

# Forward algorithm for PairHMM

Zijie Zhang

June 2022

## Contents

<b>1</b>	<b>Introduction</b>	<b>2</b>
<b>2</b>	<b>References</b>	<b>2</b>

## 1 Introduction

Bioinformatics is a fast growing field, with increasing demand for high computational capabilities for several applications like DNA sequencing.

Although sophisticated algorithms are available for DNA sequence analysis, the most commonly used algorithm is the PairHMM algorithm.

## 2 References

1. R. Durbin. Biological Sequence analysis.
2. D. Benjamin. Pair HMM probabilistic realignment in HaplotypeCaller and Mutect.