

Finding Signals

There are ways of finding signals, group testing is one of the most efficient method proposed earlier.



Warming Up

- 猜數字遊戲：我有一個介於1和63的整數，你們要如何用最少個問題來猜出它？（如何問？）



At most 6 Queries

- (1) Is the number larger than 32?
Yes or No?
- (2) If the answer is “Yes”, then ask if the number is larger than 48 or not. On the other hand, if the answer is “No”, then ask if the number is larger than 16 or not.
- Continued ...
- 6 (Binary Splitting Algorithm)
- Do you have a better idea?

Another idea

- We can also ask several questions simultaneously and then make a decision!



Magic cards

32	33	34	35	36	37	38	39
40	41	42	43	44	45	46	47
48	49	50	51	52	53	54	55
56	57	58	59	60	61	62	63

16	17	18	19	20	21	22	23
24	25	26	27	28	29	30	31
48	49	50	51	52	53	54	55
56	57	58	59	60	61	62	63

2	3	6	7	10	11	14	15
18	19	22	23	26	27	30	31
34	35	38	39	42	43	46	47
50	51	54	55	58	59	62	63

8	9	10	11	12	13	14	15
24	25	26	27	28	29	30	31
40	41	42	43	44	45	46	47
56	57	58	59	60	61	62	63

4	5	6	7	12	13	14	15
20	21	22	23	28	29	30	31
36	37	38	39	44	45	46	47
52	53	54	55	60	61	62	63

1	3	5	7	9	11	13	15
17	19	21	23	25	27	29	31
33	35	37	39	41	43	45	47
49	51	53	55	57	59	61	63

A coincidence

- It is about Christmas trees.
- How to check the light bulbs are good?

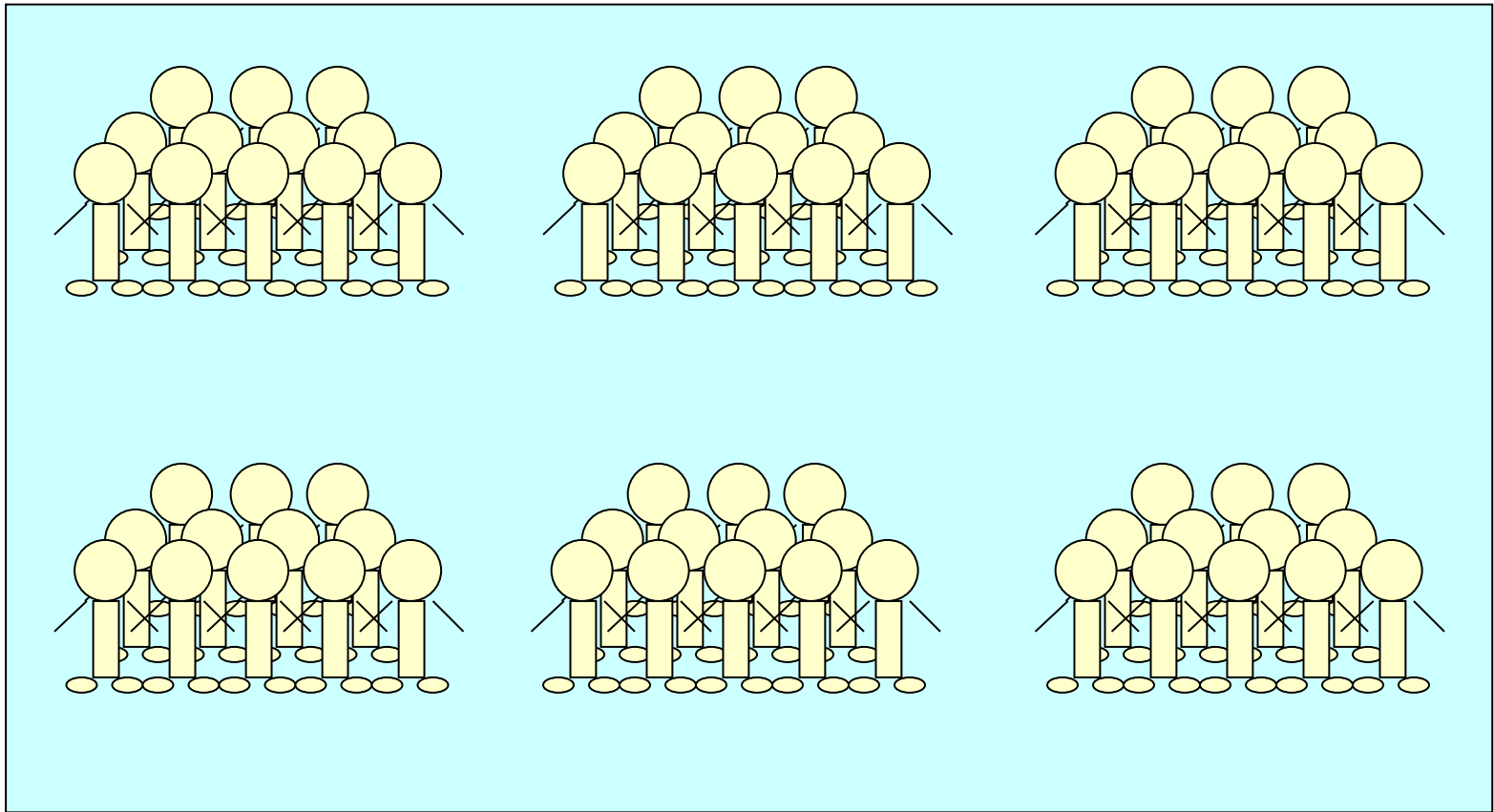


Information to Know

- Hsin Chu played the most important role in the production of Christmas light bulbs. (Before the construction of Science Based park).
- People lived along 光復路 make the key contribution!
- They knew how to apply *Group Testing* already.
- Currently, more than 80% such light bulbs are manufactured by a **Taiwanese company** located in mainland China.

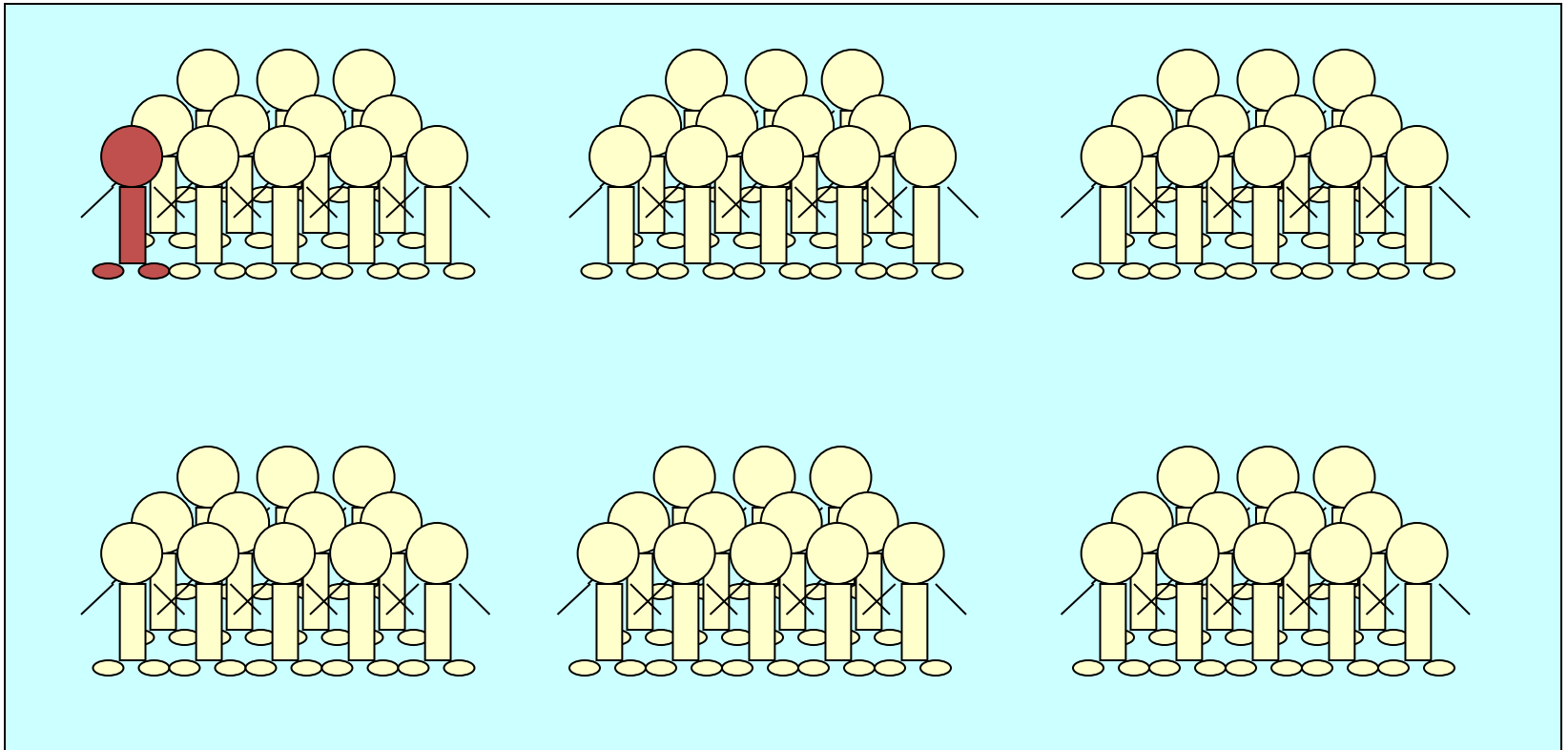
One More Example

Syphilis (梅毒) Tests (World war II, 1943)

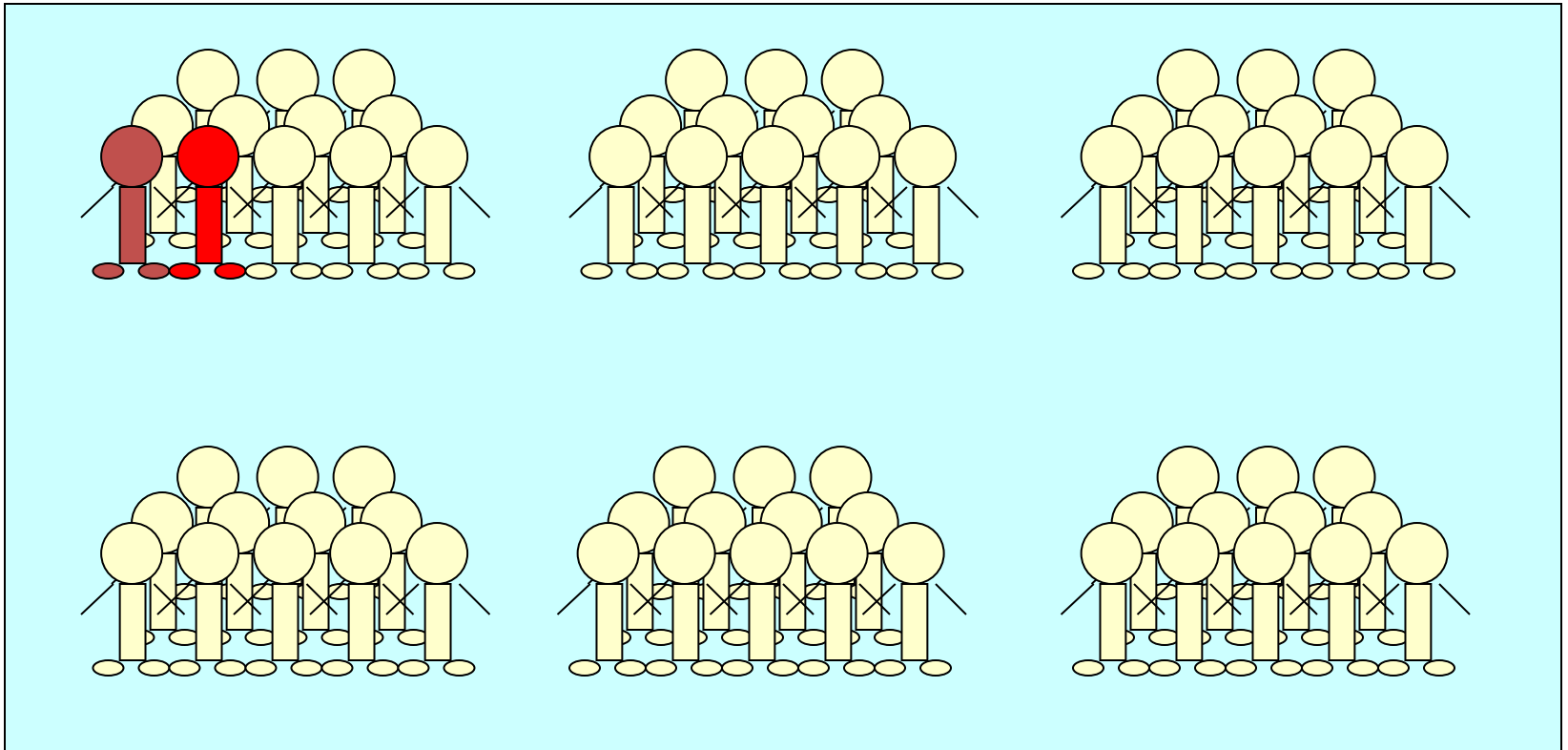


Individual Test

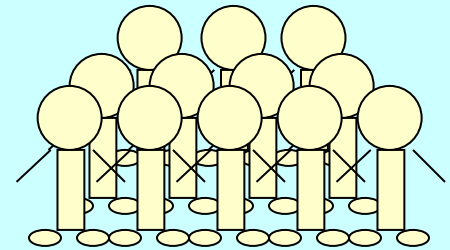
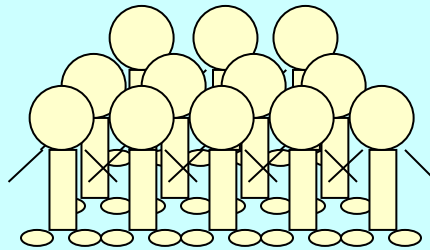
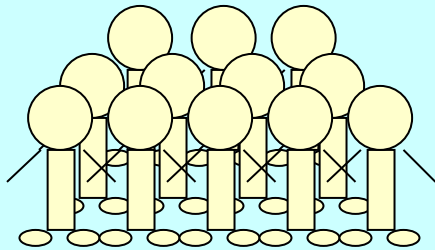
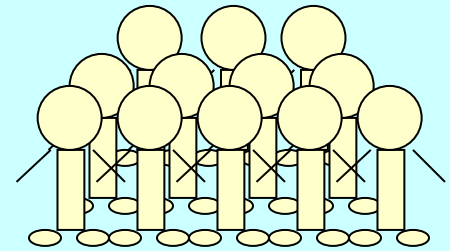
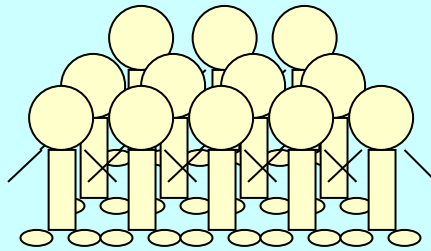
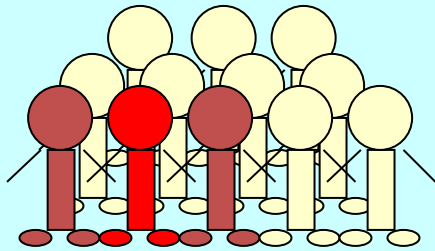
72 tests!



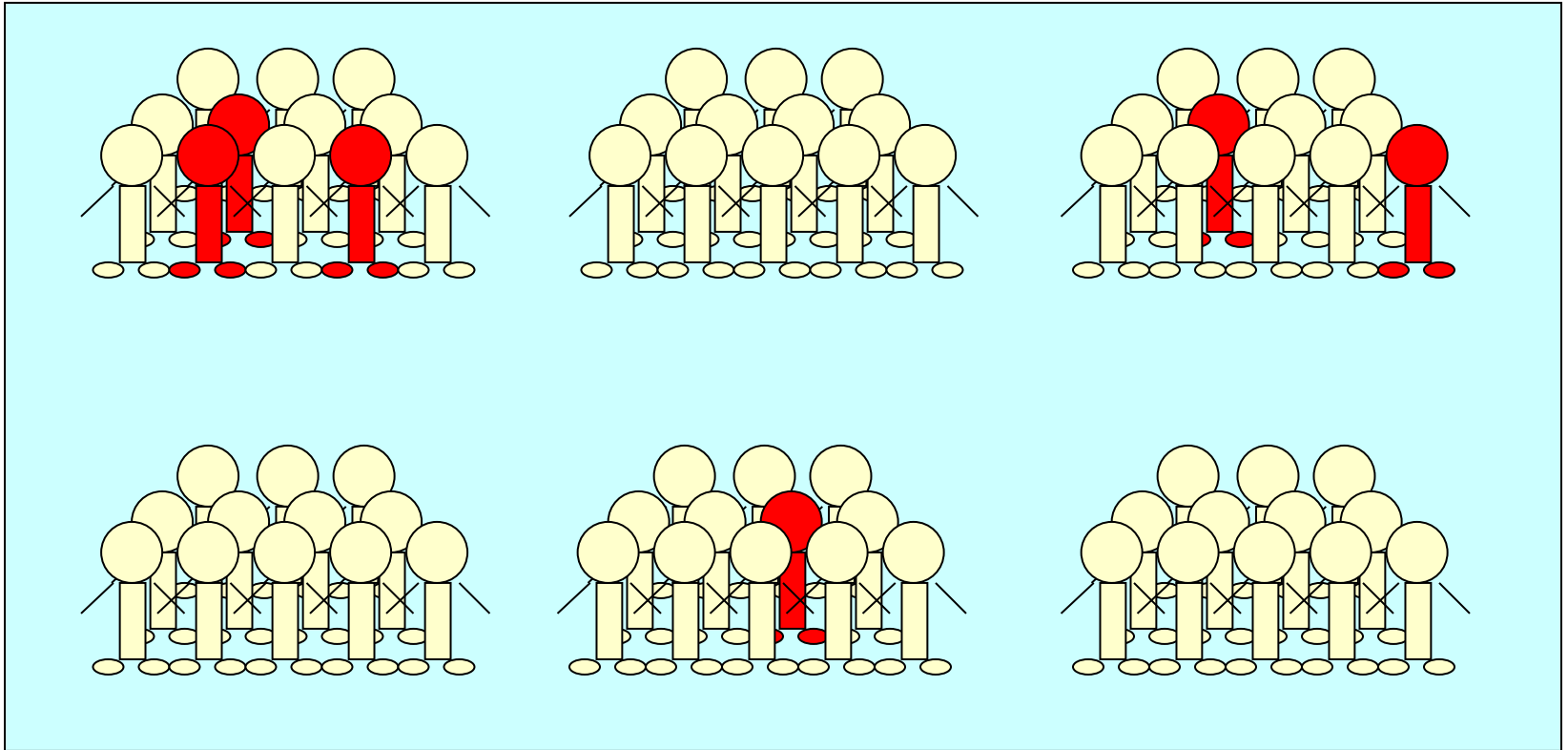
Red *is positive and* **Brown** *is negative*



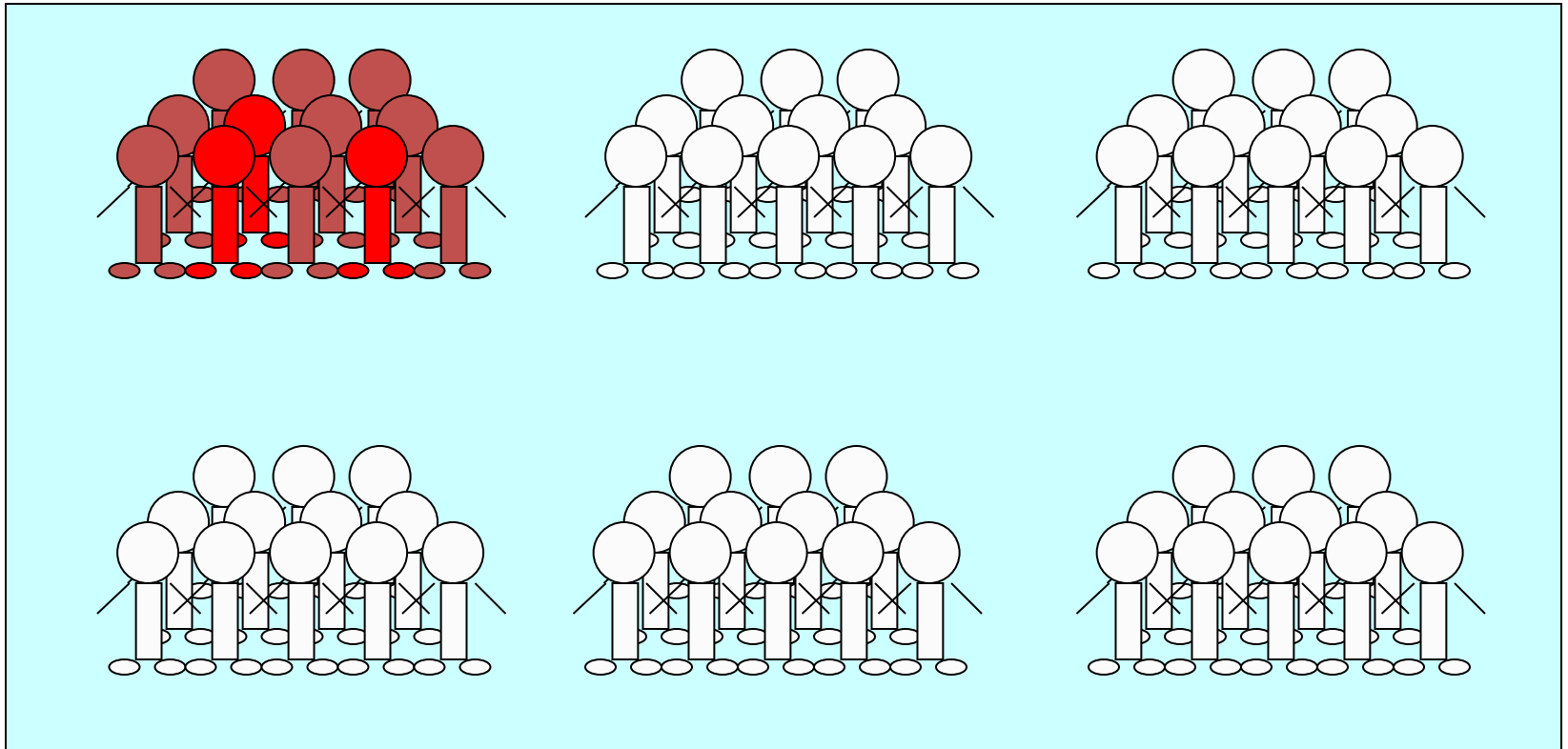
Keep going



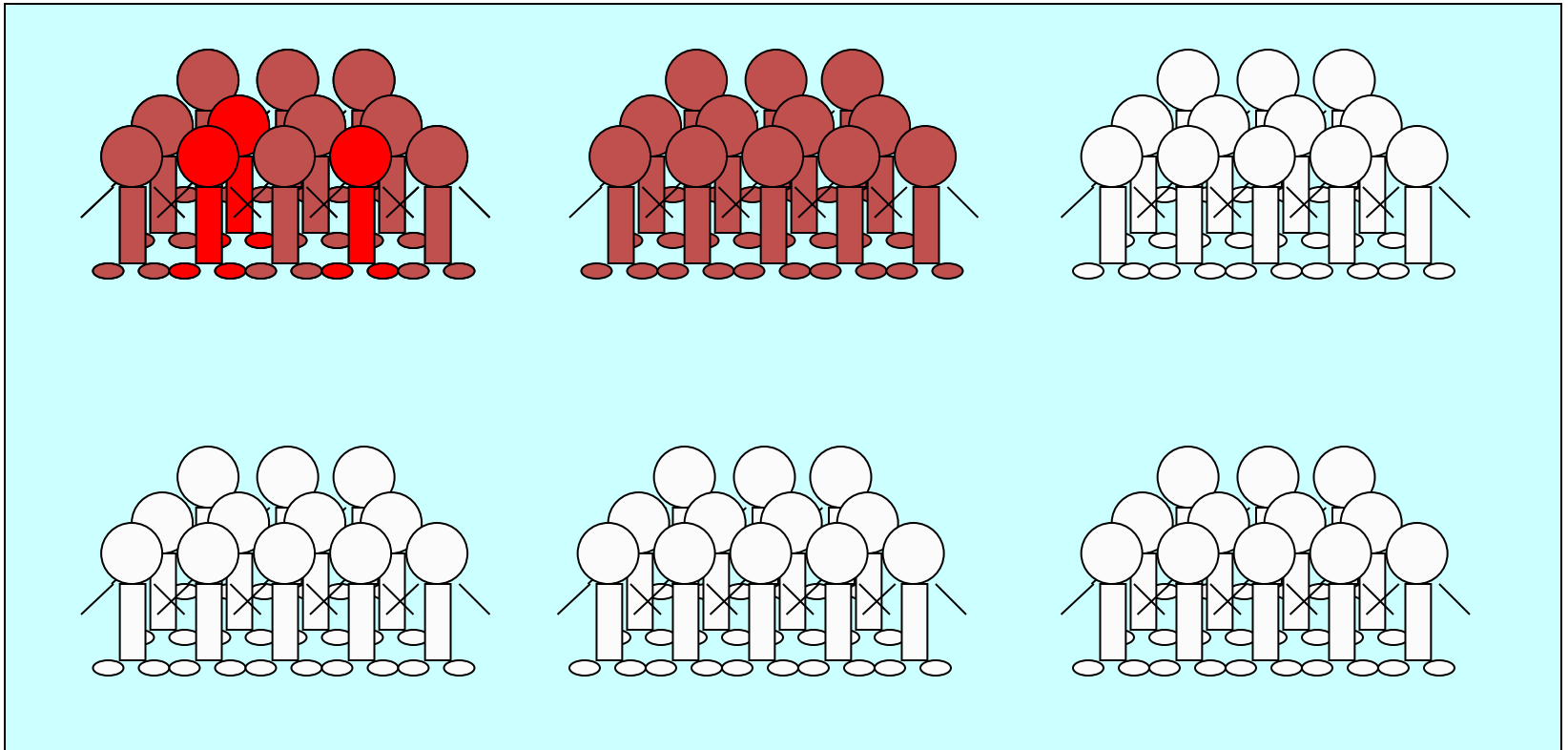
More positives (72 tests)



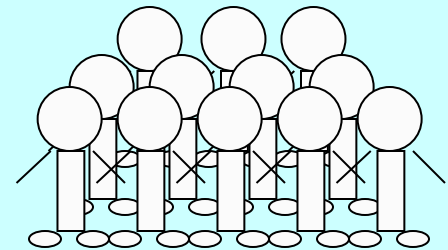
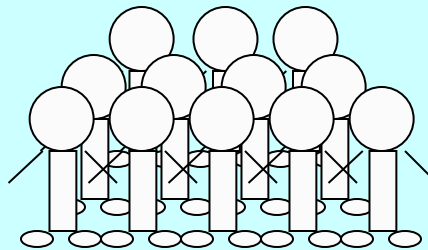
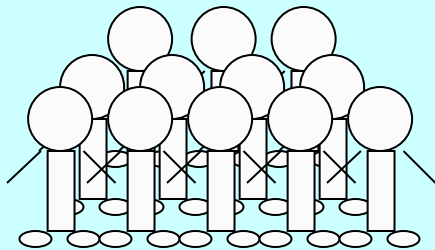
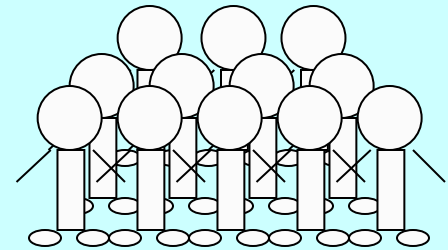
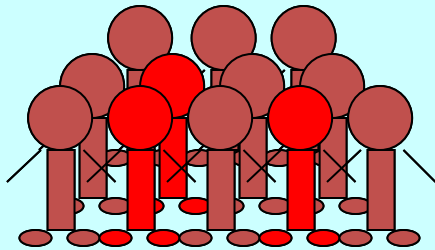
Test a group at one time



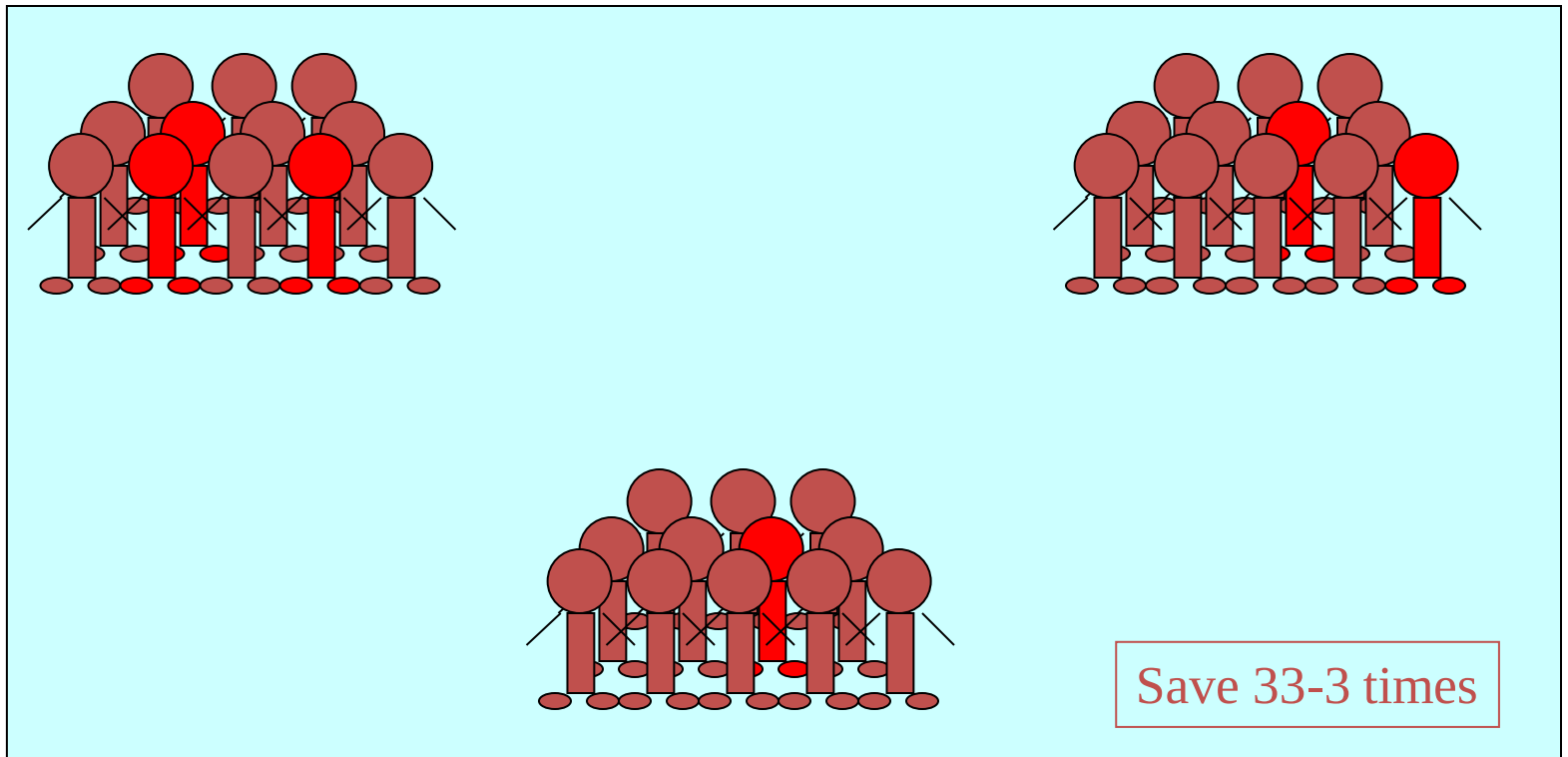
Some group is negative!



They are done!



Save a lot of Money!



What's next?

Research Facts

- The idea was proposed by a team member (Rosenblatt) of R. Dorfman and Dorfman went ahead to write a journal paper to emphasize the importance of this idea.
- The detection of defective members of large populations, Ann. Math. Statist. 14 (1943), 436 – 440.
- Upon the report, this idea has never been used then. ***People are not confident about it!***

Group testing

- Consider a set N of n items consisting of at most d *positive* (used to be called defective) items with the others being *negative* (used to be called good) items.
- A group test, sometimes called a *pool*, can be applied to an arbitrary set S of items with two possible outcomes; *negative*: all items in S are negative; *positive*: at least one positive item in S , not knowing which one or how many.

Adaptive (Sequential) and Non-adaptive

- Can you see the *difference* between the above two ways of finding the number in $[1,63]$?
- The first one (*adaptive or sequential*): You ask the second question (query) after knowing the answer of the first one and continue That is, the previous knowledge will be used later.
- The second one (*non-adaptive*): You can ask all the questions (queries) *at the same time*.

Algorithms

- Adaptive algorithm (*Count on you!*)
- Non-adaptive algorithm (*Construction of Arrays?*)
- k-stage algorithm

The most popular one is a 2-stage algorithm in which we use an algorithm (either one) in the first stage and then in the second stage we test the left “suspected” items from the first stage one by one.

Fundamental Problem

- Among all possible algorithms let $M(d, n)$ denote the minimum number of tests we need to use in the worst case. $M(1, 64) = 6$.
- **Problem: Determine $M(d, n)$.**
- For example, can we determine $M(2, 1,000)$?
- **Fact:** $d \cdot \{\log_2 n\} \geq M(d, n) \geq \{\log_2 C(n, d)\}$.
($C(n, d)$ denotes n -choose- d .)
- The inequality of the right hand side is known as the information lower bound. (?)

Development of GT (1)

- - 1999 Complex model: Molecular biology (Torney)
- - 1998 Mutually obscuring defetives (Damaschke)
- - 1997 Inhibitor model (Farach *et al.*)
- - 1993 Combinatorial group testing (堵丁柱與黃光明)
- - 1984 Multiple-access communication (Berger et al.)
- - 1943 Blood testing (Dorfman & Rosenblatt)

Development of GT (2)

- 2006 – Present: Our contributions- See references.
- 2006 Pooling designs and nonadaptive group testing (堵丁柱與黃光明).
- Graph reconstruction (contig sequencing)
- Non-unique probe selection problem
- - 2006 Inhibitor complex model (Chang *et al.*)
- - 2001 Drug discovery (Xie *et al.*)
- - 2000 Combinatorial group testing, 2ed (堵丁柱與黃光明)

Non-adaptive Algorithm

We can use a matrix to describe a non-adaptive algorithm.

Items are indexed by columns and the tests are indexed by rows. Therefore, the (i, j) entry is **1** if the item j is included in the *pool* i (for test), and **0** otherwise.

An example (12 items and 9 tests)

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.

Items: 010000010000 (2 & 8)

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.

Decoding Idea

- Let each input be a 12-dim column vector $\mathbf{x}$ and A be the above 9×12 matrix. Then the outcome (0,1)-vector $\mathbf{y}$ is obtained by $A\mathbf{x}$ such that its i^{th} component is 1 if the i^{th} component of $A\mathbf{x}$ is positive and 0 otherwise.
- If the mapping A is 1-1, then we are able to find the positives, that is to determine $\mathbf{x}$, see it?

Outcome Vectors

- The vector $\mathbf{y}$ is an *outcome vector* which is corresponding to an input $\mathbf{x}$.
- If A is 1-1, then we can decode $\mathbf{x}$ long as we know its outcome vector.
- In order to get the job done with lower decoding complexity, extra properties for A is needed.

Set notation

- It is easier to apply combinatorial structures to construct pooling designs, therefore, we use sets (or codewords) for columns in non-adaptive algorithms.
- We shall use set notation most of the time.
- The set corresponding to a codeword (binary vector) is called the *support* of the codeword.

Relation with designs

- Let $M = [m_{i,j}]$ be a $(0,1)$ $t \times n$ matrix. Then we can use n sets (ordered) S_i 's to represent the columns of M where
$$S_k = \{i : m_{i,k} = 1, i = 1, 2, \dots, t\}, k = 1, 2, \dots, n.$$
- The following sets represent the columns the $(0,1)$ -matrix mentioned above:
 $\{1,2,3\}, \{4,5,6\}, \{7,8,9\}, \{1,4,7\}, \{2,5,8\}, \{3,6,9\}, \{1,5,9\},$
 $\{2,6,7\}, \{3,4,8\}, \{1,6,8\}, \{2,4,9\}, \{3,5,7\}.$
- This a collection of subsets of $[1,9]$, so a design.
- In fact, this design is the **Affine plane of order 3**.

Remark

- A *design* is a pair (X, B) where X is a v -set and B is a collection of subsets of X . So, the matrix mentioned above can be viewed as a *design*.
- A design defined on a v -set can be viewed as a *binary code of length v* .
- A design (X, B) can also be viewed as a *hypergraph* with vertex set X and edge set B .

Find Positives?

- We can do it, if the number of positives is not too many, say **at most 2**, by running the **9** tests simultaneously corresponding to rows.
- The reason is that the union of (**at most**) 2 columns are all distinct. In a word, the matrix is indeed an injective mapping.

d-separable and d-disjunct matrices

- A matrix is *d-separable* if $\cup D \neq \cup D'$ for any two distinct d-sets D and D' (columns), i.e. no two unions of d columns are the same.
- A matrix is *d-disjunct* if no column is contained in the union of any other d columns.
- A *d-disjunct* matrix is *d-separable*, *but the other way around may not be correct. (?)*

Important Facts

- *A d -disjunct matrix can be applied to find $k (\leq d)$ positives.*

Proof. The union of $k (\leq d)$ columns corresponds to distinct *outcome vector*. (This is also true for d -separable matrices.)

- *d -disjunct matrices have a simple decoding algorithm, namely, a column is positive if and only if it does not appear in a negative row.*

Various Models

- *Errors* occurred (*in experiments*).
- There are *inhibitors* (*cancel the positive effects*).
- There is a *threshold* (*enough positives*).
- Defective items are sets: *complex* model.
- *Competitive* model: the number of defectives is unknown.
- The defectives are *mutually obscuring*.

Further Remarks

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

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…。

Twenty Questions Game with Genes

- Given an unknown set S of integers in the interval $[1, n]$, reconstruct the set S by asking the minimum number of queries of the form “does a given interval contain an integer from S ?”
- In this formulation, the interval $[1, n]$ corresponds to cDNA (original gene with cut-out introns), S corresponds to exon boundaries in cDNA, and the queries correspond to PCR reactions defined by a pair of primers.

Facts

- If the number of exon boundaries k is known, then we need at least $\log_2(m)$ queries where m is equal to n chooses k .
- If a biologist tolerates Δ error, then the number of queries will be about $k \cdot \log_2(n/\Delta) - k \cdot \log_2 k$.
- For typical cDNA, we use about 30 primers and 3 rounds to find exon boundaries.

Another Example of Group Testing

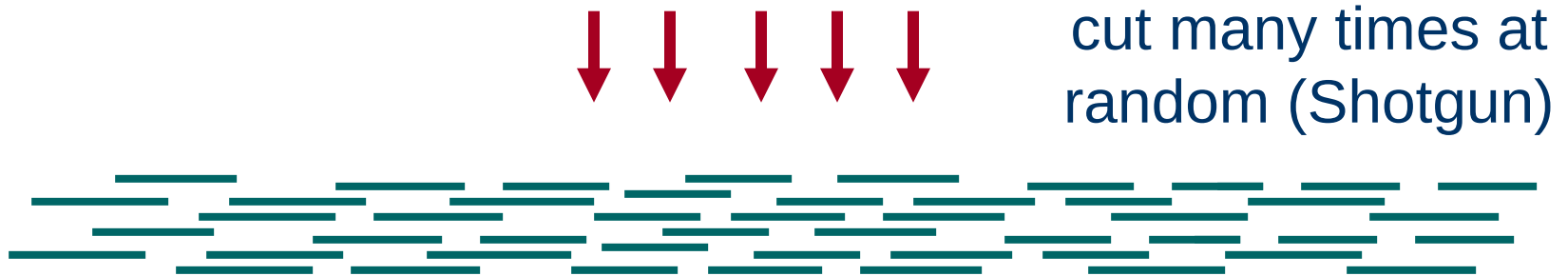
- In screening clone library the goal is to determine which clones in the clone library hybridize with a given probe in an efficient fashion. A clone is said to be **positive** if it hybridize with the **probe(探針)**, and **negative** otherwise.

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 ...**

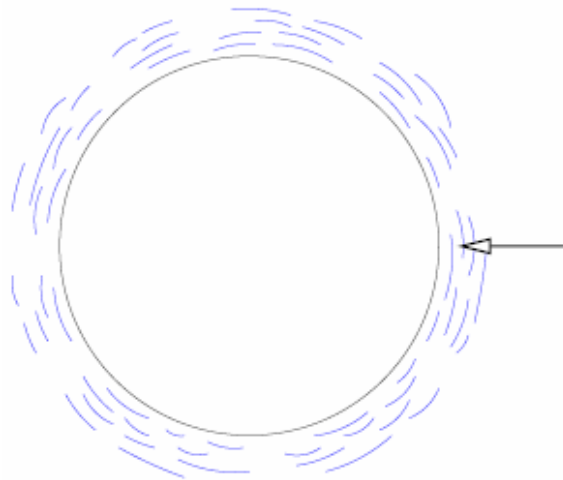
Shotgun approach

genomic segment



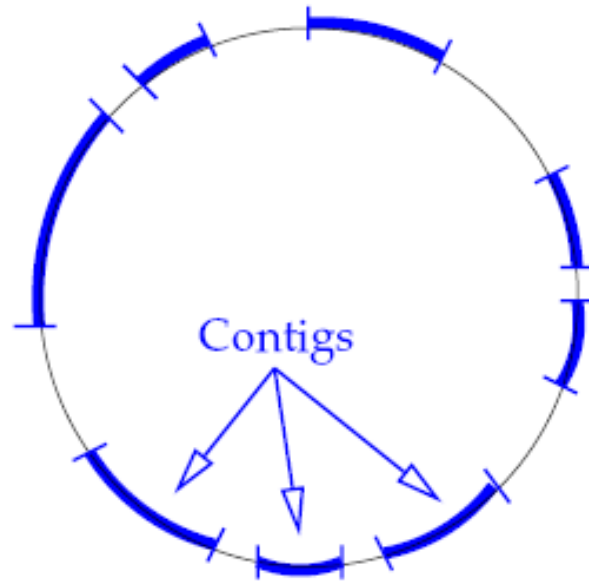
Whole-genome shotgun sequencing

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

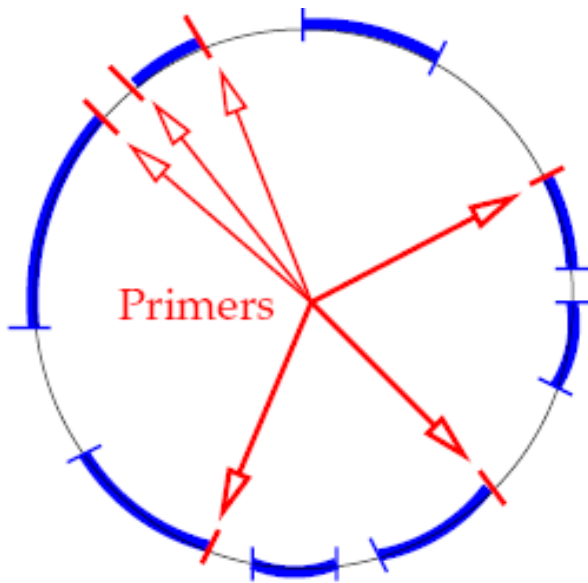


Circular genome

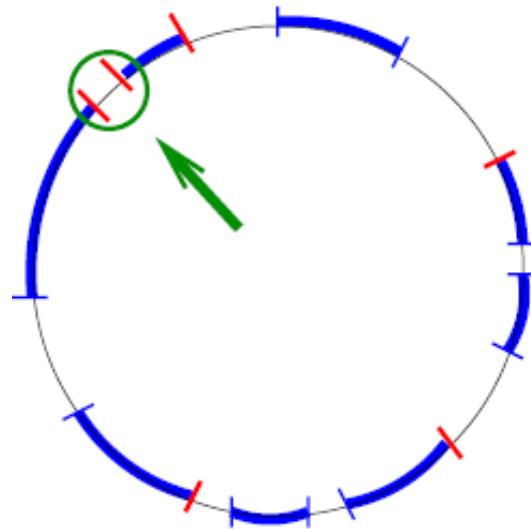
- Reads are assembled into contigs with unknown relative placement.

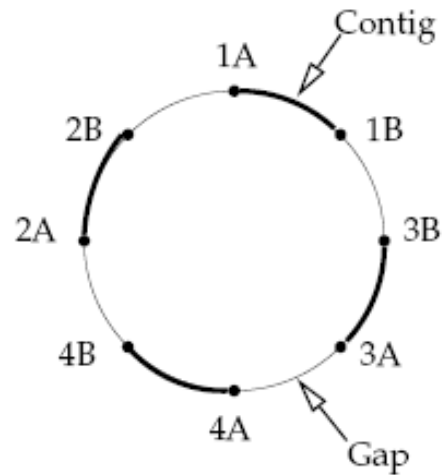


– **Primers** : (short) fragments of DNA characterizing ends of contigs.



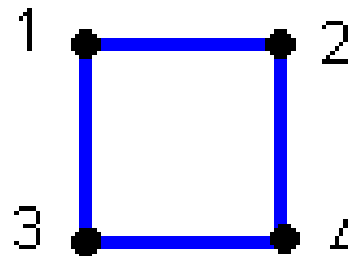
- A **PCR (Polymerase Chain Reaction)** reaction reveals if two primers are proximate (adjacent to the same gap).
- **Multiplex PCR** can treat multiple primers simultaneously and outputs if there is a pair of adjacent primers in the input set and even sometimes the number of such pairs.

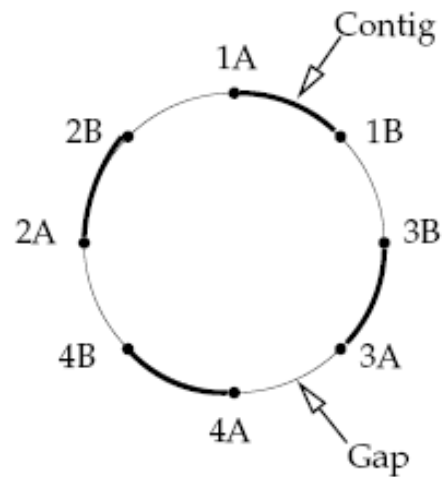




- Two primers of each contig are “mixed together”
 - Find a Hamiltonian cycle by PCRs!

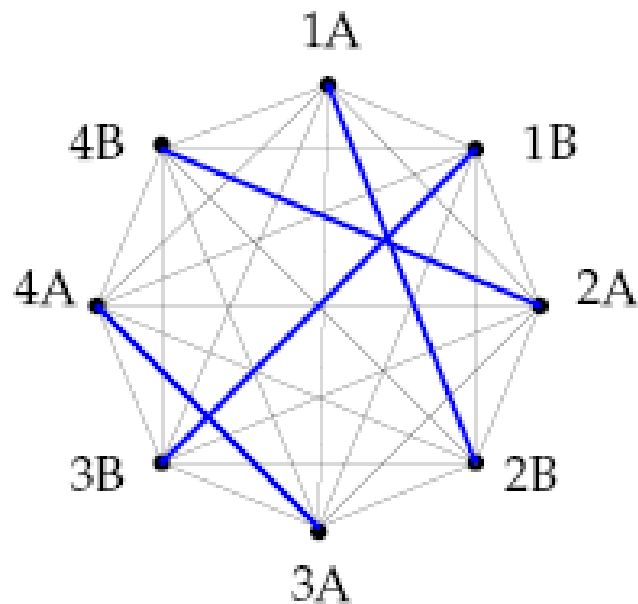
1A ——— 1B
 2A ——— 2B
 3A ——— 3B
 4A ——— 4B





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 or Hypergraphs (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

References

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- 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.
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- 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.
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- *Threshold* group testing on *inhibitor* model (Huilan Chang and Chie-Huai Shih), **J. Computational Biology**, Vol. 20, No. 6, 2013, 1 – 7.

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- New bound on *2-bar-separable* codes of length 2 (with Minquan Cheng, J. Jiang, Yuan-Hsun Lo and Ying Miao), **Des. Code Cryptography**, 74(2015), no. 1, 31 – 40.
- Codes with the identifiable parent property for *multimedia fingerprinting* (with Minquan Cheng, J. Jiang, Yuan-Hsun Lo and Ying Miao), **Des. Code Cryptography**, 83(2017), no. 1, 71 – 82.
- Learning a hidden *uniform hypergraph* (with Huilan Chang and Chi-Huai Shih), **Optim. Lett.**, 12(2018), 55 - 62.

Keep Moving Forward!

