1. Compute the partition function for the binary $NK$ model where $K = 0$, and
the fitness function for allele $a_i \in \{0, 1\}$ is uniformly $f^i(a_i) = ca_i + b$, for given
constants $c, b \in \mathbb{R}$.

2. Design an algorithm for finding a globally optimal genotype in a binary $NK$
model with $K = 1$. (The inputs to your algorithm are the “dependency graph”
of the model, indicating for each locus $i$ the one other locus $i' \neq i$ on which its
fitness depends, and the associated local fitness functions $f^i(a_i, a_{i'})$, which may
be viewed as $2 \times 2$ real matrices.) Estimate the efficiency of your algorithm.

3. Compute the expected number of (a) edges, (b) $r$-cliques (complete subgraphs $K_r$) in a random graph $G \in \mathcal{G}(n, p)$.

4. Derive Theorem 4.1 of the lecture notes (given any fixed graph $H$, a.e. $G \in \mathcal{G}(n, p)$ for $0 < p < 1$ contains an induced copy of $H$) from Lemma 4.2 of the notes (for
any fixed $k, l \in \mathbb{N}$, a.e. $G \in \mathcal{G}(n, p)$ for $0 < p < 1$ has property $Q_{kl}$).

5. Prove that the graph property “$G$ has maximum degree at least $k$” has a threshold
function for $k \geq 1$, and compute it.

6. Prove that the graph property “$G$ contains a $d$-dimensional cube” has a threshold
function for $d \geq 1$, and compute it. (The “$d$-dimensional cube” has $2^d$ vertices
represented as $\{0, 1\}^d$, and two vertices are connected by an edge if and only if
their representations differ in exactly one position.)