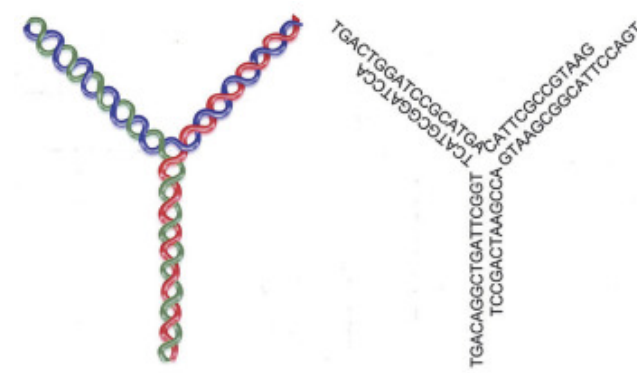
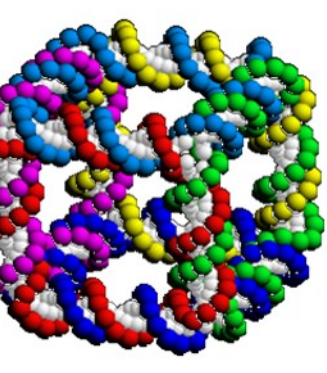
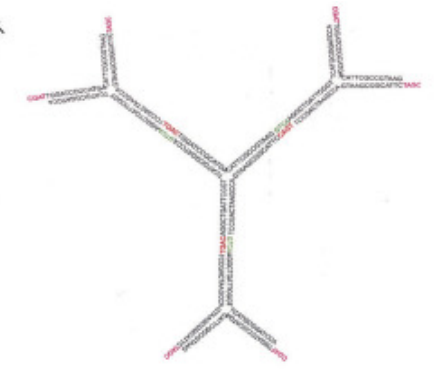


Introduction

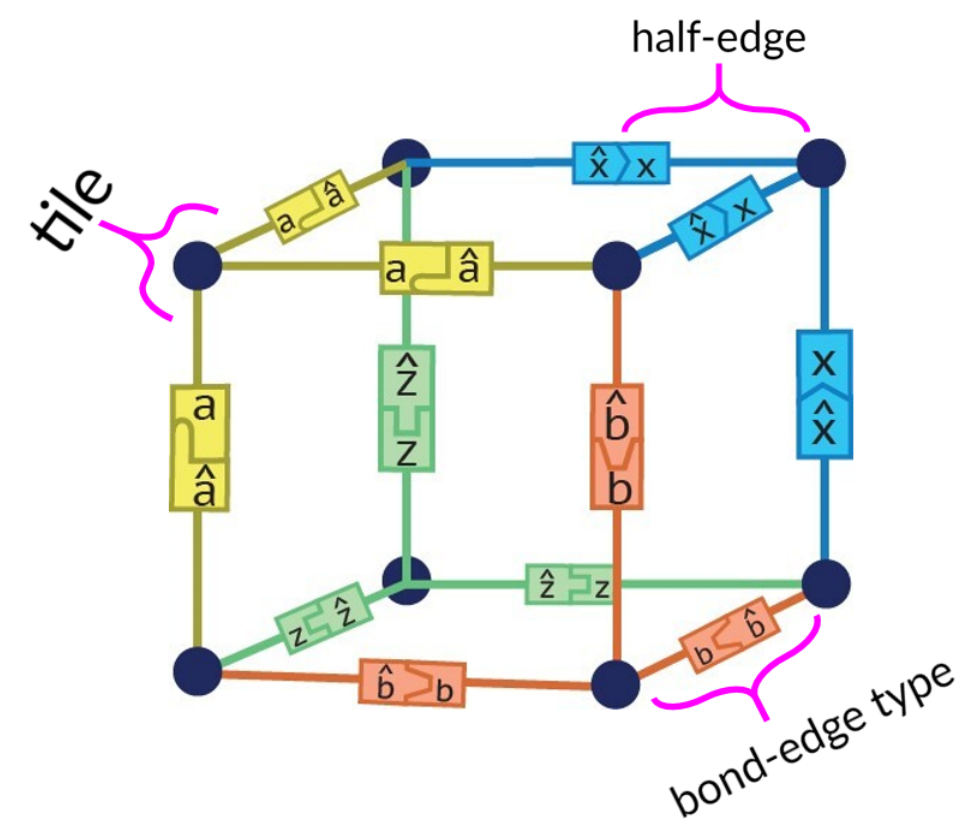
Self-assembling nanostructures are constructed through the process of branched-junction DNA molecules bonding with each other without external guidance. We use graph theory and a *flexible* tile-based model to predict what structures can be produced in a laboratory setting. [1]



3-armed junction-branched DNA molecules [3]



DNA cube



Graph realized by pot $P = \{\{a^3\}, \{\hat{a}, \hat{x}, \hat{z}\}, \{x^3\}, \{\hat{a}, \hat{b}, \hat{x}\}, \{\hat{a}, \hat{b}, z\}, \{z, \hat{z}^2\}, \{\hat{b}, \hat{x}, z\}, \{b^3\}\}$ using tile distribution (1, 1, 1, 1, 1, 1, 1)

Goal

Given a pot of tiles, P , can we algorithmically construct at least one graph and possibly all non-isomorphic graphs realized by P ?

- Input: A pot containing any number of bond-edge types
- Output: All non-isomorphic graphs realized by P

Construction Matrix Algorithm

Input: $P = \{\{\hat{a}, b\}, \{\hat{a}, \hat{b}\}, \{a^2, b\}, \{a^2, \hat{b}\}\}$

$$\begin{bmatrix} t_1 & t_2 & t_3 & t_4 \\ -1 & -1 & 2 & 2 \\ 1 & -1 & 1 & -1 \\ 1 & 1 & 1 & 1 \end{bmatrix} \begin{matrix} a \\ b \\ 0 \\ 0 \end{matrix} \xrightarrow{RREF} \begin{bmatrix} t_1 & t_2 & t_3 & t_4 \\ 1 & 0 & 0 & -1 \\ 0 & 1 & 0 & 1 \\ 0 & 0 & 1 & 1 \end{bmatrix} \begin{matrix} 1/6 \\ 1/2 \\ 1/3 \\ a \\ b \end{matrix}$$

Output: Minimum possible order = 6

Tile proportions = $(\frac{1}{6}, \frac{3}{6}, \frac{2}{6}, \frac{0}{6}), (\frac{2}{6}, \frac{2}{6}, \frac{1}{6}, \frac{1}{6}), (\frac{3}{6}, \frac{1}{6}, \frac{0}{6}, \frac{2}{6})$

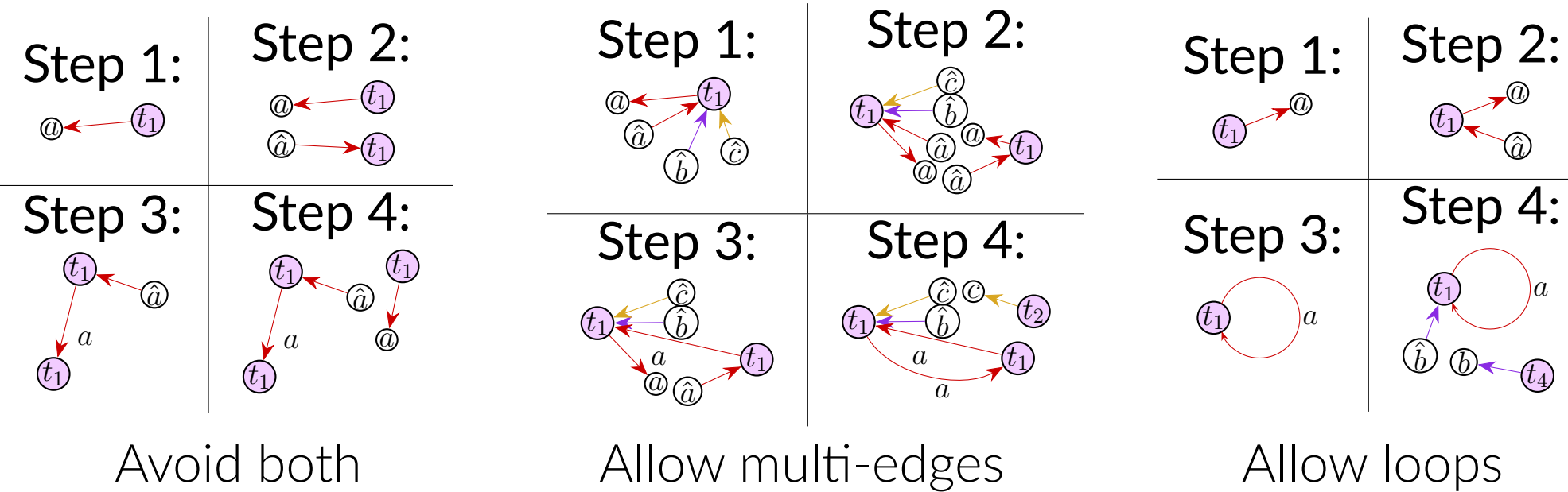
Prioritization Algorithms

Organizing

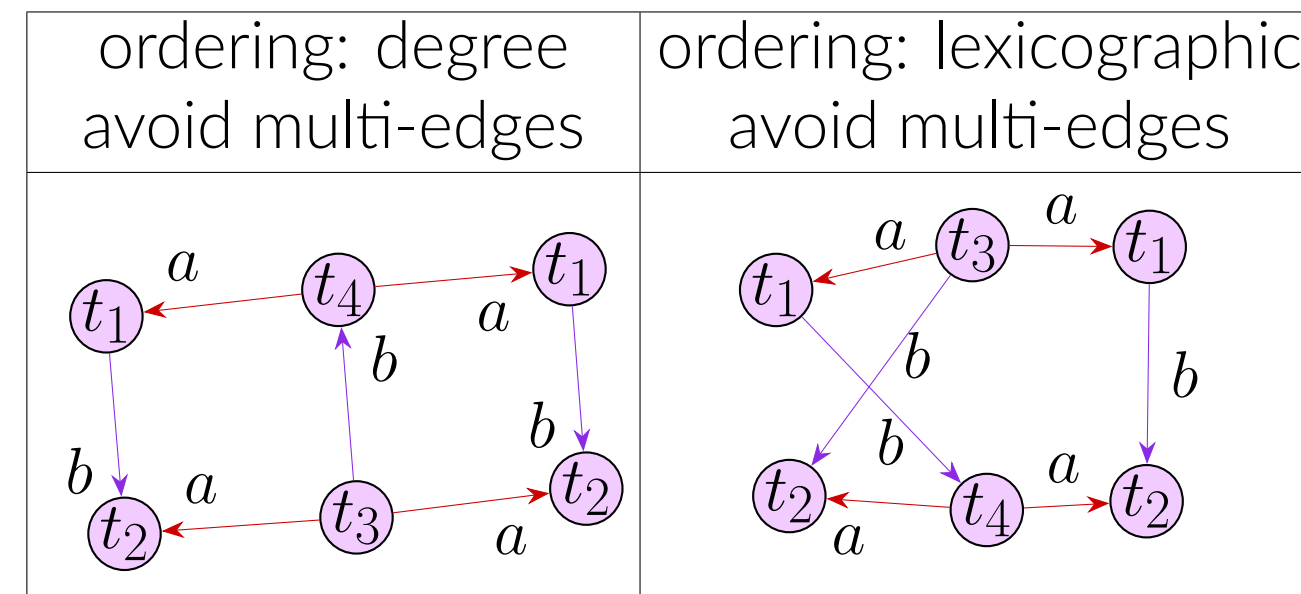
We can order the list of tiles by:

degree	$\{a^2, b\}, \{a^2, \hat{b}\}, \{\hat{a}, b\}, \{\hat{a}, \hat{b}\}$
diversity	$\{\hat{a}, b\}, \{\hat{a}, \hat{b}\}, \{a^2, b\}, \{a^2, \hat{b}\}$
lexicographic	$\{a^2, b\}, \{a^2, \hat{b}\}, \{\hat{a}, b\}, \{\hat{a}, \hat{b}\}$

Connecting Process



Connected Examples



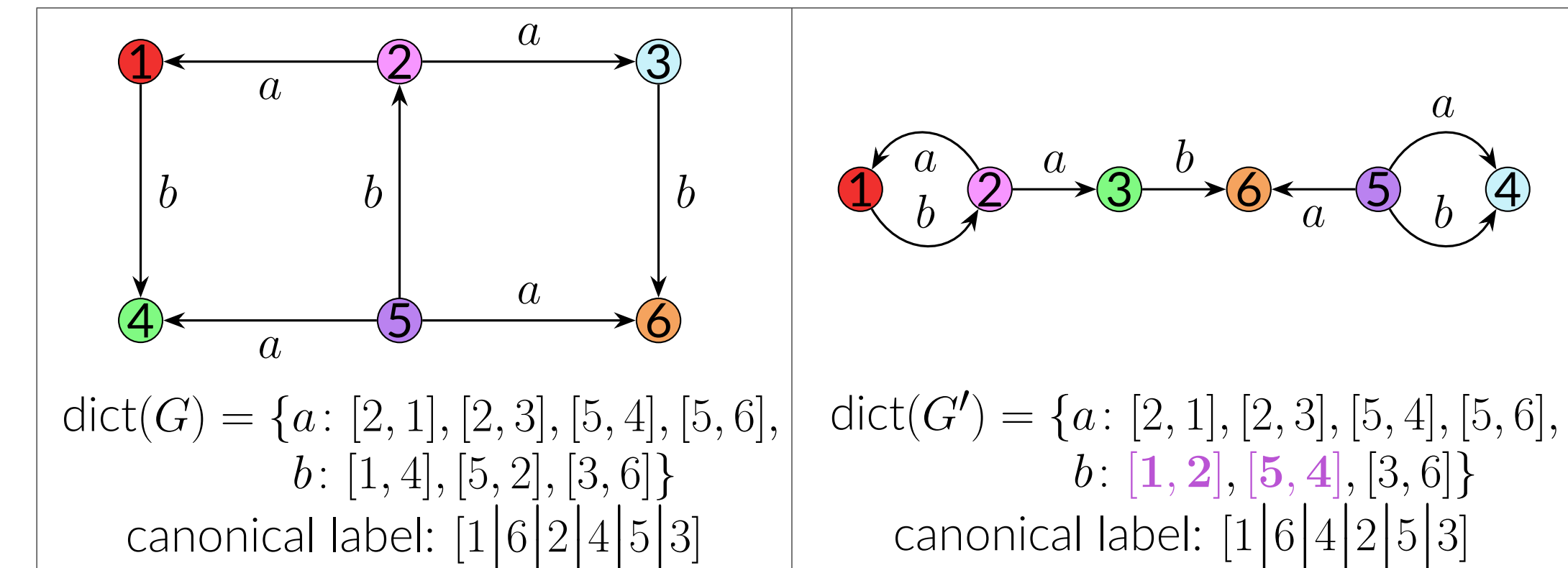
Combinatorics

We count the number of permutations of edge-swaps.

$P = (\{\hat{a}, b\}, \{\hat{a}, \hat{b}\}, \{a^2, b\}, \{a^2, \hat{b}\})$, Tile Distribution = (2, 2, 1, 1)

$$\prod_{\alpha \in A} \binom{e_\alpha(G)}{\deg_\alpha(v_1)} \binom{e_\alpha(G) - \deg_\alpha(v_1)}{\deg_\alpha(v_2)} \dots \binom{e_\alpha(G) - \deg_\alpha(v_1) - \dots - \deg_\alpha(v_{k-1})}{\deg_\alpha(v_k)} = 36$$

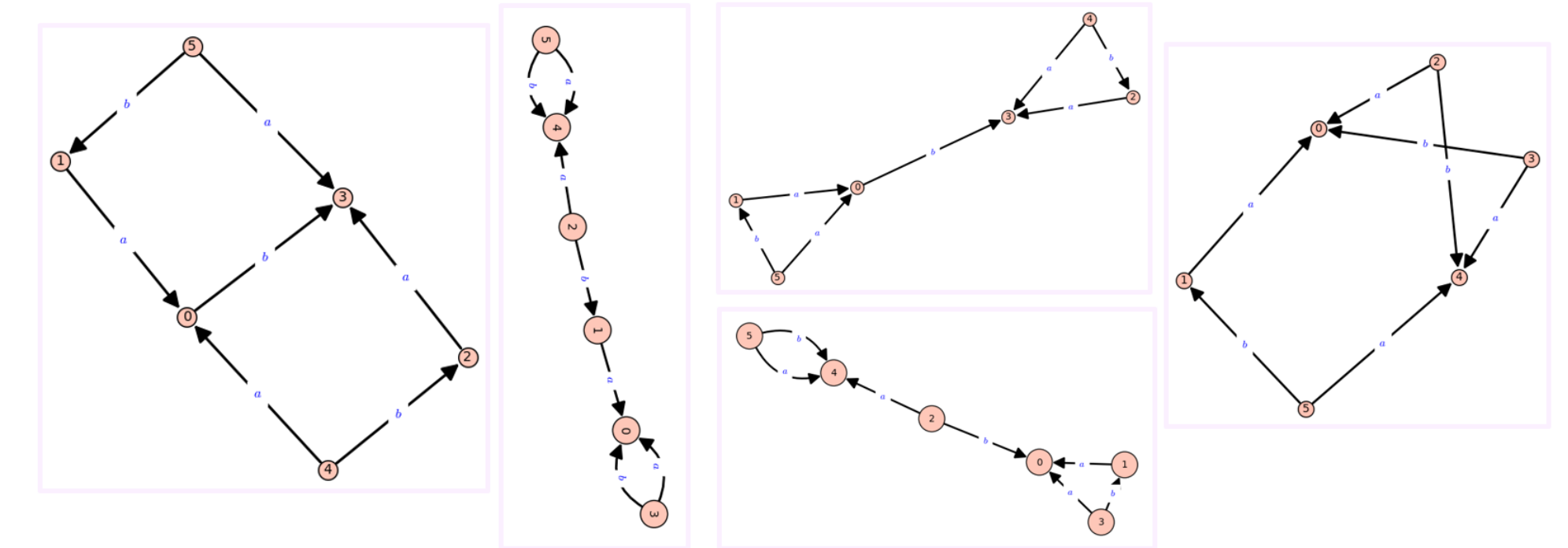
Isomorphism Algorithm



Permuting graph G using (2, 1, 3) gives graph G' . G and G' are non-isomorphic

Theorem (Canonical Labeling) [2]: $G_1 \cong G_2$ iff $c(G_1) = c(G_2)$

Algorithm Output



The given pot with tile distribution (2, 2, 1, 1) has 5 non-isomorphic graphs

Acknowledgement

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References

- [1] Leyda Almodóvar, Jo Ellis-Monaghan, Amanda Harsy, Cory Johnson, and Jessica Sorrells. Computational complexity and pragmatic solutions for flexible tile based dna self-assembly. *arXiv preprint arXiv:2108.00035*, 2021.
- [2] Robert A Beezer and Chris Godsil. Explorations in algebraic graph theory with sage. 2015.
- [3] Dan Luo. The road from biology to materials. *Materials Today*, 6(11):38–43, 2003.