# Abstract

# Introduction

# Materials and Methods

## Synthetic DNA Dataset

## H1N1 Influenza Samples

# Results

## Model Structure

### Figure 1: Graphical Model

### Generative Algorithm

## Inference Algorithm and Variant Calling

### Metropolis-within-Gibbs

### Parameter Estimation

### Variant Calling Test

## Simulation Results

### We simulated data from the model and test the performance varying the read depth, n, sequence length, J, and number of replicates, N.

### Figure 2: ROC curves for synthetic data

## Comparison Results on Synthetic DNA

### We tested the performance of our model on real sequence data with known variant positions.

### Figure 3: Error-rate by Location Plot

### Comparison to RVD, (others).

### Figure 4: ROC comparison with other methods

## Empirical Results on Clinical Data

### We tested our method on sequence data from clinical H1N1 influenza samples.

### We expect to see that…

### Table: Table of variants

## Performance with Read Depth

### We subsampled the reads in the synthetic DNA data and compared the performance of our method to XXX, XXX and XXX.

### Figure 4: ROC by read depth.

# Discussion