

# Thermodynamics of a multistranded one-dimension Scaffolded DNA Computer

Ahmed Shalaby

1<sup>st</sup> year PhD

Computer Science Department

Supervisor: Damien Woods

# Agenda

- What is 1D Scaffolded DNA Computer?
- What is the thermodynamic aspects we are interested in?
  - Minimum free energy.
  - Partition function.
- How to compute Partition function efficiently?
- SDC kinetic simulation and experimental results.



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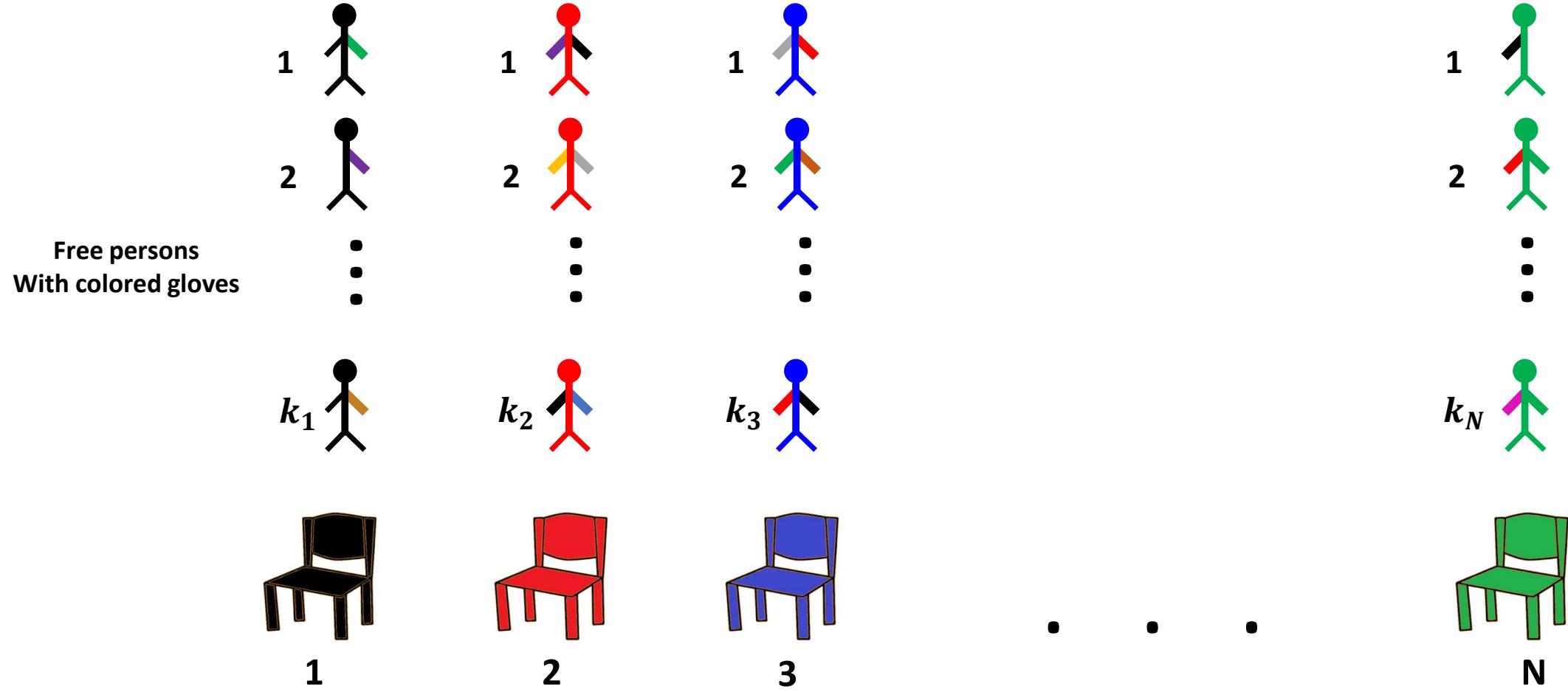
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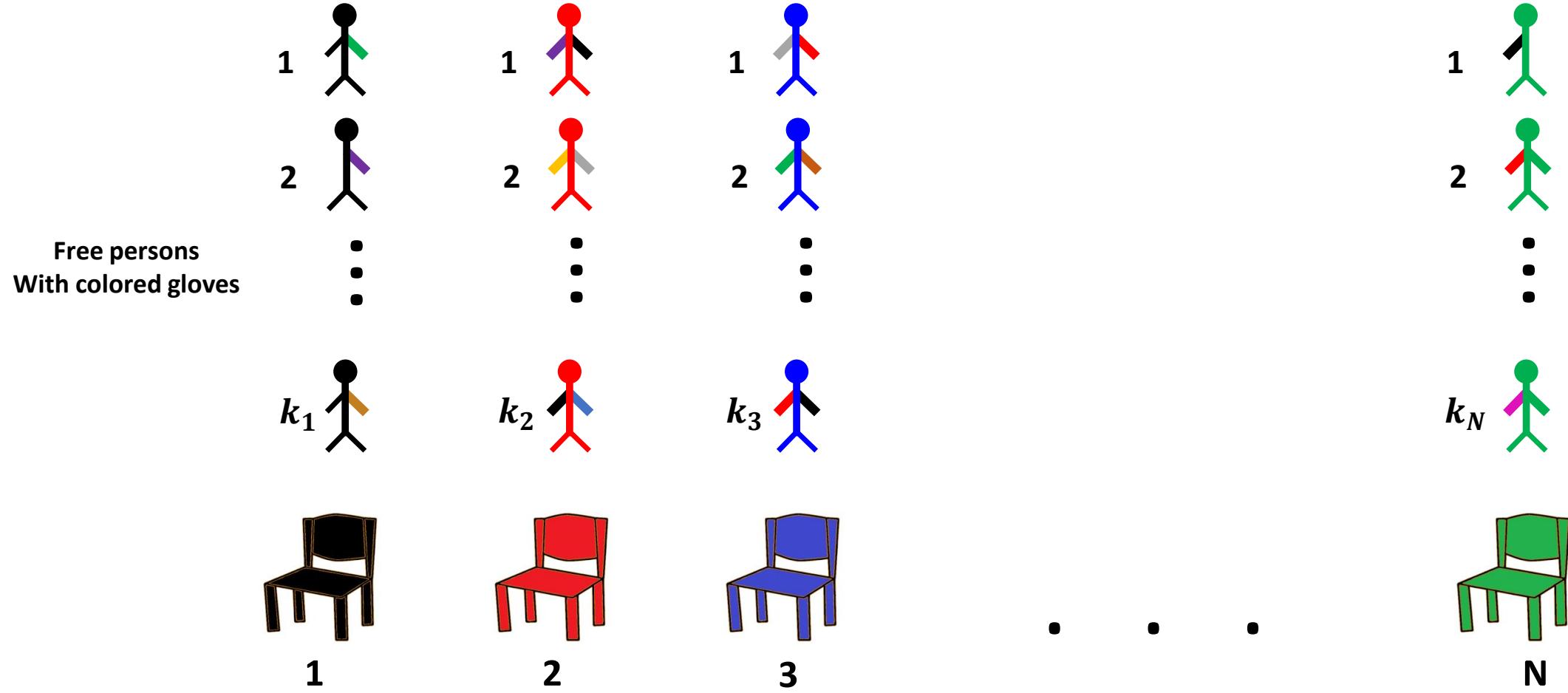
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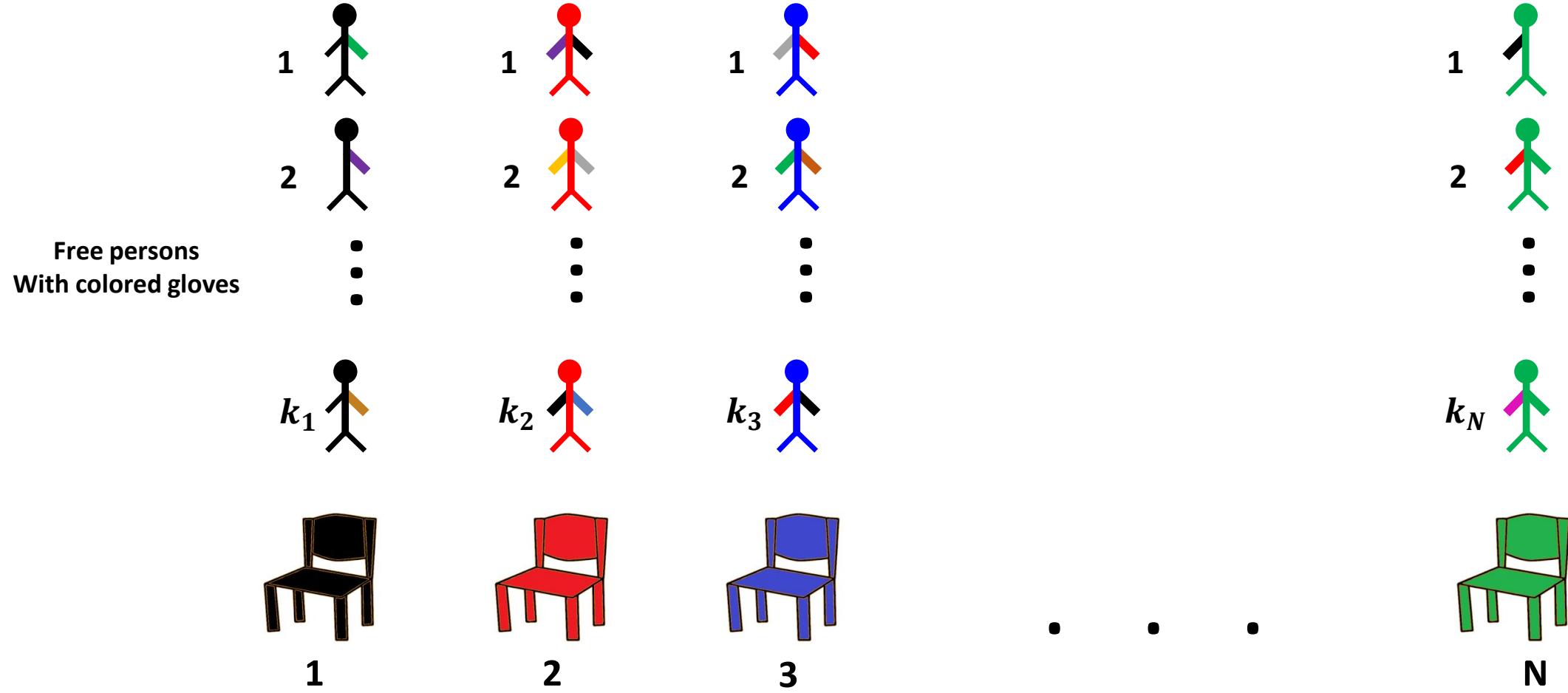


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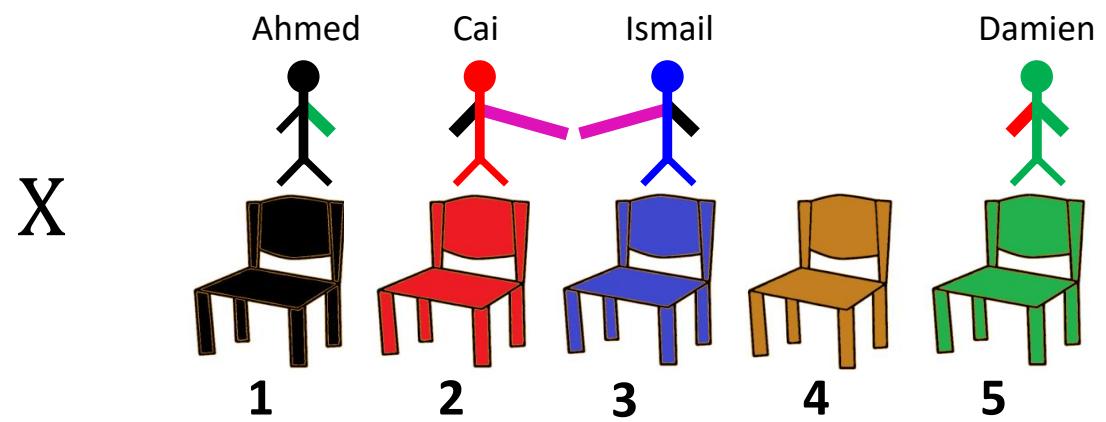


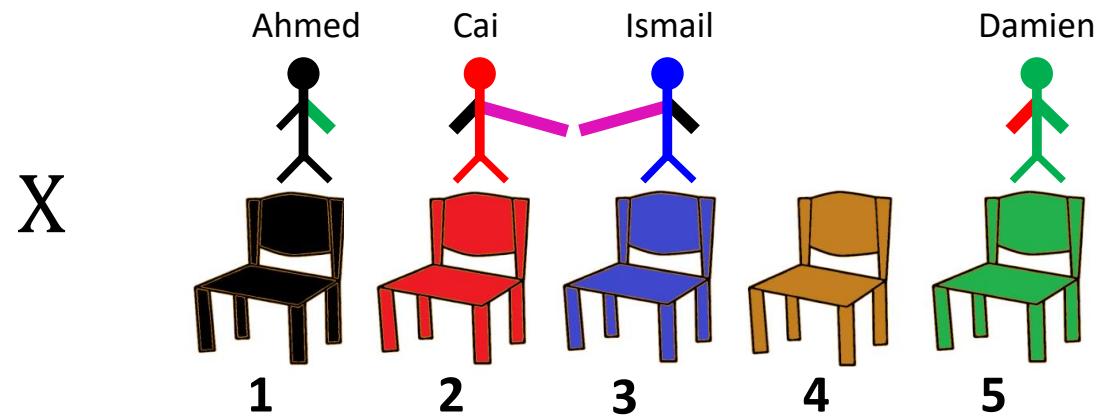
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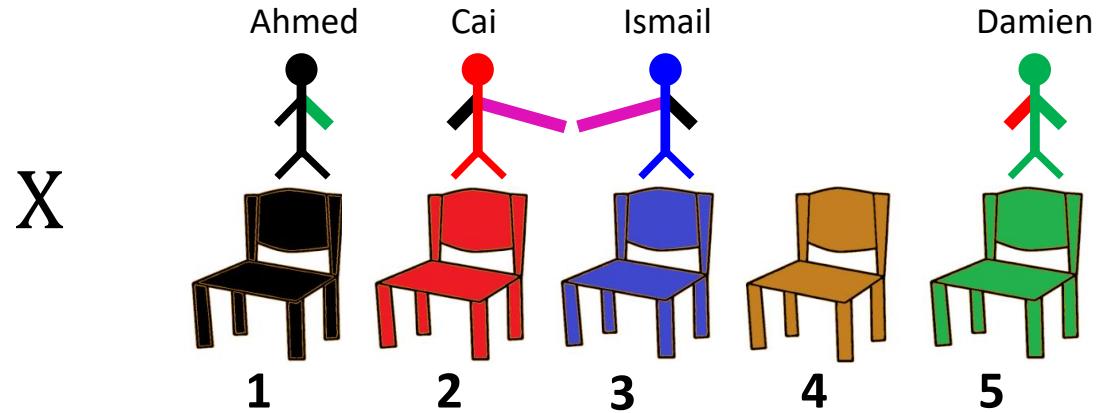
**(Exponential in the # of chairs)**





$$E(X) = \text{sit(Ahmed)} + \text{sit(Cai)} + \text{sit(Ismail)} + \text{sit(Damien)} + 4 * \text{sit\_convincing\_cost} + \text{handshake(Cai, Ismail)}.$$

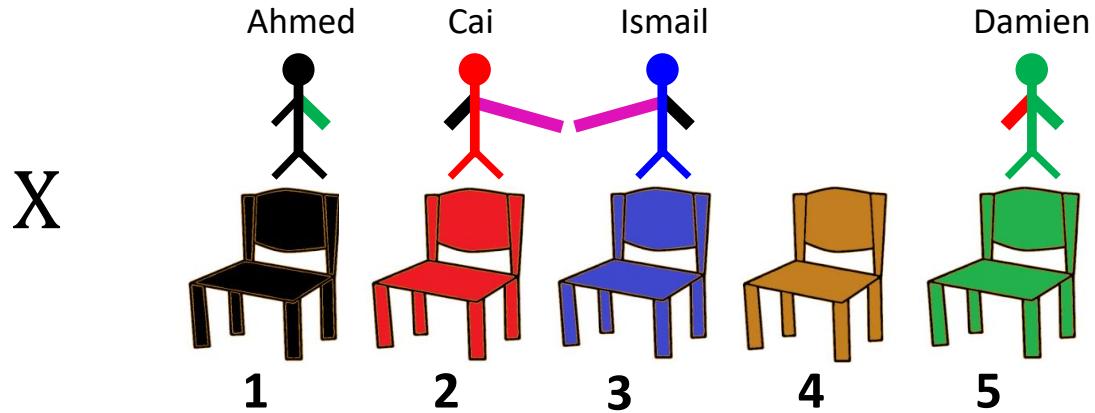
+      +      +      +      -      +



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+      +      +      +      -      +

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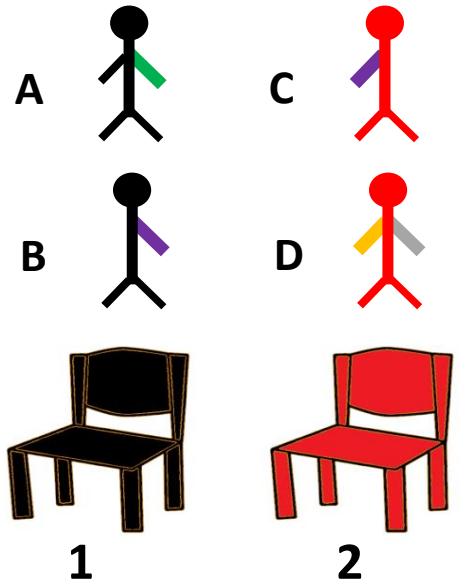
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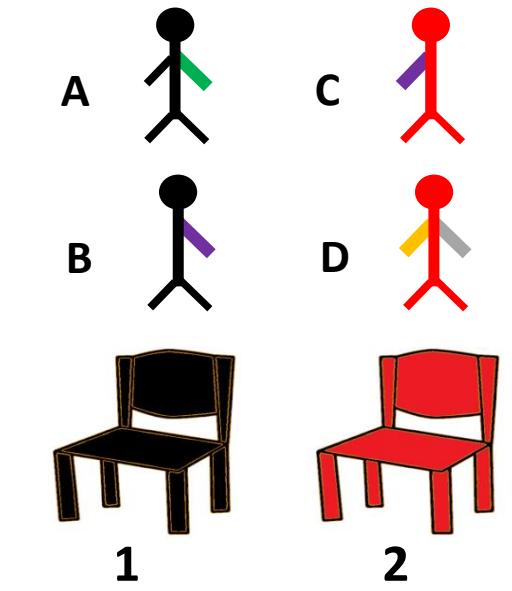
We further assume the following:

- $|\text{sit}(p)| > |\text{sit\_convincing\_cost}|$ . (you always gain by convincing a person to sit)

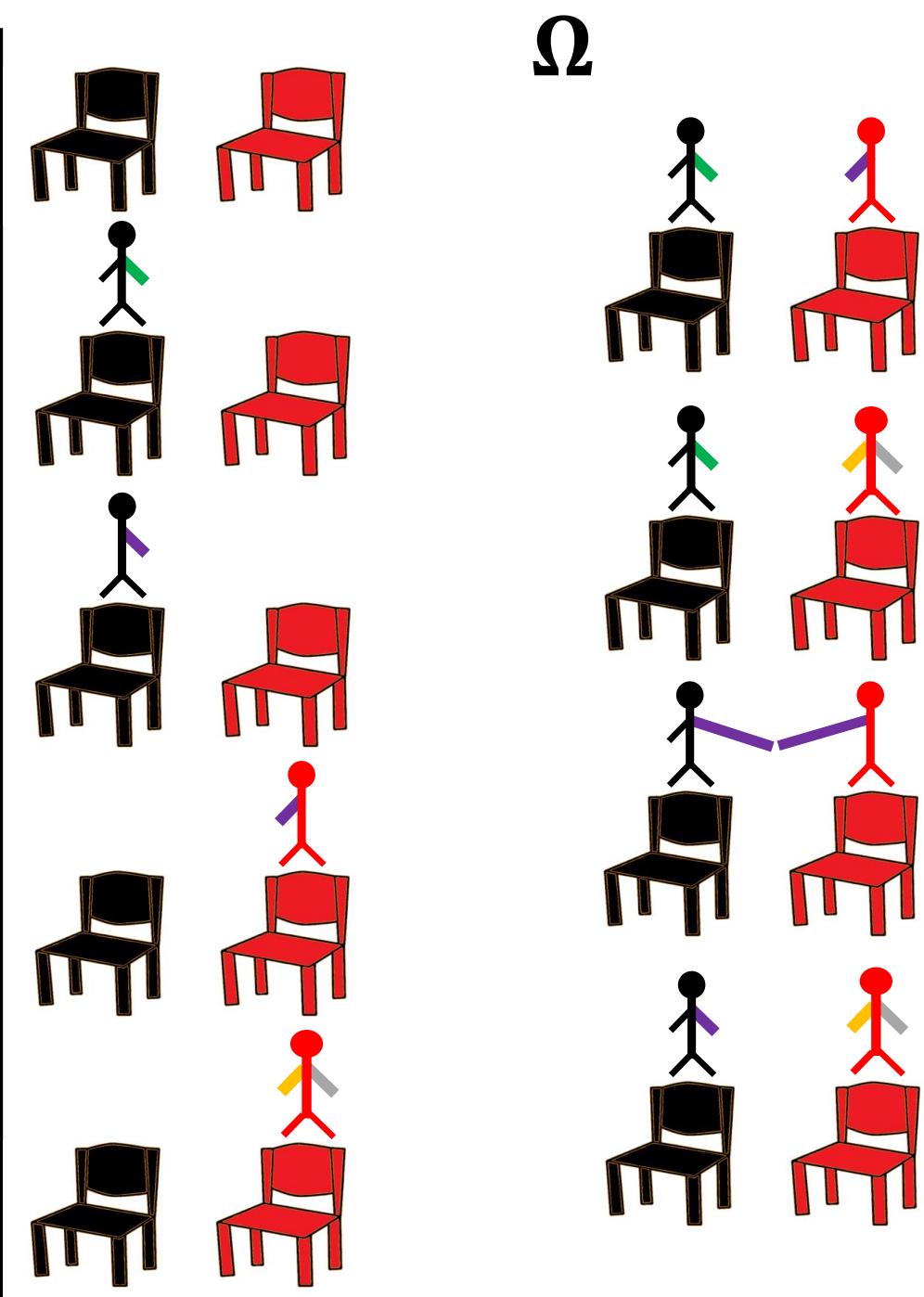


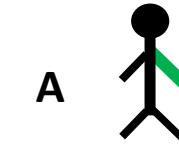
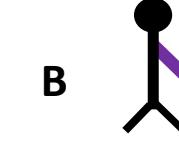
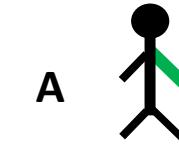
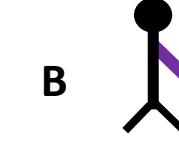


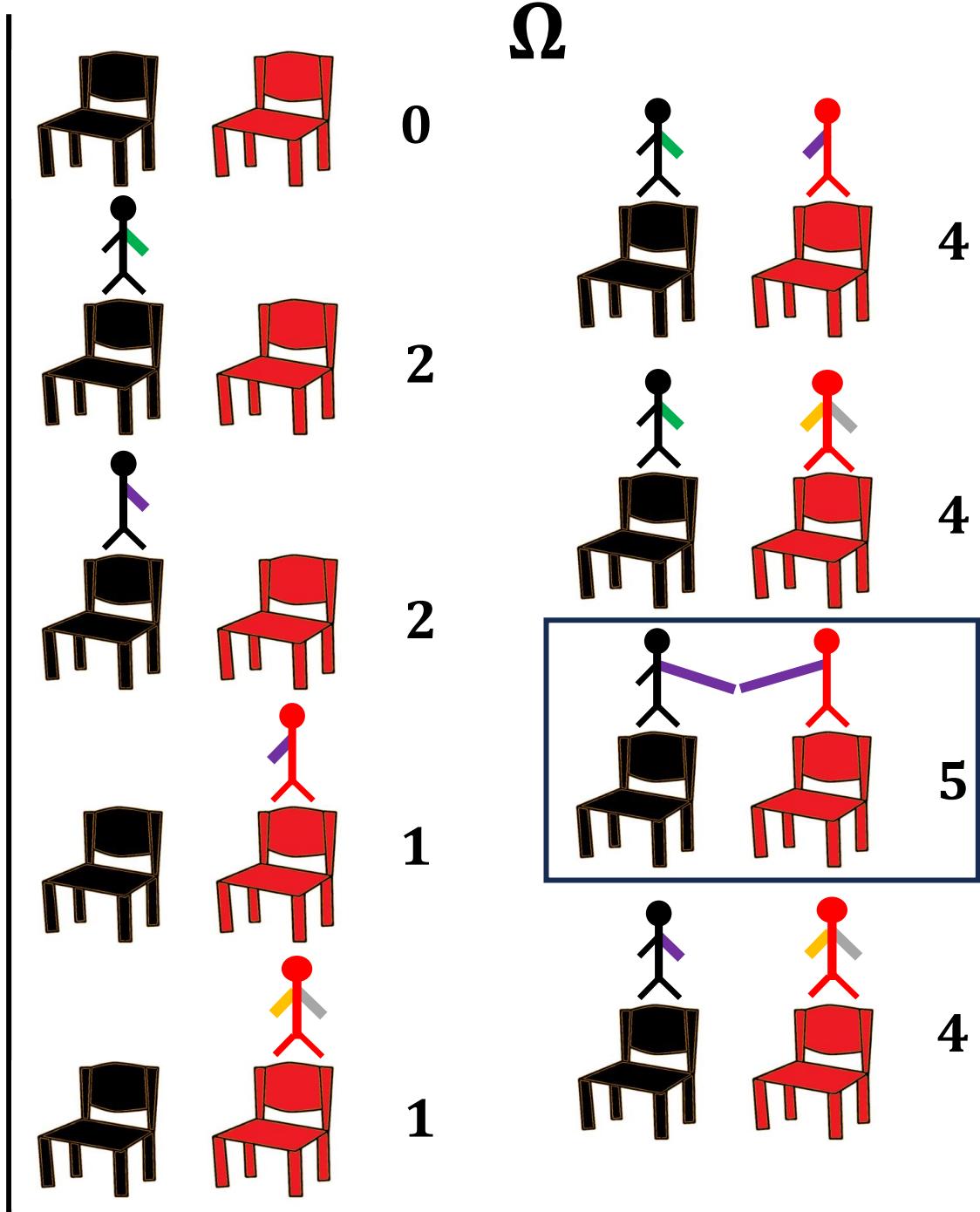
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- $\text{sit\_convincing\_cost} = -1$

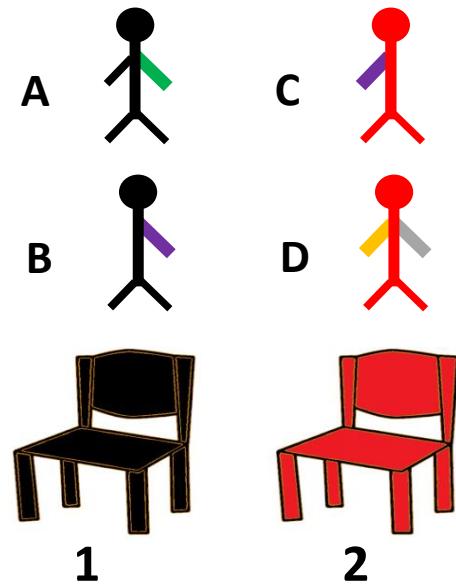


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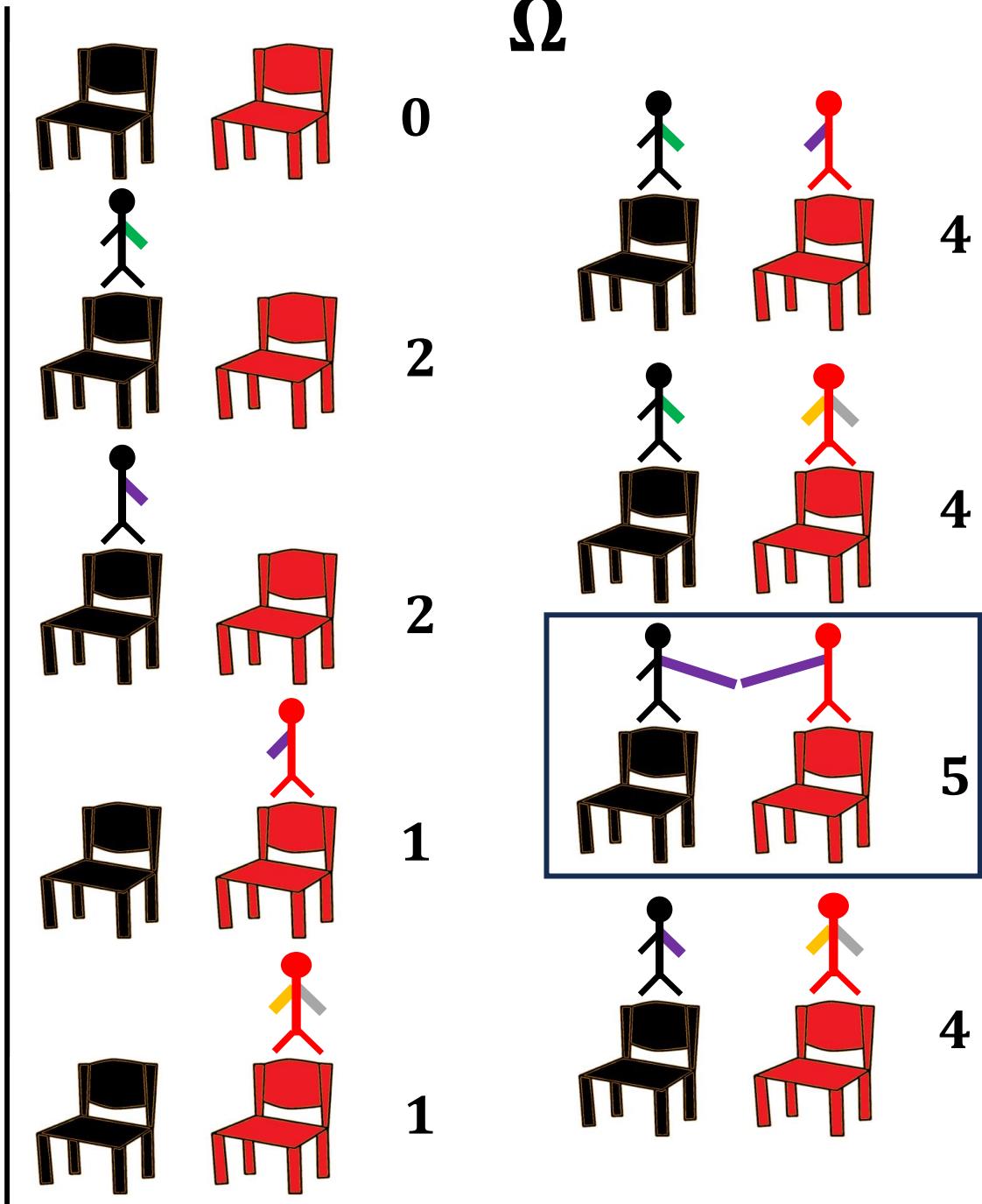


- A   
 B   
 C   
 D 
- 1   
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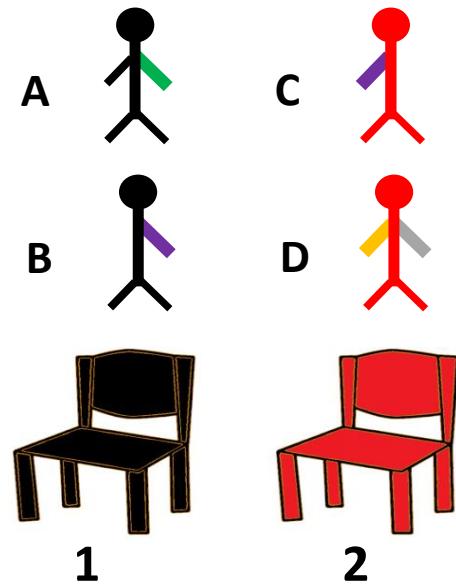
## The Maximum Energy $M$

$$M := \max_{X \in \Omega} \{E(X)\}$$

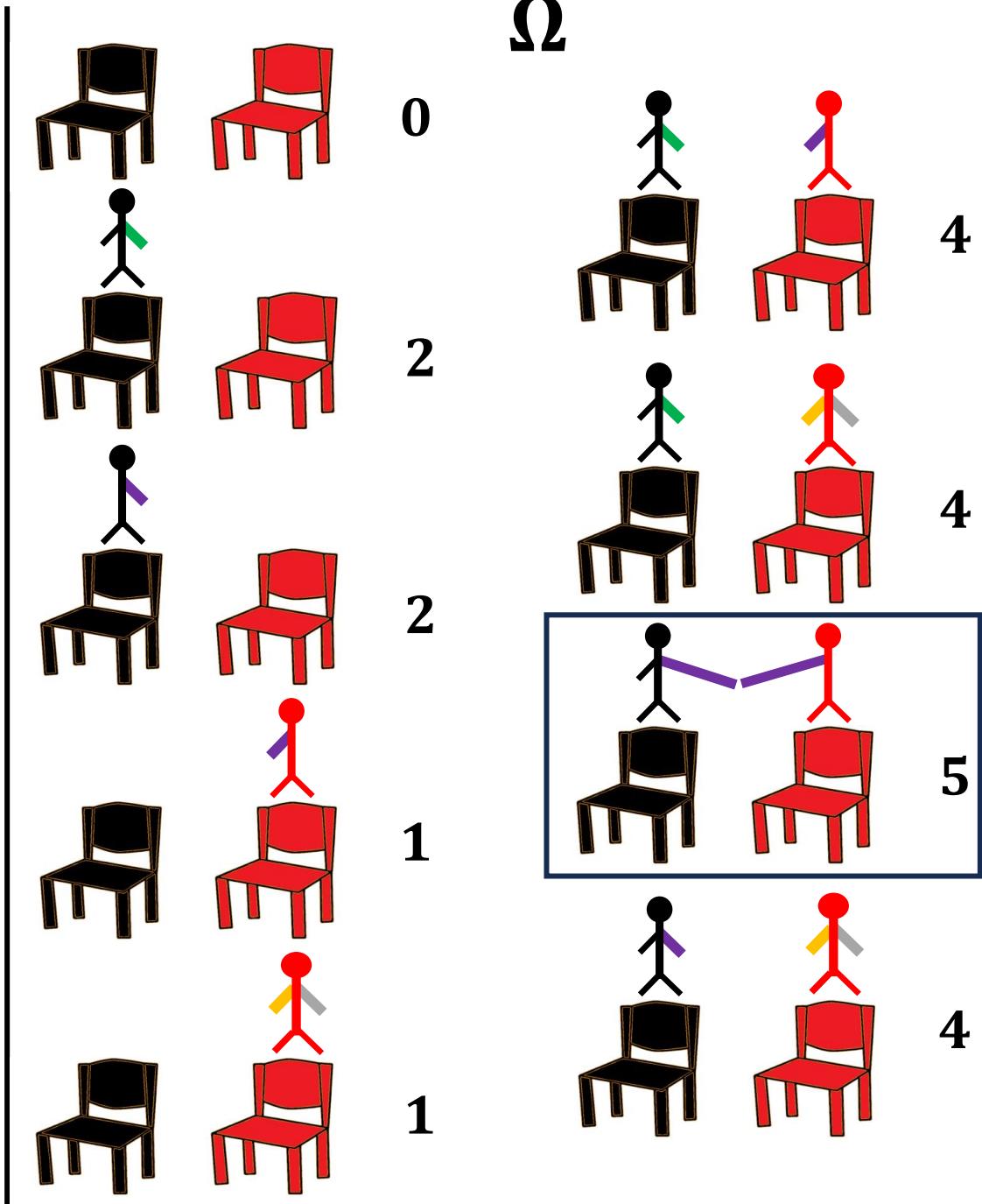
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Where  $c$  is some specific constant



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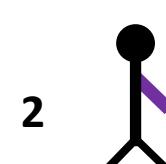
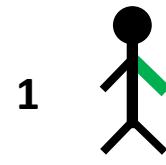
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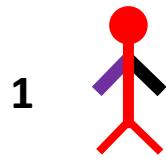
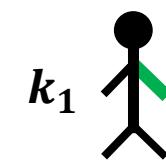
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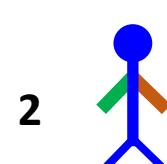
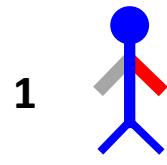
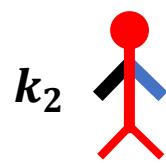
**Why are we interested in this ?**



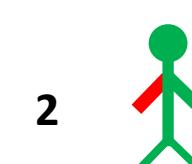
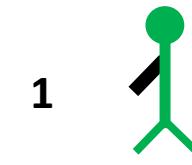
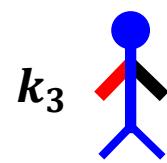
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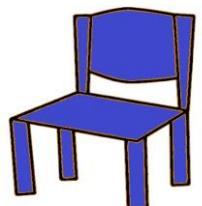
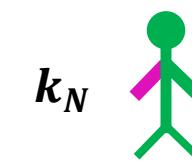
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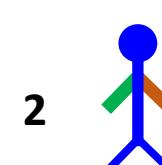
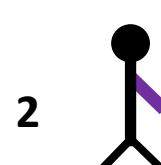
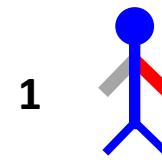
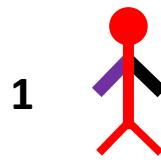
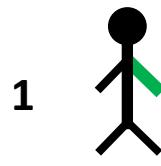


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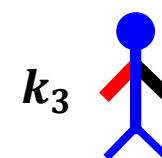
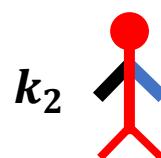
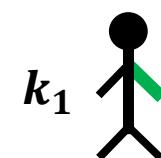




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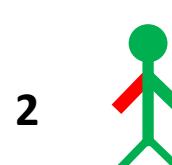
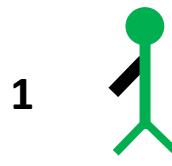
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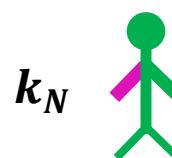
$k_1$

$k_2$

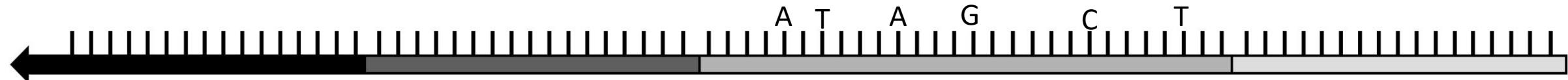
$k_3$

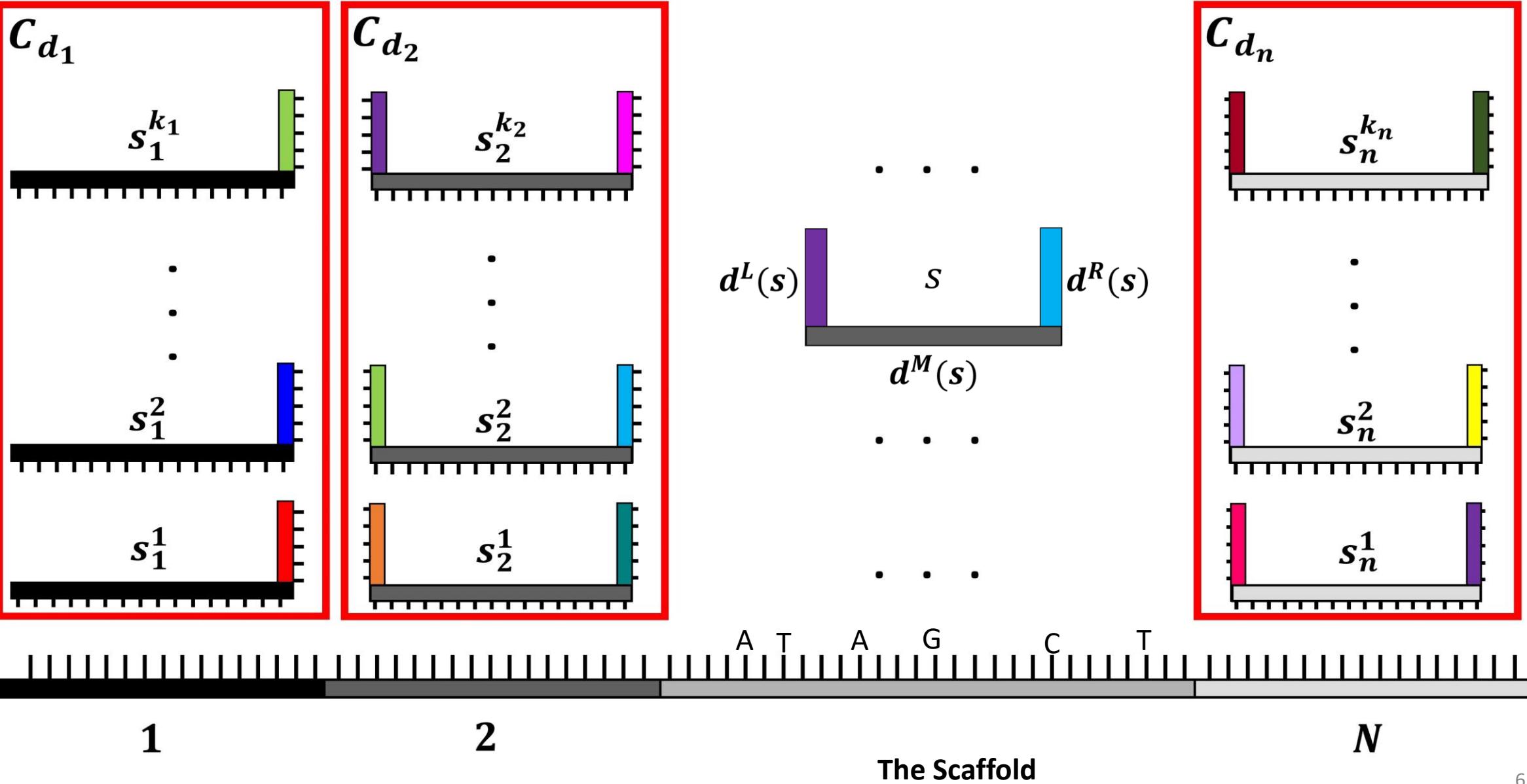


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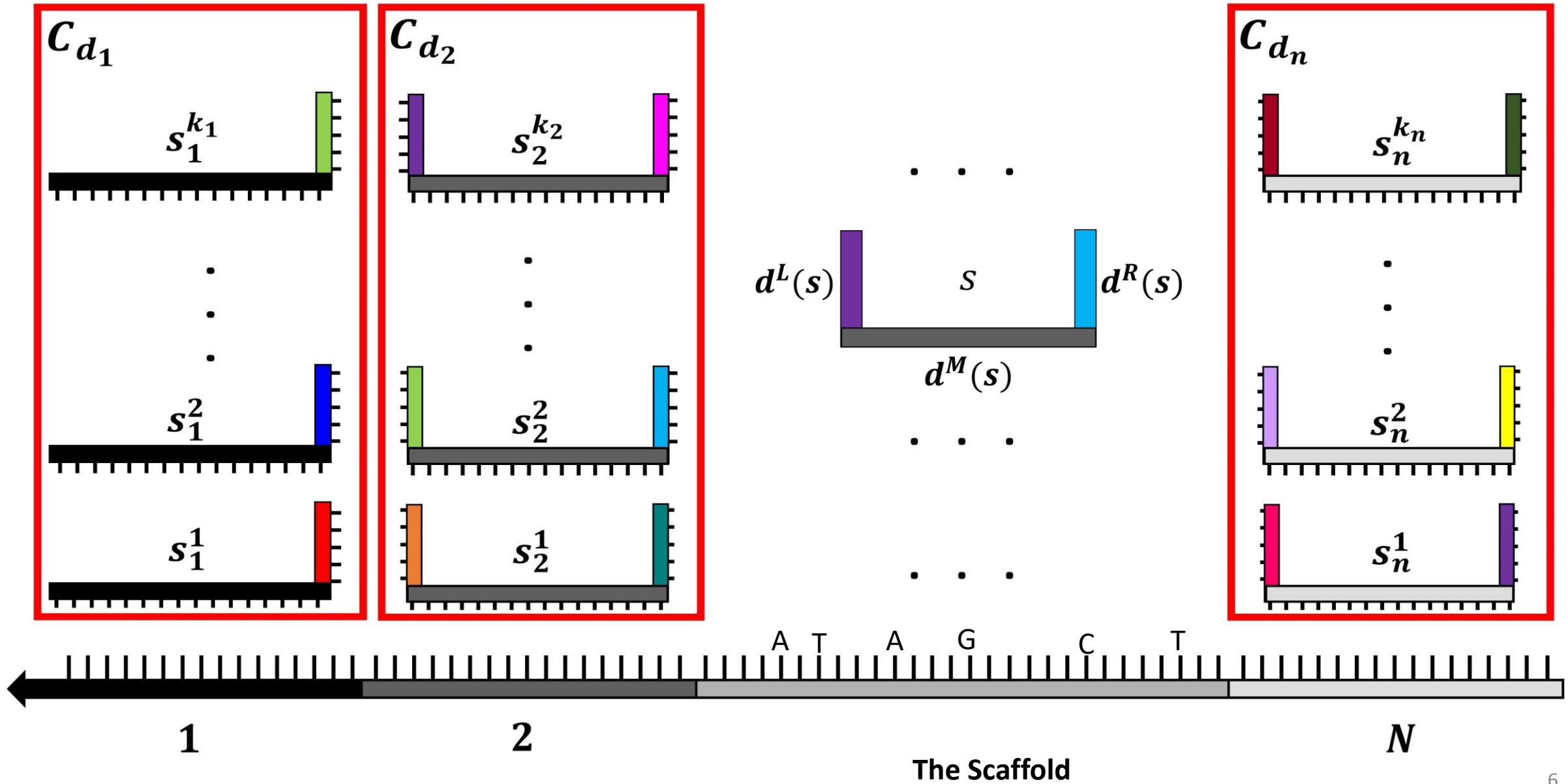


$k_N$





# This is 1D Scaffolded DNA Computer



# 1D Scaffolded DNA Computer Energy model and thermodynamic features

For any configuration  $X$  of size  $l$ :

**DNA**       $\Delta G^S(X) = \sum_{s \in X} \Delta G(d^M(s)) + l \cdot \Delta G^{\text{assoc}} + \sum_{s_i, s_{i+1} \in X} \Delta G(d^R(s_i), d^L(s_{i+1})).$

**Chair**       $E(X) = \sum_{p \in X} \text{sit}(p) + l * \text{sitcost} + \sum_{p_i, p_{i+1} \in X} \text{handshake}(p_i, p_{i+1}).$

$$\text{MFE}^S = \min_{X \in \Omega^S} \{\Delta G^S(X)\}$$

$$Q^S = \sum_{X \in \Omega^S} e^{-\Delta G^S(X)/kT}$$

**NP-Hard** in base level case

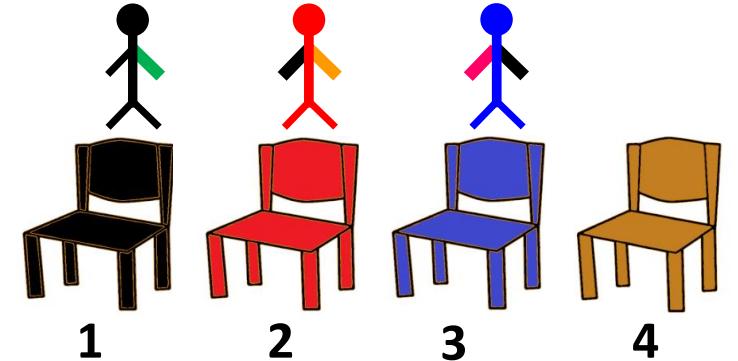
$T$  is the temperature in (kelvin) and  $k$  is Boltzmann constant.

- Intuitively, the MFE is the energy of the most favored configuration(s) of the system.
- The partition function is a Boltzmann-weighted sum of the energies of every configuration of the system and typically used as a normalization factor to calculate the probability of any configuration  $X$  at **equilibrium**:  $p(X) = (e^{-\Delta G^S(X)/kT})/Q^S$ .

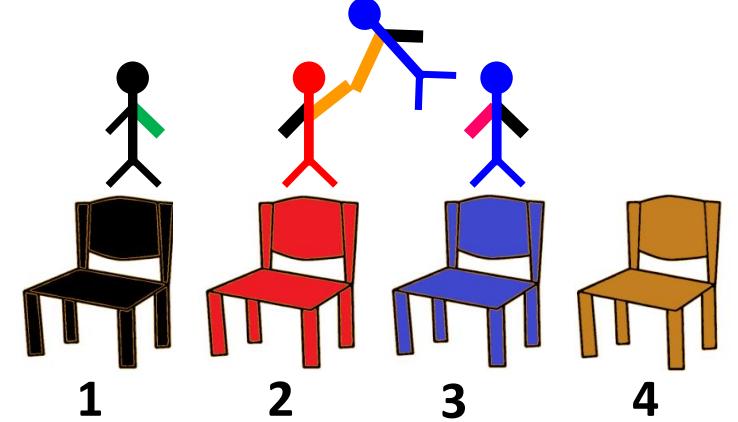
# **What is interesting in Scaffolded DNA Computer (SDC) ?**

**What is interesting in Scaffolded DNA Computer (SDC) ? DNA strand displacement**

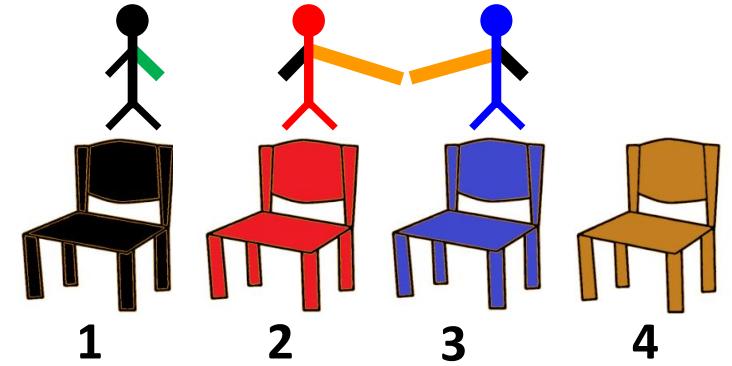
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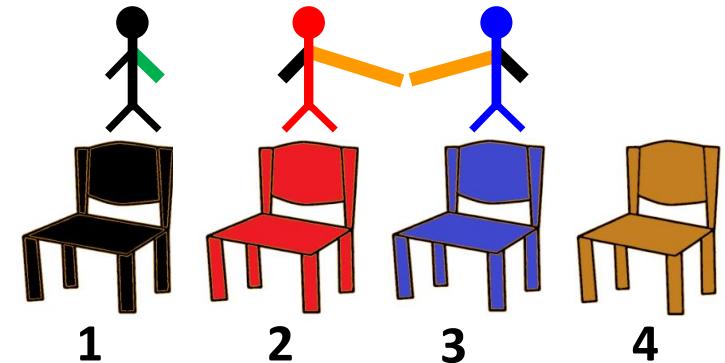


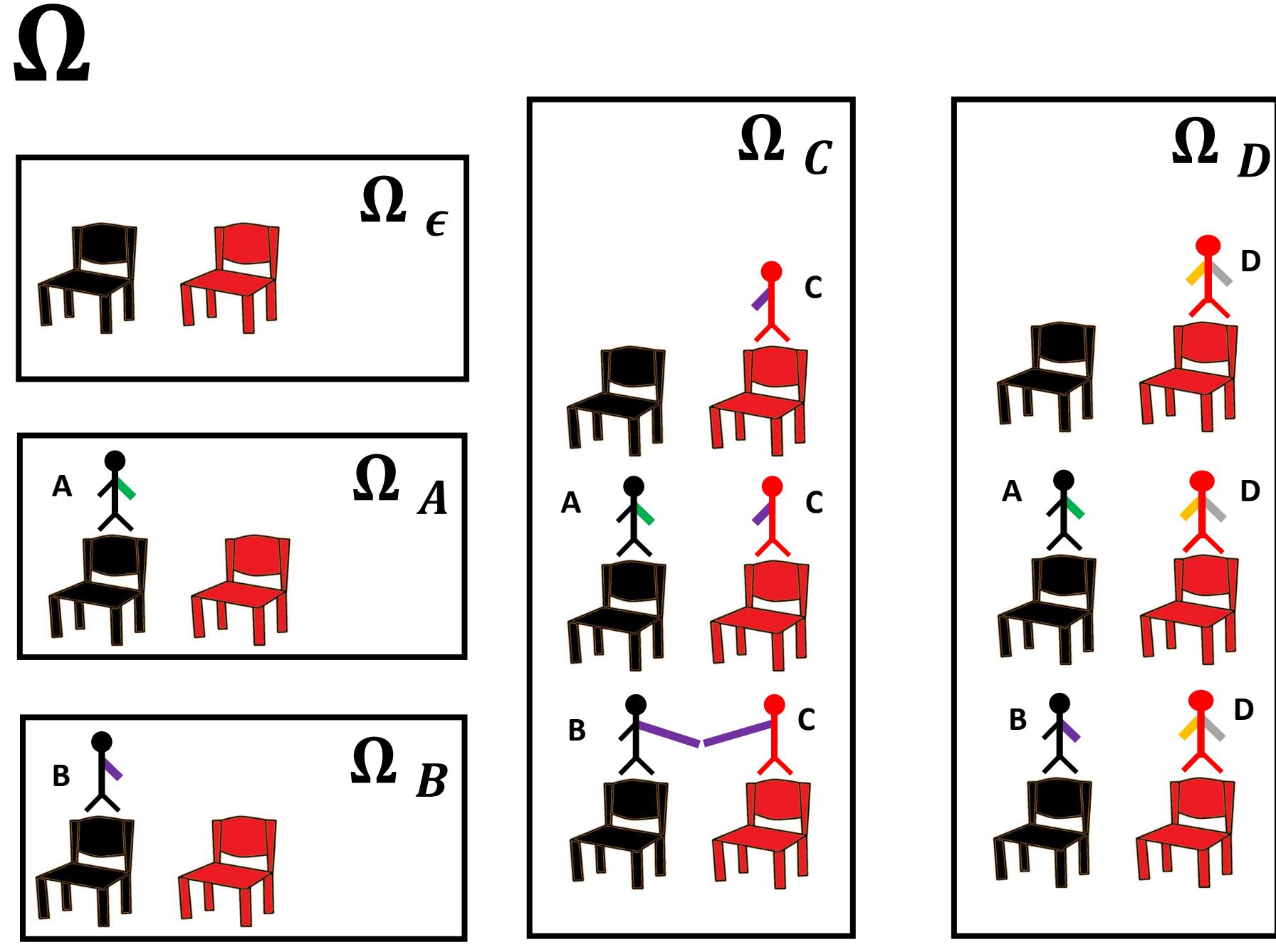
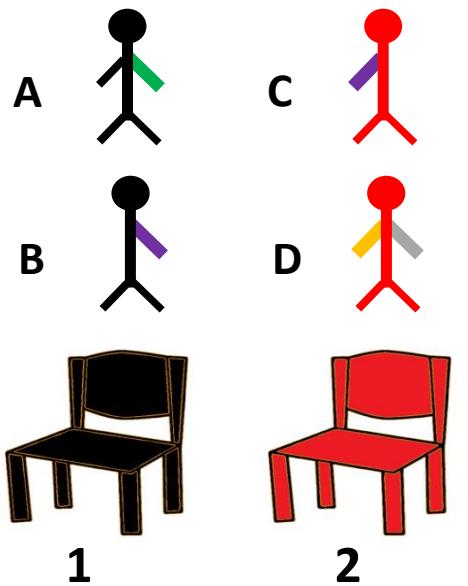
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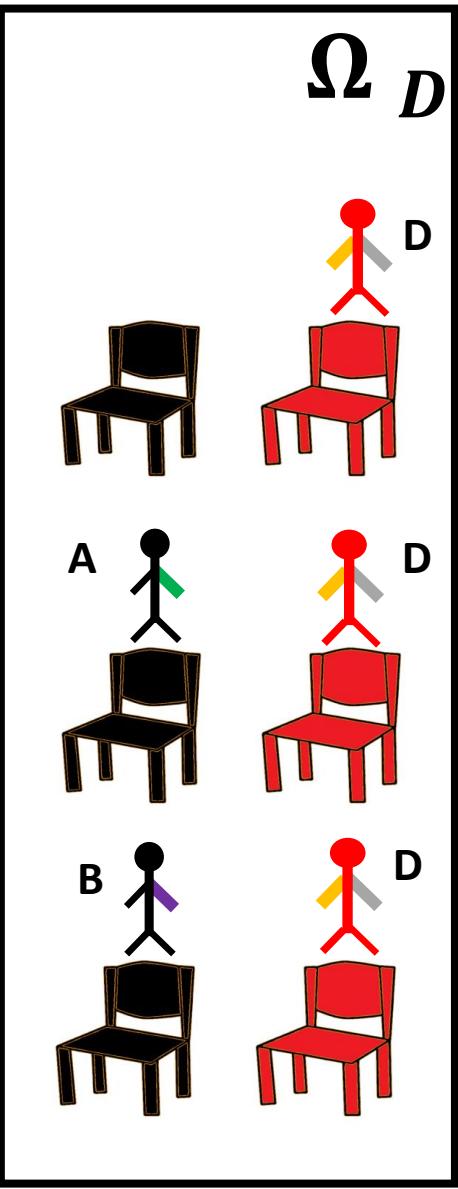
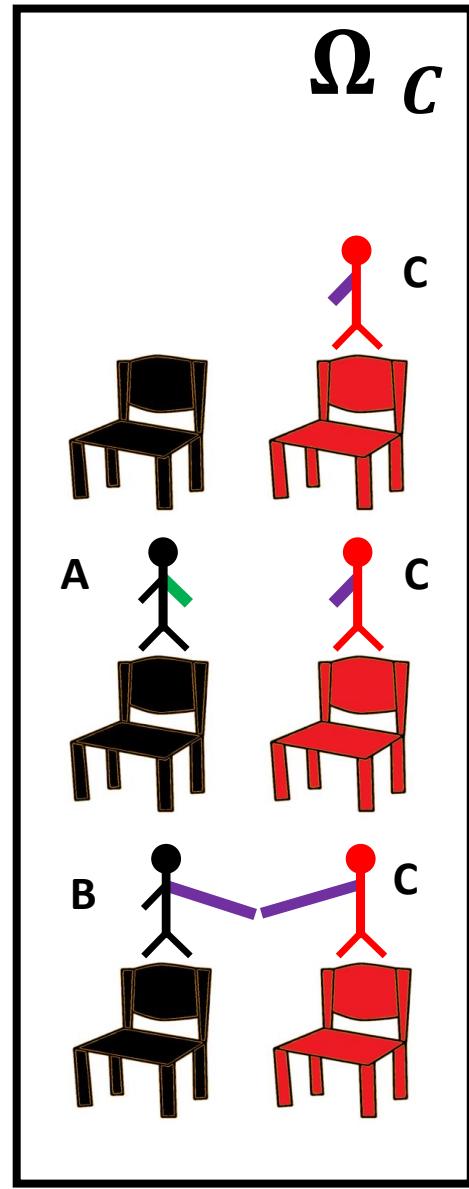
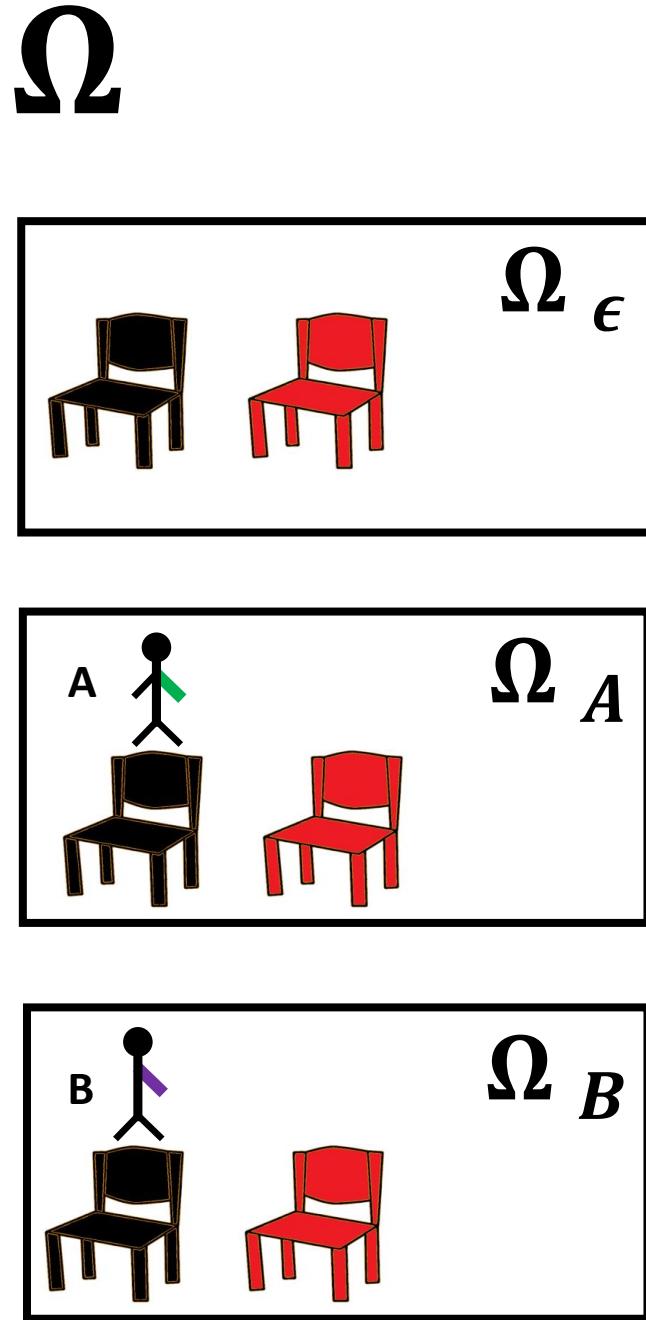
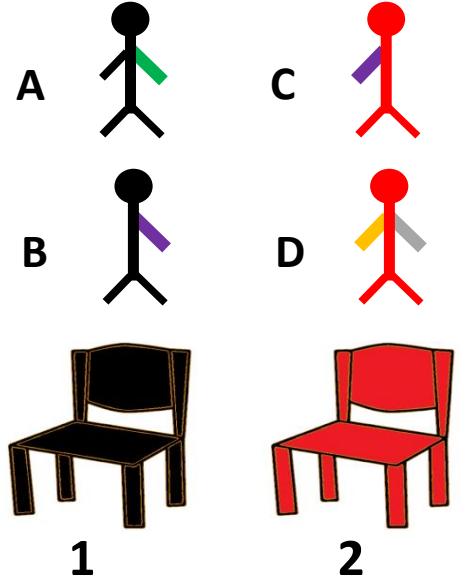
# What is interesting in Scaffolded DNA Computer (SDC) ? DNA strand displacement

- computationally expressive:
  - simulate finite state machines in 1D.
  - Boolean circuits in 2D.
- amenable to DNA storage applications.
- The SDC has been implemented experimentally in 1D, showcasing a total of 10 programs that solve problems such as
  - Bit-copy
  - Addition of two 4-bit numbers
  - Parity of an 8-bit input (is the number of 1s odd?)
  - Graph Reachability (is there a path in an input graph from a source node  $s$  to a target node  $t$ )
- Initial designs and results in 2D include Addition of two 7-bit numbers and a simple Bit-Copy program.

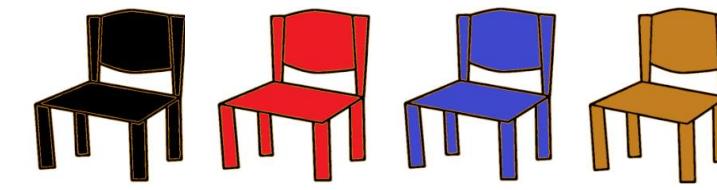




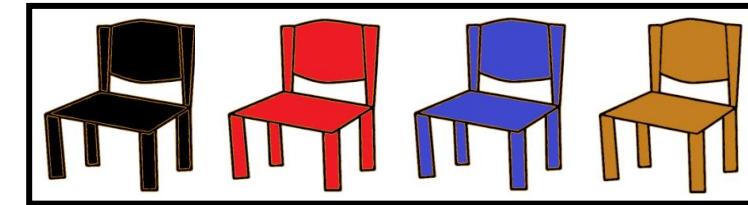
Is there recursive way  
to build these classes  
from themselves?





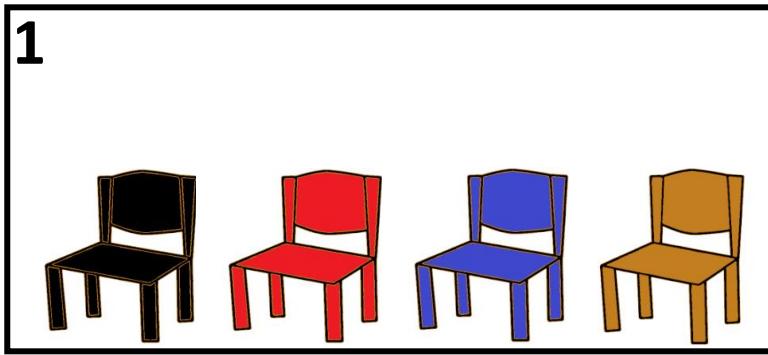
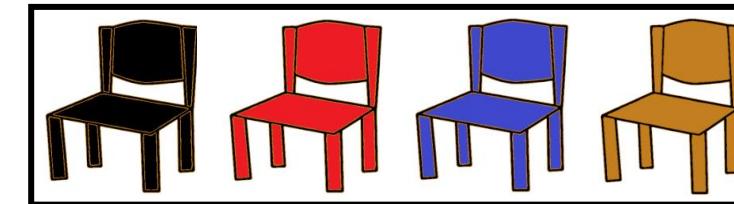


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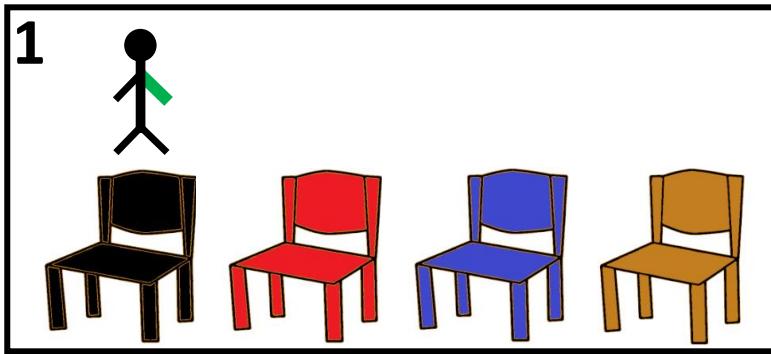
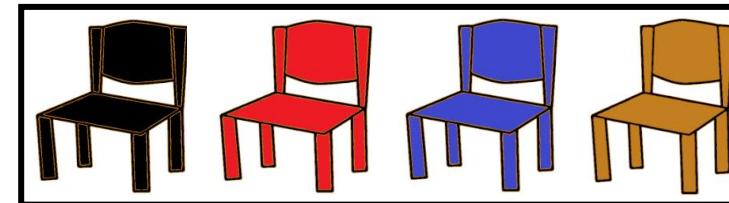


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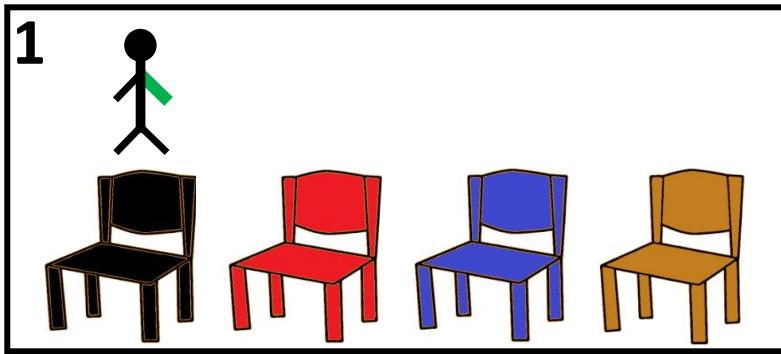
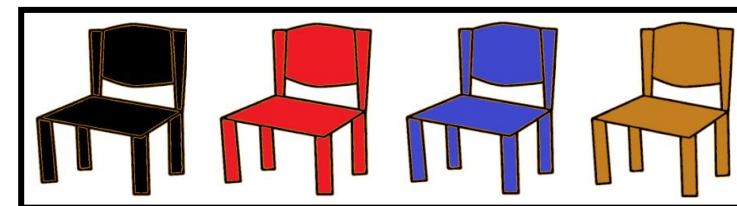
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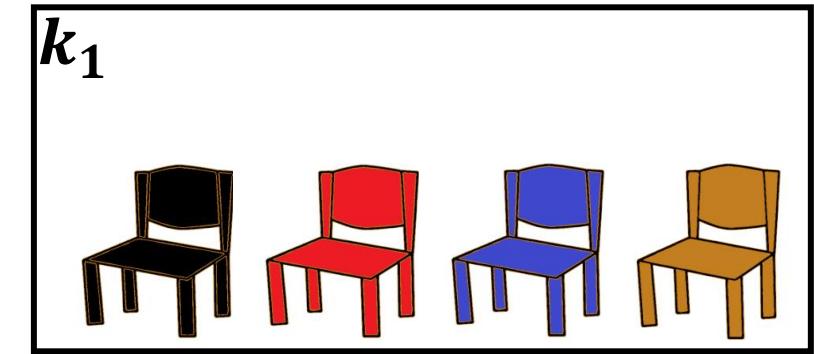
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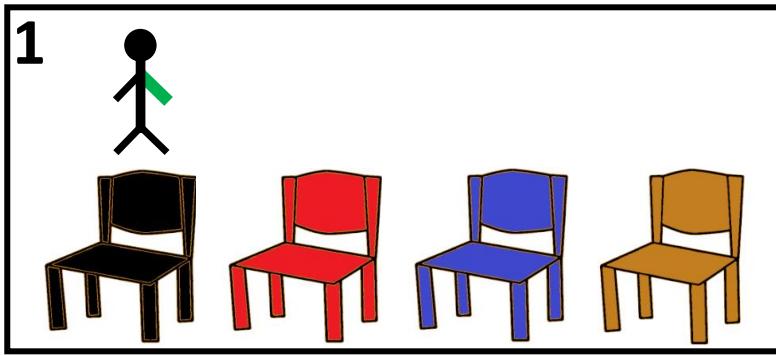
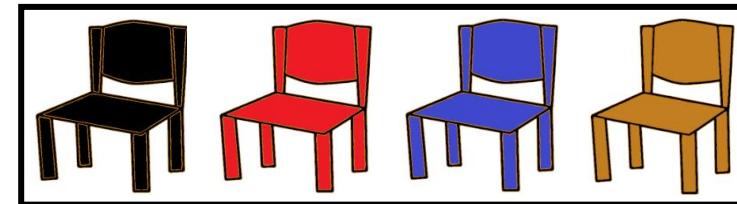
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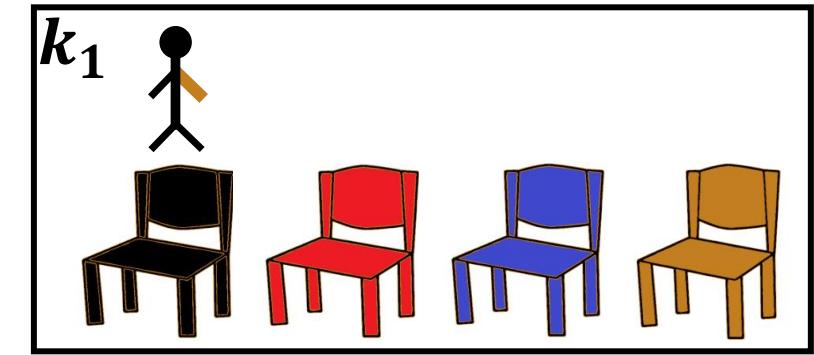


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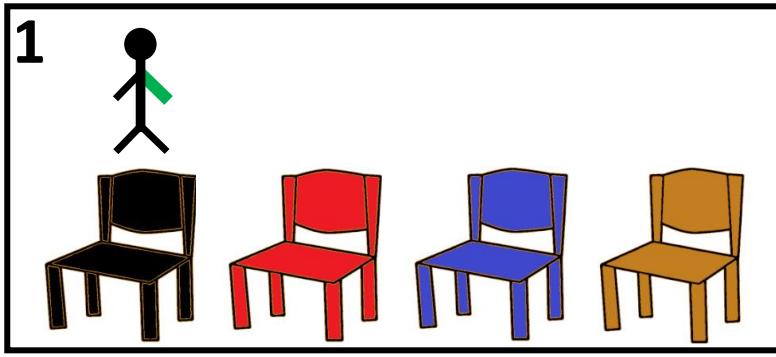
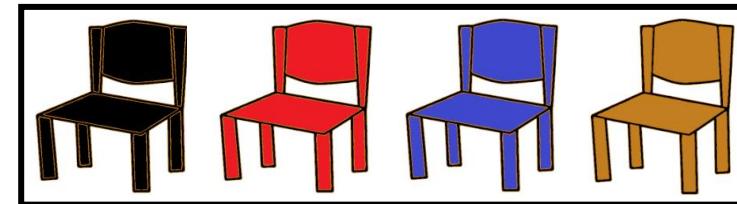


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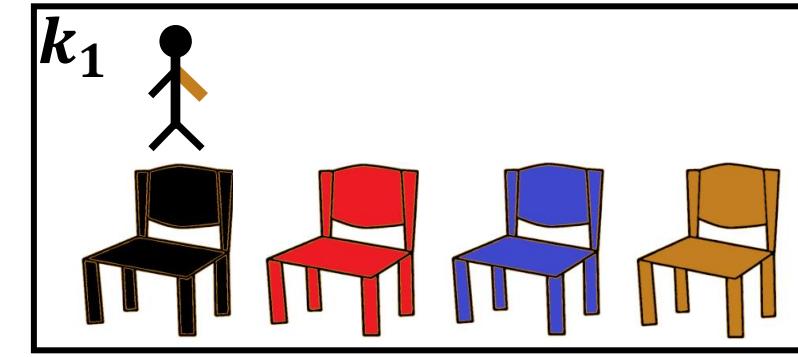
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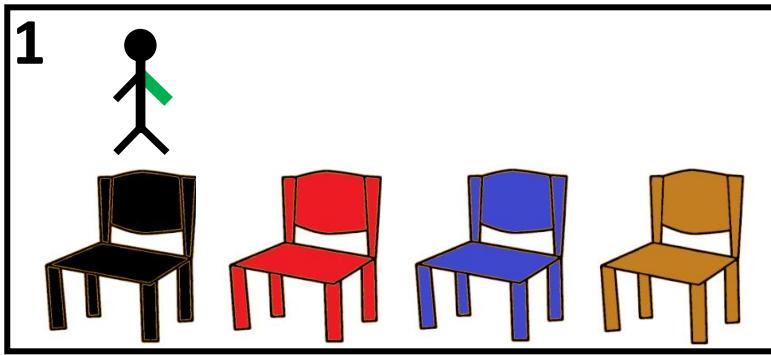
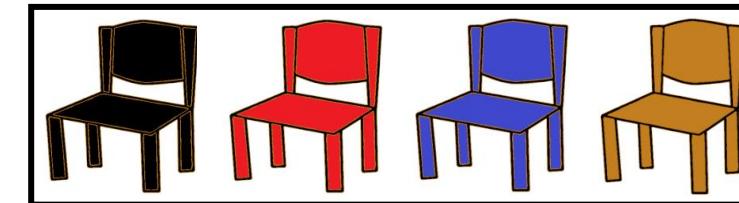
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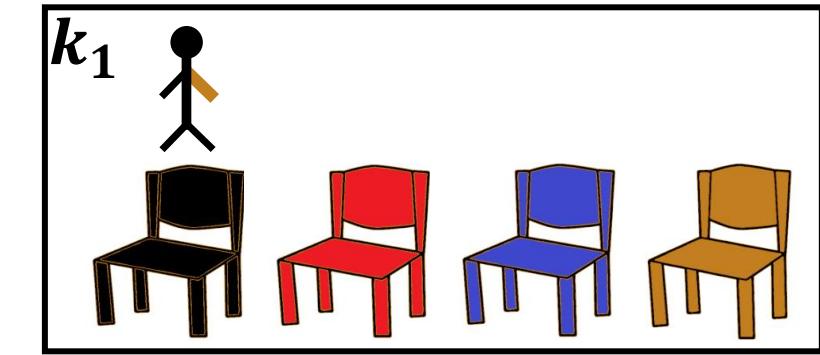
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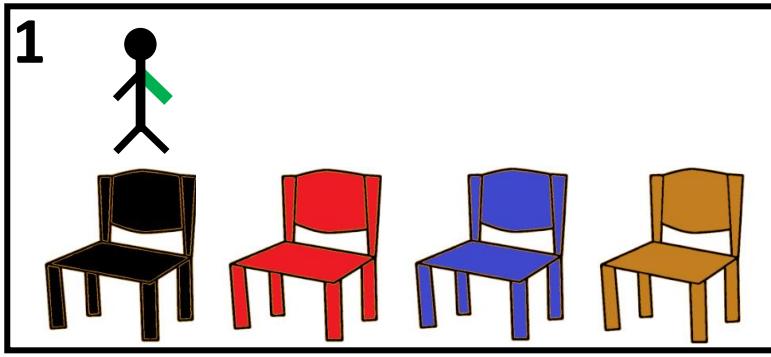
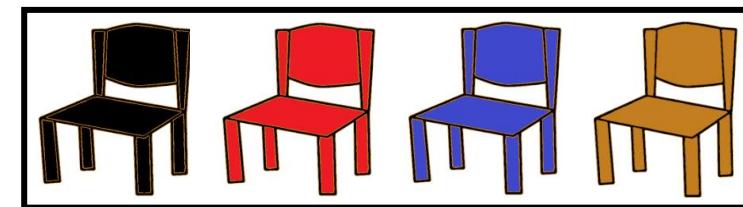
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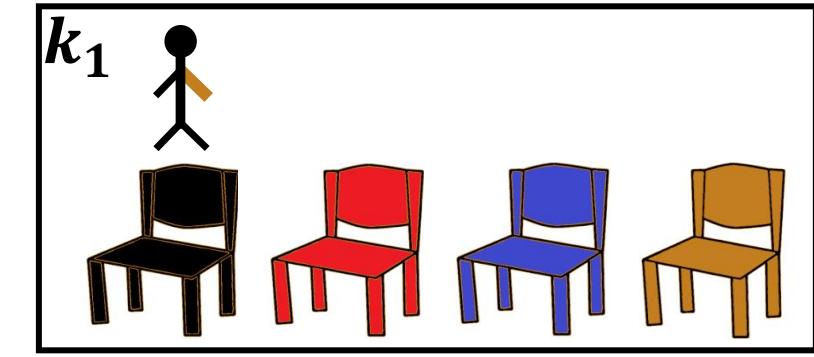
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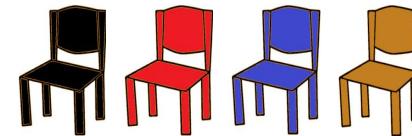
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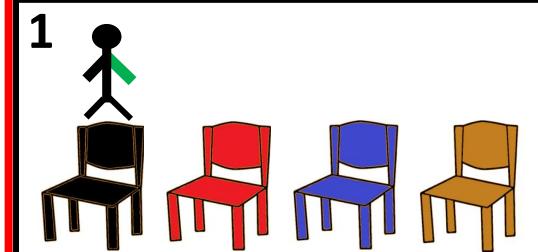
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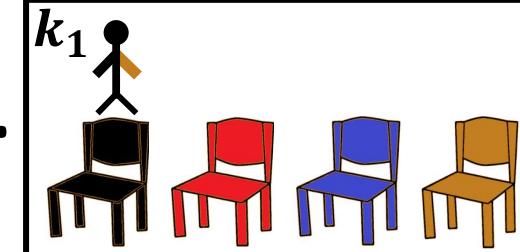
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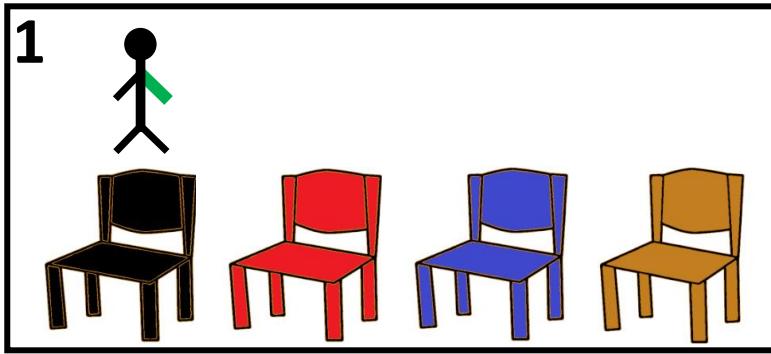
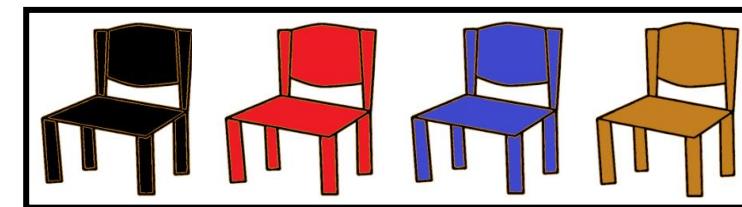
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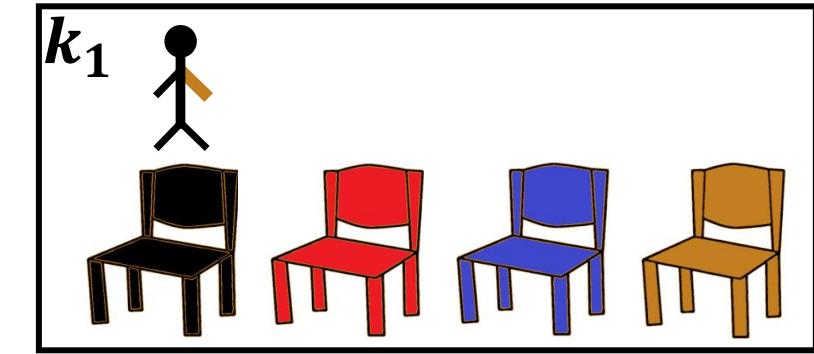
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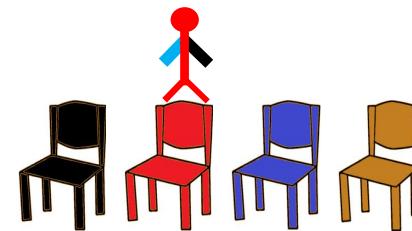
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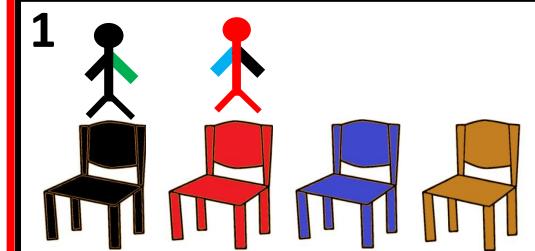
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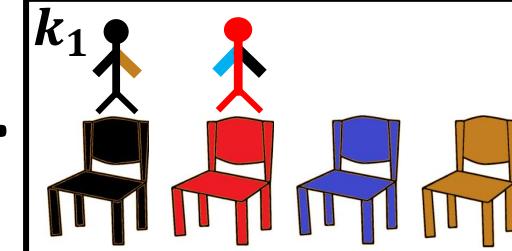
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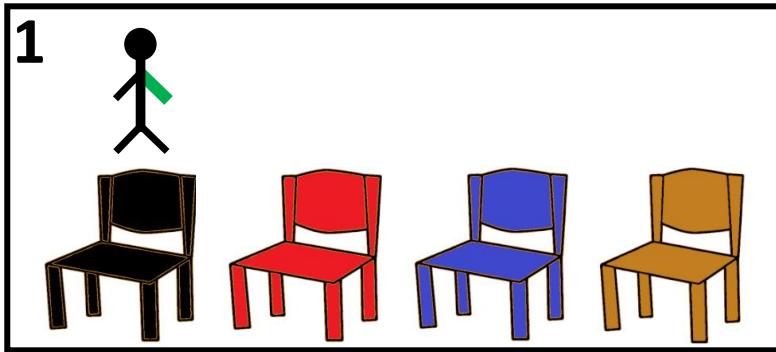
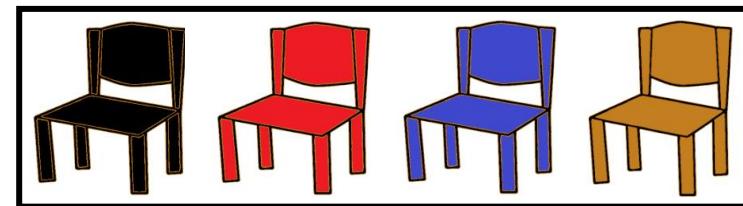
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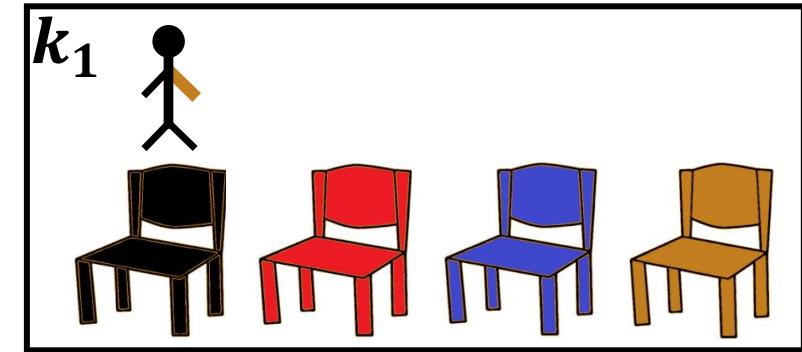
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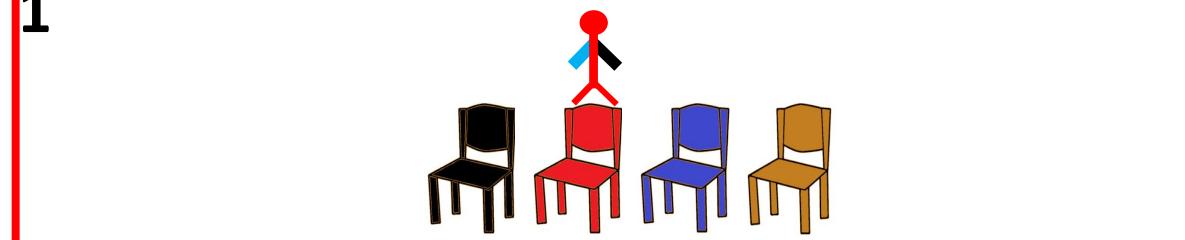
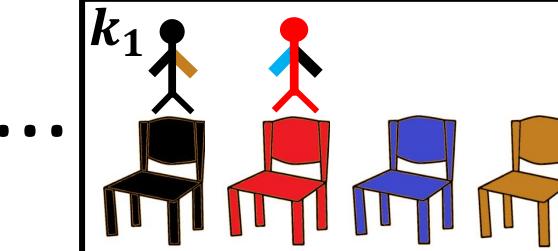
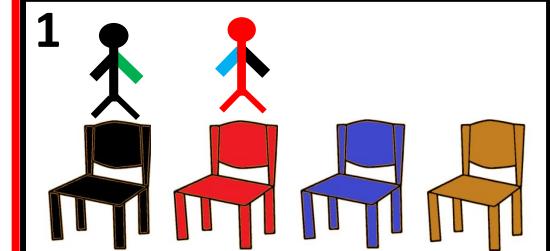
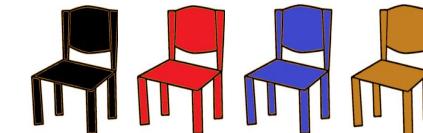
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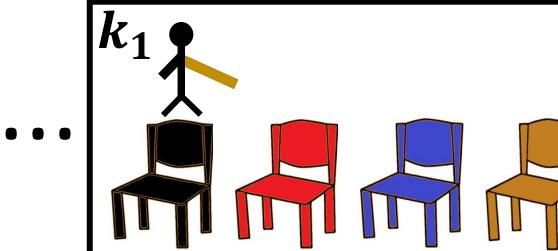
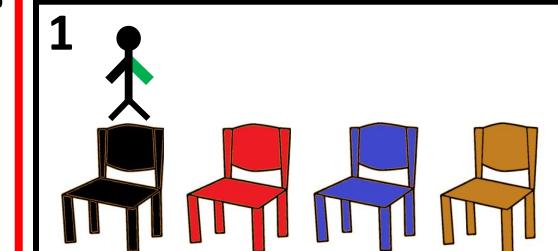
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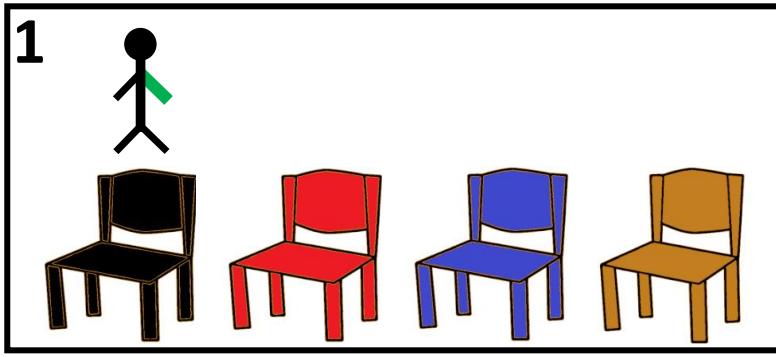
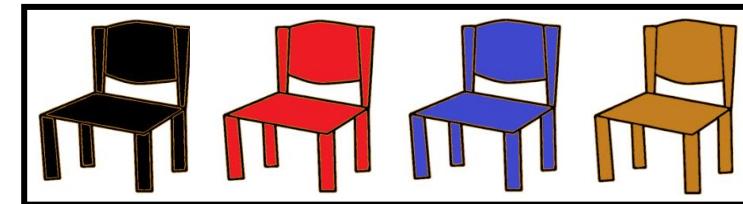
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 $k_2$ 

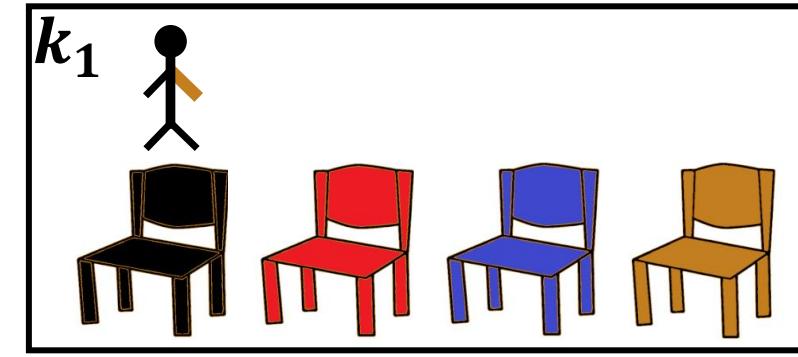
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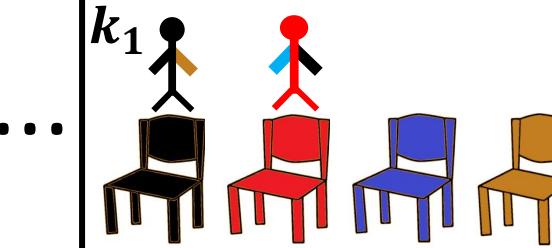
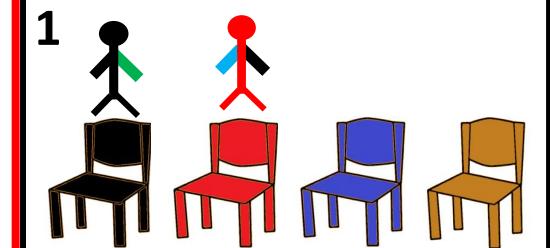
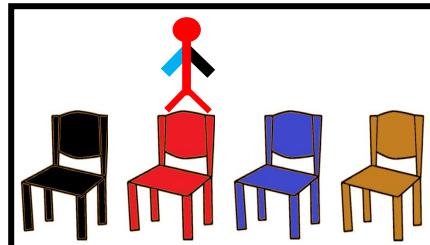
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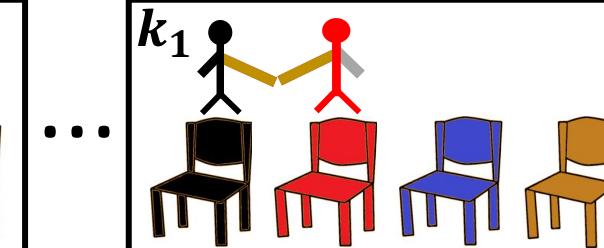
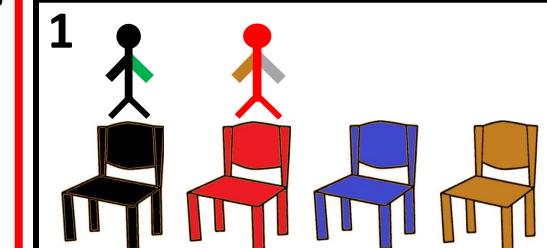
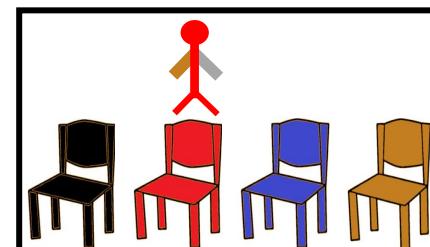
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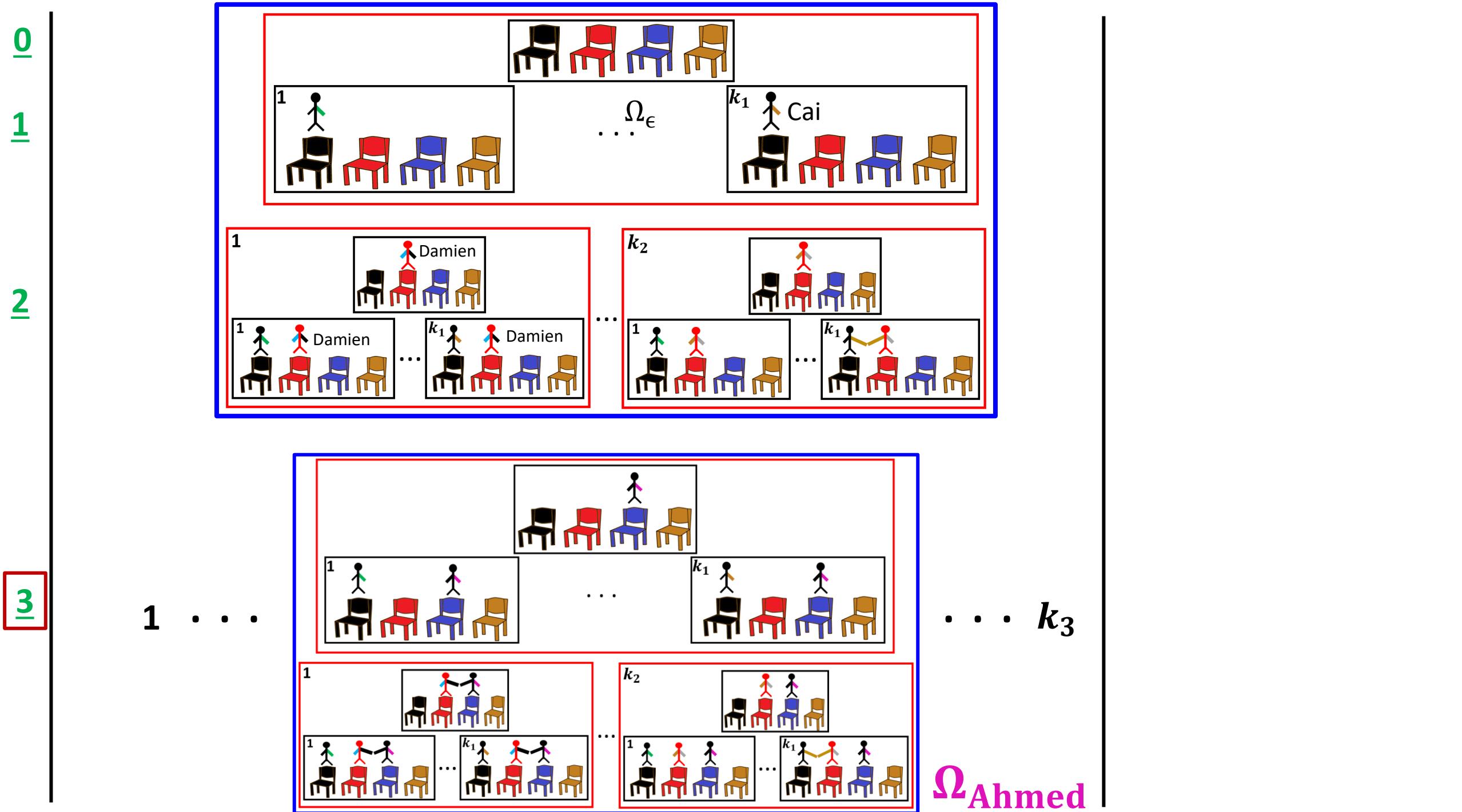


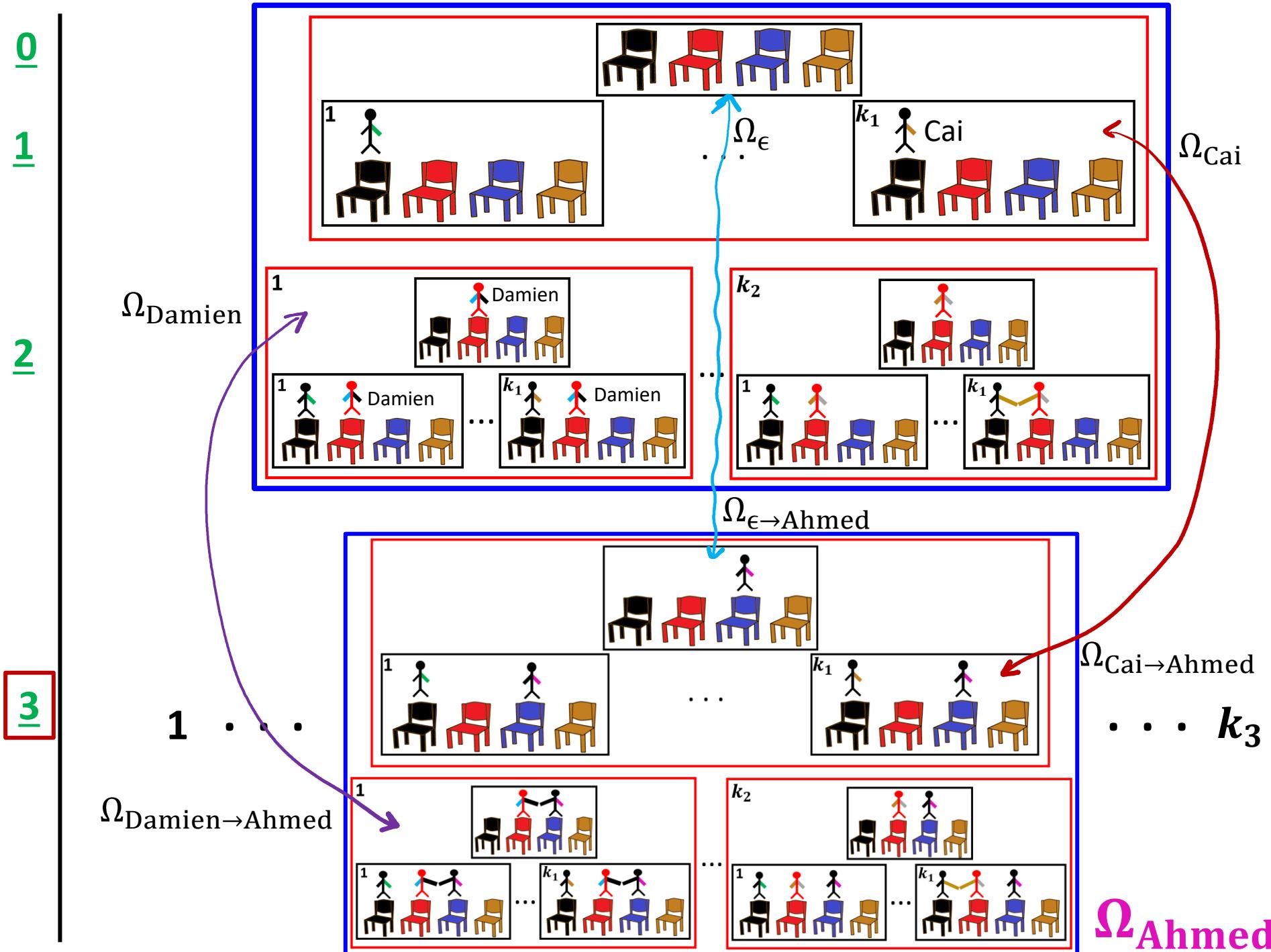
1



...

 $k_2$ 





Layer = chair

There is a 1-1 correspondence between each **class** of higher layers and a **sub-class** of any class in current layer.

$$\Omega_p$$

$$\uparrow$$

$$\Omega_{p \rightarrow p'}$$

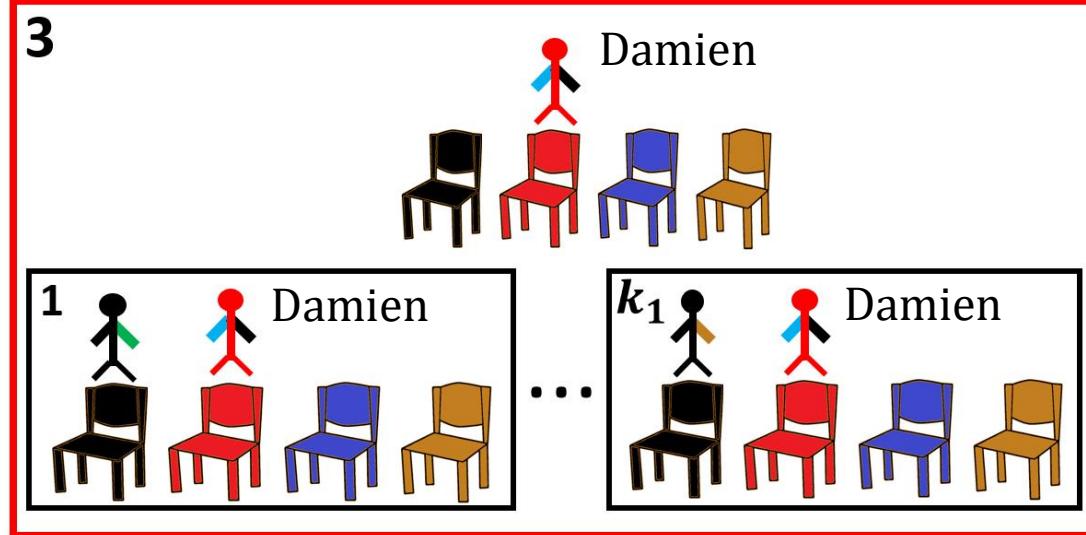
a **sub-class** of the class  $\Omega_{p'}$ , where  $p$  is the nearest neighbour to  $p'$ .

**Can we use this inductive construction process to propagate information through this hierarchy ?**

Can we use this inductive construction process to propagate information through this hierarchy ?

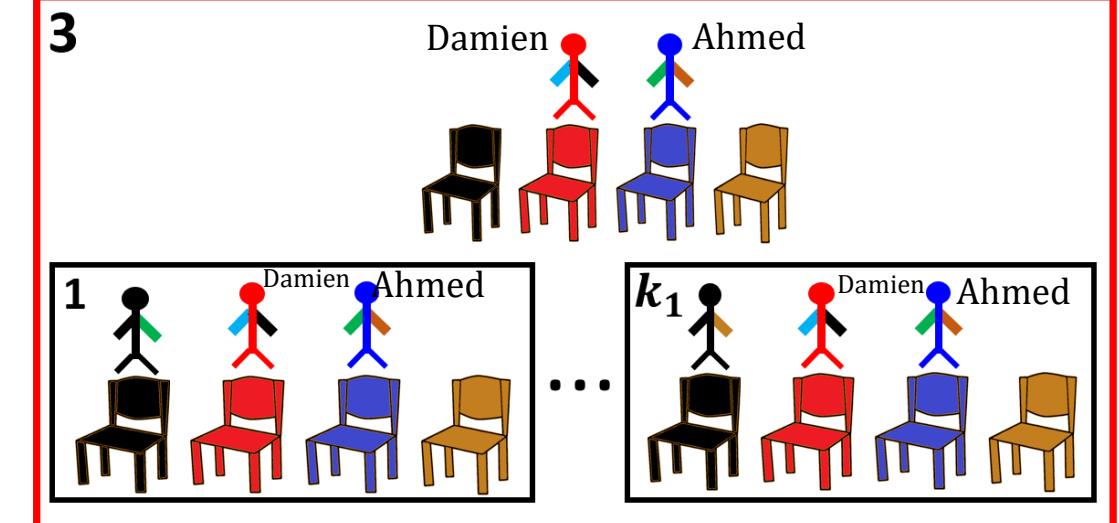
1 - Propagate information from exactly the previous layer (Direct neighbour handshaking possibility).

$\Omega_{\text{Damien}}$



Information given:  $Q(\Omega_{\text{Damien}})$

$\Omega_{\text{Damien} \rightarrow \text{Ahmed}}$

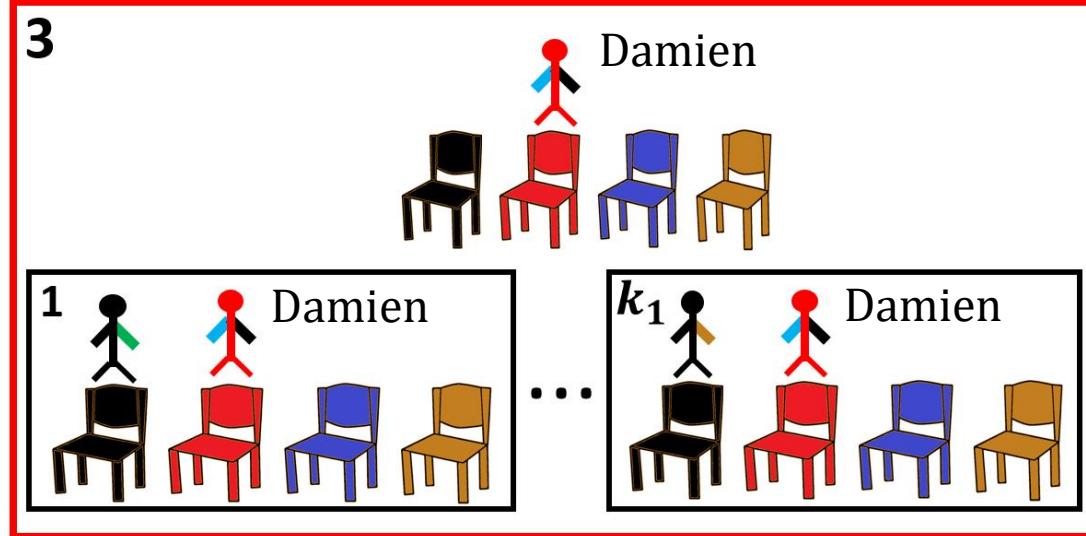


Information needed:  $Q(\Omega_{\text{Damien} \rightarrow \text{Ahmed}})$

Can we use this inductive construction process to propagate information through this hierarchy ?

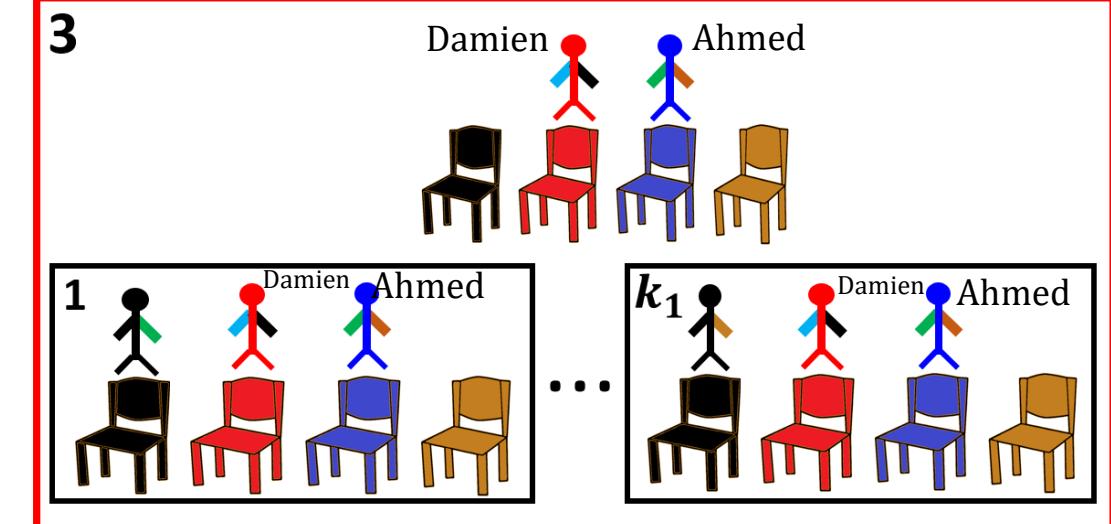
1 - Propagate information from exactly the previous layer (Direct neighbour handshaking possibility).

$\Omega_{\text{Damien}}$



Information given:  $Q(\Omega_{\text{Damien}})$

$\Omega_{\text{Damien} \rightarrow \text{Ahmed}}$

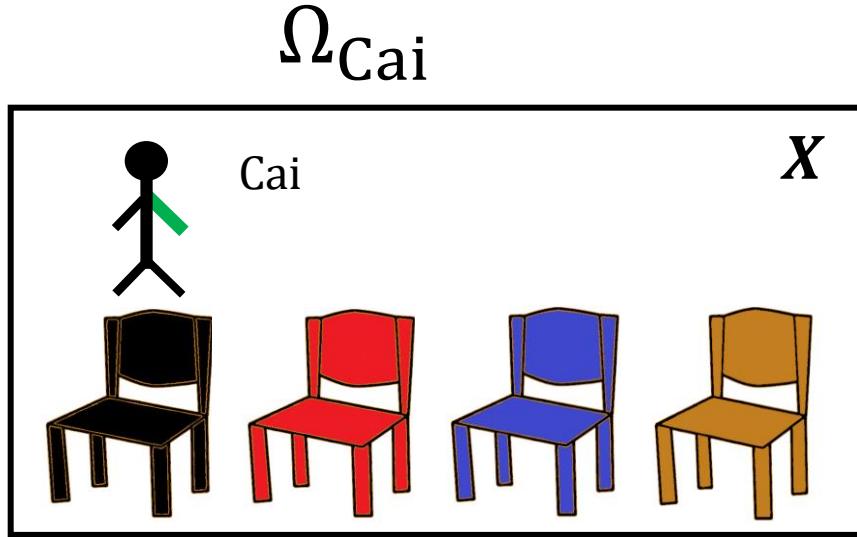


Information needed:  $Q(\Omega_{\text{Damien} \rightarrow \text{Ahmed}})$

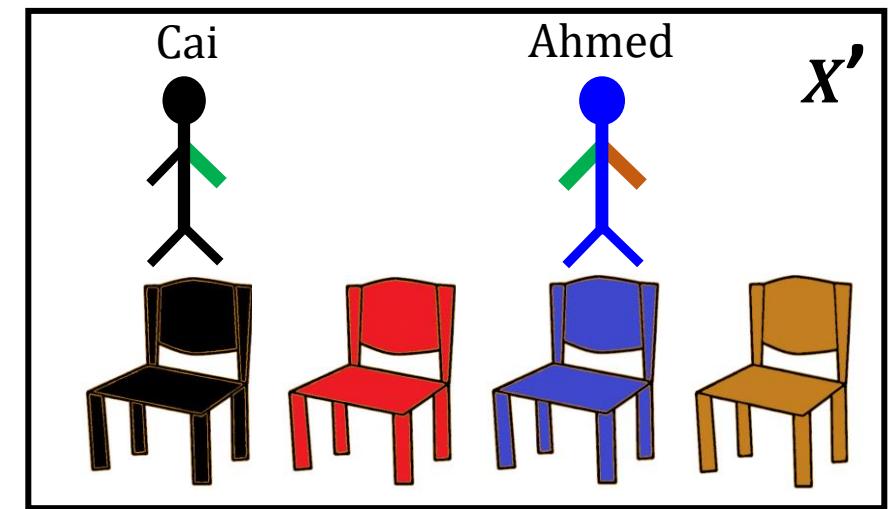
$$Q(\Omega_{\text{Damien} \rightarrow \text{Ahmed}}) = \dots = e^{\frac{\text{sit(Ahmed)} + \text{Sit\_Cost}}{c}} * e^{\frac{\text{handshake(Damien,Ahmed)}}{c}} * Q(\Omega_{\text{Damien}})$$

2 - Propagate information from the rest (**No handshaking possibility**).

$\Omega_{\text{Cai} \rightarrow \text{Ahmed}}$



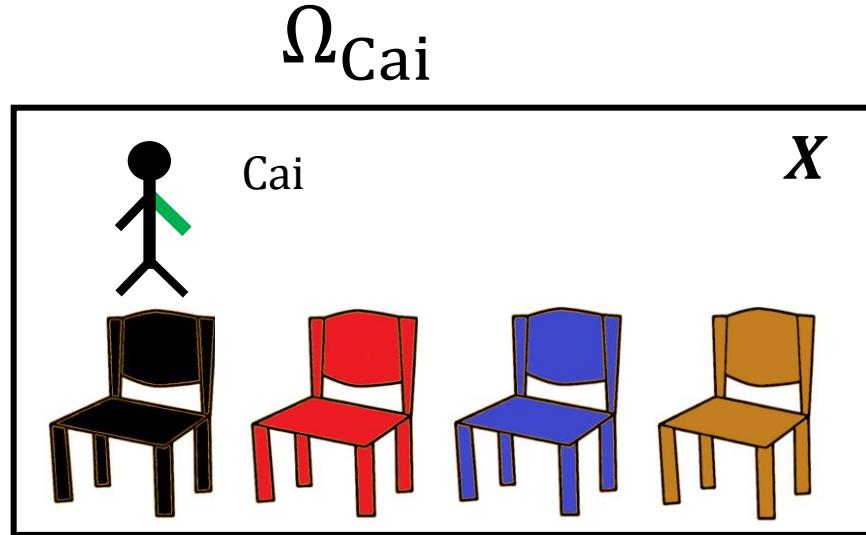
Information given:  $Q(\Omega_{\text{Cai}})$



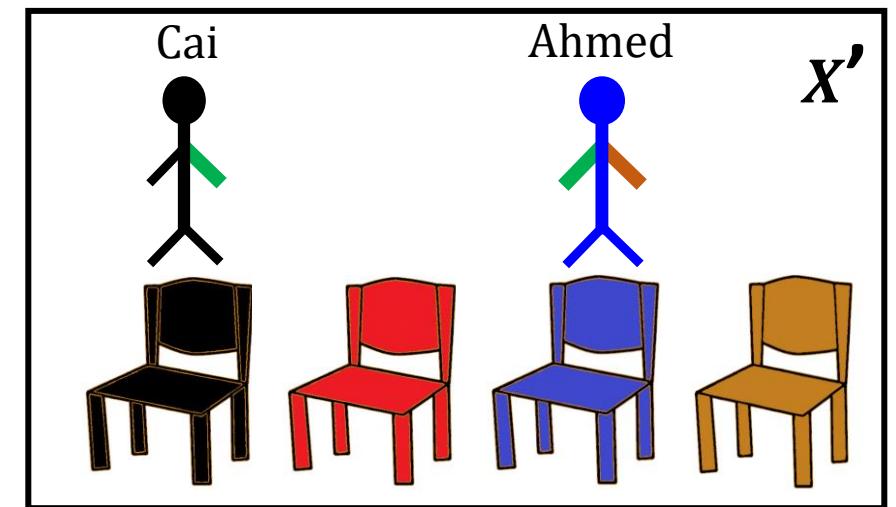
Information needed:  $Q(\Omega_{\text{Cai} \rightarrow \text{Ahmed}})$

2 - Propagate information from the rest (**No handshaking possibility**).

$\Omega_{\text{Cai} \rightarrow \text{Ahmed}}$



Information given:  $Q(\Omega_{\text{Cai}})$



Information needed:  $Q(\Omega_{\text{Cai} \rightarrow \text{Ahmed}})$

$$Q(\Omega_{\text{Cai} \rightarrow \text{Ahmed}}) = \dots = e^{\frac{\text{sit(Ahmed)} + \text{sit\_cost}}{c}} * Q(\Omega_{\text{Cai}})$$

$$Q(\Omega_p) = e^{\frac{sit(p)+sit\_cost}{c}} * \left[ \left( \sum_{\substack{p' \text{ is} \\ \text{direct neighbour}}} e^{\frac{handshake(p',p)}{c}} * Q(\Omega_{p'}) \right) + 1 + \sum_{\substack{p' \text{ is not} \\ \text{direct neighbour}}} Q(\Omega_{p'}) \right]$$

$$Q = 1 + \sum_p Q(\Omega_p)$$

$$Q(\Omega_p) = e^{\frac{sit(p)+sit\_cost}{c}} * \left[ \left( \sum_{\substack{p' \text{ is} \\ \text{direct neighbour}}} e^{\frac{handshake(p',p)}{c}} * Q(\Omega_{p'}) \right) + 1 + \sum_{\substack{p' \text{ is not} \\ \text{direct neighbour}}} Q(\Omega_{p'}) \right]$$

► **Theorem** There is an  $O(k^2N)$  time algorithm for the domain-level partition function for a 1D SDC of length  $N$  with  $\leq k$  computation strands competing at each scaffold domain.

$$Z^S = 1 + \sum_{s \in T} Z_s^S \quad (6)$$

$$Z_s^S = \left( e^{-(\Delta G(d^M(s)) + \Delta G^{\text{assoc}})/kT} \right) \cdot \left[ 1 + \sum_{s' \in L_s} Z_{(s', s)} * Z_{s'}^S + \sum_{s' \prec s \text{ and } s' \notin L_s} Z_{s'}^S \right] \quad (7)$$

where  $Z_{(s', s)} = e^{-\Delta G(d^R(s'), d^L(s))/kT}$ .

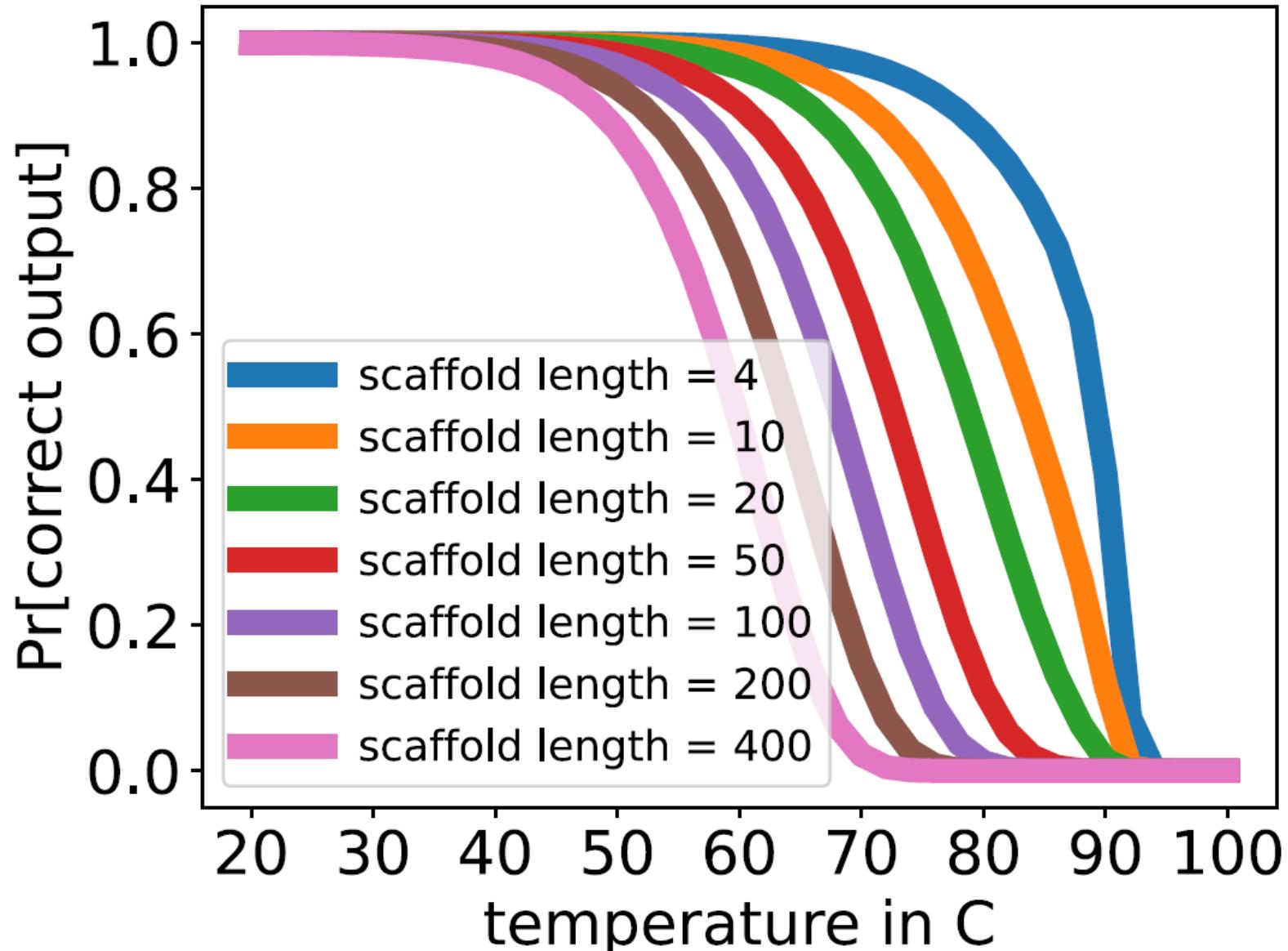
■ **Algorithm 2** 1D SDC partition function algorithm. The proof of Theorem 2 argues that this algorithm returns  $Z^S$  as defined in Equation (6). Note that arrays are indexed from 1, and recall that  $k_1, \dots, k_N$  are the counts of competing strands at scaffold domains  $d_1, \dots, d_N$ , and we let  $s_i^j$  be the  $j^{\text{th}}$  strand competing at domain  $d_i$ .

---

```

1:  $Z_{\text{curr}} = [0, 0, \dots, 0]$            ▷ size  $k = \max(k_1, \dots, k_N)$ , current (partial) partition function
2:  $Z_{\text{prev}} = [0, 0, \dots, 0]$            ▷ size  $k = \max(k_1, \dots, k_N)$ , previous (partial) partition function
3:  $Z^S \leftarrow 1$ ;  $\text{sum}_a \leftarrow 0$ 
4: for  $i \leftarrow 1 \dots N$  do
5:    $\text{sum}_a \leftarrow \text{sum}_a + \sum_{i \in \{1, \dots, k\}} Z_{\text{prev}}[i]$            ▷  $\text{sum}_a$ : rightmost summation Equation (7)
6:    $Z_{\text{prev}} \leftarrow Z_{\text{curr}}$ 
7:    $Z_{\text{curr}} = [0, 0, \dots, 0]$ 
8:   for  $j \leftarrow 1 \dots k_i$  do           ▷ each iteration computes Equation (7) for a strand
9:      $t_1 = e^{-(\Delta G(d^M(s_i^j)) + \Delta G^{\text{assoc}})/kT}$ 
10:    if  $i = 1$  then           ▷ first domain where is no neighbors at all
11:       $Z_{\text{curr}}[j] = t_1$ 
12:    else
13:       $t_2 \leftarrow 0$ 
14:      for  $m \leftarrow 1 \dots k_{i-1}$  do
15:         $t_2 \leftarrow t_2 + \left( e^{-(\Delta G(d^R(s_{i-1}^m), d^L(s_i^j))/kT)} \right) \cdot Z_{\text{prev}}[m]$ 
16:      end for
17:       $Z_{\text{curr}}[j] \leftarrow t_1 + t_2 + \text{sum}_a$ 
18:    end if
19:     $Z^S \leftarrow Z^S + Z_{\text{curr}}[j]$            ▷ computing Equation (6)
20:  end for
21: end for
22: return  $Z^S$ 
```

► **Theorem** There is an  $O(k^2N)$  time algorithm for the domain-level partition function for a 1D SDC of length  $N$  with  $\leq k$  computation strands competing at each scaffold domain.



# Thanks