋方框內的單字

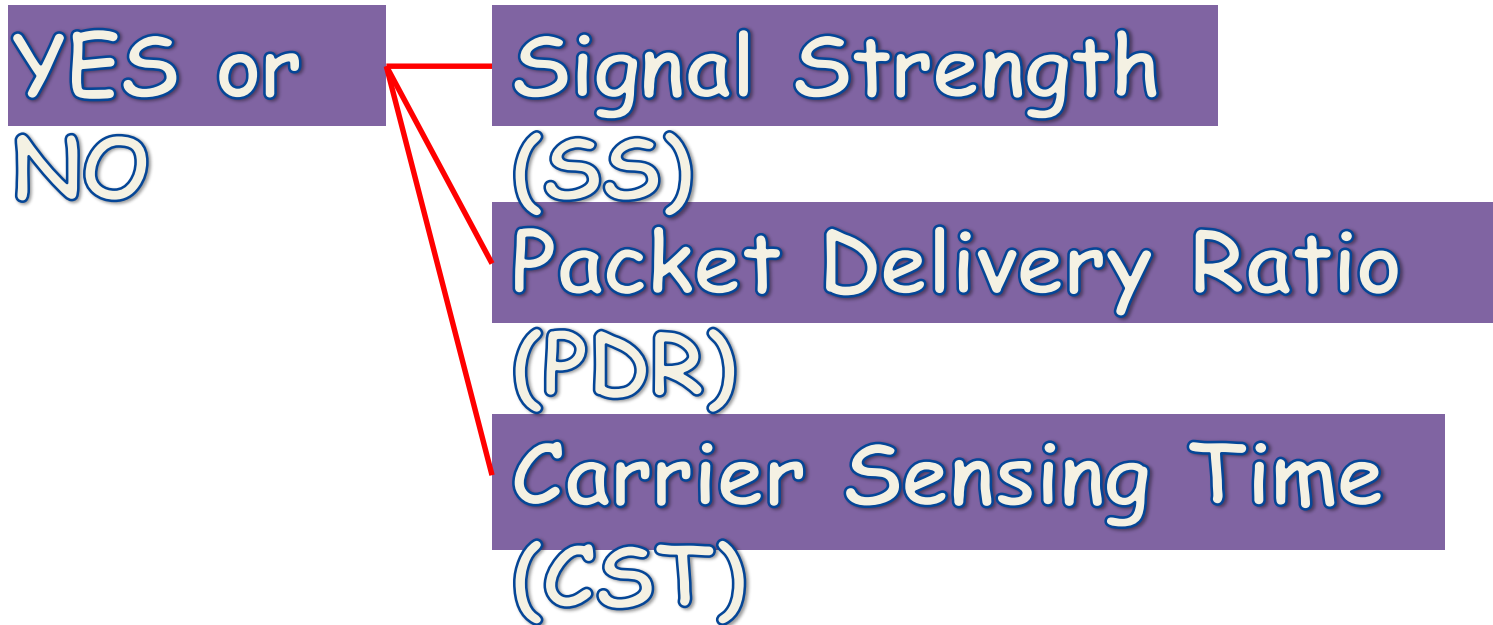
n. 名詞

1. 【無】干擾發射機(臺)
2. 【機】U型鋼絲芯撐

Jammer



Detection for Jammers



Further Information

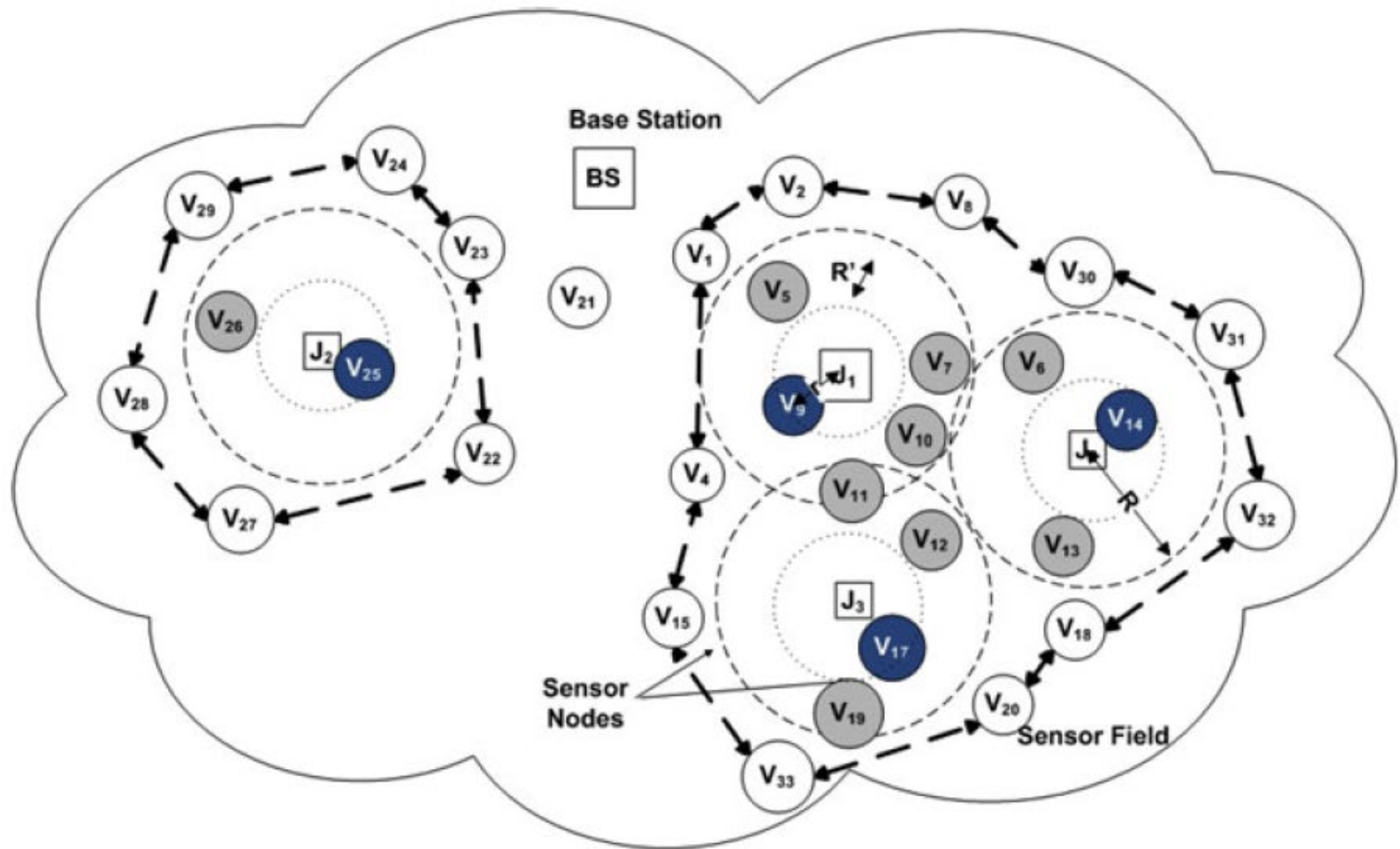
Coping with Reactive Jammers

Finding

Trigger nodes

1. Constructing a routing algorithm :
triggers be only receivers.
2. For triggers to send,
applying channel surfing becomes efficient.
3. Properly utilizing victim nodes (VN).

Basic Model



Identifying Trigger Nodes

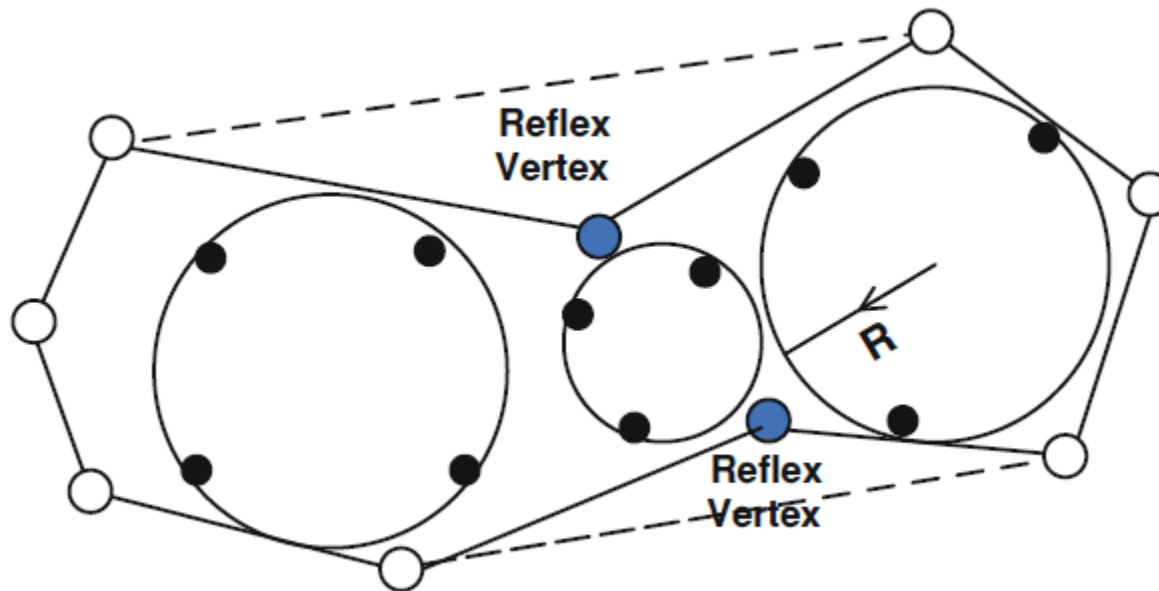
- Preprocessing

A diagram showing the 'Preprocessing' step branching into two sub-steps: 'Node Classification' and 'Jamming Range Estimation'. Red lines connect the word 'Preprocessing' to the start of each sub-step box.

 - Node Classification
 - Jamming Range Estimation
- Interference Free Group Testing (**IFGT**)
Algorithm
- Non-Adaptive Group Testing Detection (**NGTD**)
Algorithm

Jamming Range Estimation

- Dense-jammer case



- *Group testing?*
- *Please refer to the book
“Group Testing Theory in
Network Security” written by
My T. Thai.*

References

- A new construction of 3-bar-*separable* matrices via improved decoding of Macula construction (with F. K. Hwang), **Discrete Optim.**, 5(2008), 700-704.
- An upper bound of the number of tests in pooling designs for the *error-tolerant complex model* (with Hong-Bin. Chen and F. K. Hwang), **Optimization Letters**, 2(2008), no. 3, 425-431.
- The minimum number of e-vertex-cover among *hypergraphs* with e edges of given rank (with F. H. Chang, F. K. Hwang and B. C. Lin), **Discrete Applied Math.**, 157(2009), 164-169.
- Non-adaptive algorithms for *threshold* group testing (with Hong-Bin Chen), **Discrete Applied Math.**, 157(2009), 1581-1585.

Continued

- Identification and classification problem on pooling designs for *inhibitor* models (with Huilan Chang and Hong-Bin Chen), **J. Computational Biology**, 17(2010), No. 7, 927-941.
- Reconstruction of *hidden graphs and threshold* group testing (with Huilan Chang, Hong-Bin Chen and Chi-Huai Shih), **J. Combin. Optimization**, 22(2011), no. 2, 270 – 281.
- Group testing with multiple *mutually-obscuring positives* (with Hong-Bin Chen), **Lecture Notes Computer Science**, 7777(2013), 557 – 568.
- *Threshold* group testing on *inhibitor* model (Huilan Chang and Chie-Huai Shih), **J. Computational Biology**, Vol. 20, No. 6, 2013, 1 – 7.

Continued

- New bound on *2-bar-separable* codes of length 2 (with Minquan Cheng, J. Jiang, Yuan-Hsun Lo and Ying Miao), **Des. Code Cryptography**, to appear.
- Learning a *hidden graph* (with Huilan Chang and Chie-Huai Shih), under review of Optimization Letters.
- *Expanded separable codes* (with Minquan Cheng, J. Jiang, Yuan-Hsun Lo and Ying Miao), under review of IEEE Transaction of Information Theory.

Keep Moving Forward!

