

The application of noisy-channel coding techniques to DNA barcoding

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January 18, 2018

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Introduction

The premise of this project is to investigate the different types of error-correcting codes, and how these might be applied to DNA barcoding. The challenge in this comes from the fact that most error-correcting codes are designed in base-2 (binary) whereas DNA strings are fundamentally base-4 (quaternary). The applicability of this project is that in oligonucleotide synthesis, some samples may need to be identified later on using a subsection of the sample (a barcode). These could just be linearly assigned codes, but this would leave them very susceptible to mutation.

Here is an example: say that we're given a barcode of length four, to encode two different samples. If we worked methodically up from the bottom (using the ordering ACGT - orderings will be discussed further later on) we might end up with the codes AAAA and AAAC. However, either string would only require a single mutation (where we say a mutation is the changing of a single base) to become identical to the other one. Therefore, in this case, it would clearly be far more optimal to make a choice like, for example, AAAA and CCCC.

There have been a few assumptions and glossed over definitions here:

- What constitutes a mutation?
- What is the best way to represent DNA mathematically?

There are also a number of parameters to the problem, and as they change the problem becomes very much nontrivial:

- What if the barcode size changes?
- What if we want more codes than two?
- What if rather than number of codes and barcode size, the parameters are set to barcode size and maximum number of mutations that can occur?

All of these will be further explored in this dissertation.

Implementing the Hamming code

Source