test

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1 Introduction

In this project we will be looking at attempting to implement a model to predict, based on data from blood analysis, whether a given person potentially has cancer. The method in which we will be doing this, is by looking at methylized/unmethylized cell-free dna in peoples blood, specifically the fragmentation patterns. This is preferable to other methods, since it is both less invasive, and less expensive.

The data we will be looking at in this project, has been provided to us by Søren Bessenbacher, and contains information regarding fragmentation patterns for approximately 230 people diagnosed with cancer, and 230 people as a control group.