# Abstract

# Introduction

# Materials and Methods

## Material

Synthetic DNA dataset

H1N1 Influenza samples

## Model structure

Generative process and model structure

## Inference algorithm and variant calling

Metropolis-within-Gibbs

Parameter estimation

Variant calling test: Bayesian Hypothesis Testing

# Result

Figure 1 Overall of the process

## Simulation Results

Figure 2 ROC curves for synthetic data

## Comparison Results on Synthetic DNA

Figure 3 ROC comparison with other methods: varScan/Samtools/RVD

## Empirical Results on Clinical Data MS samples

We tested our method on sequence data from clinical H1N1 influenza samples. We expect to see that…

Table: Table of variants

Figure 4

## Performance with Read depth

Samtools way to thin segment data, showing performance as read depth nij decreasing

Figure 5 ROC by read depth