IMPROVING MIN HASH FOR METAGENOMIC TAXONOMIC PROFILING

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Abstract. Abstract here.

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1. Introduction

(1) Min hash recently has been used to great success on biological data
(2) Mash, Titus' sourmash
(3) originally designed for sets of relatively similar size and appreciable intersection size
(4) metagenomic taxonomic profiling the setup is different: many relatively small database entries, one very large metagenomic sample, very small intersection sizes in general
(5) we modify the min hash paradigm to this particular situation so it can handle a sample of much greater size than the reference database entries.

2. Methods

Definitions, derivation of mathematical results here.

2.1. Definitions.

(1) Definitions of database entries, query sample, k-mer size, note size disparity
(2) define classic min hash (k-independent version and k-mins version)
(3) define the containment approach

2.2. Min Hash via containment.

2.3. Time and space complexity.

(1) Chernoff bound estimates
(2) comparison of number of hashes required for same accuracy
(3) time complexity
(4) space complexity (all with examples of the numbers in practice).

3. Results

In this section, we compare classic min hash to the proposed method.

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3.1. **Synthetic data.** Here we illustrate the improved accuracy of containment min hashover classical min hash in estimating the Jaccard index. To that end, we generated two random strings w_A and w_B on the alphabet $\{A, C, T, G\}$. We set $|w_A| = 10,000$ and $|w_B| = 15$ to simulate the situation of interest where one wishes to estimate the Jaccard index of two sets of very different size. We then appended a common string w_C of increasing length to each of w_A and w_B so that $\text{Jac}_k(w_A w_C, w_B w_C)$ ranges between 0 and 1. We picked the k-mer size of 11 and utilized a signature size of 100. Figure 1 depicts the comparison of containment min hashwith the classical min hash Jaccard estimate on this data and effectively illustrates the results in section 2.2 which proved that the containment approach has a higher probably of being closer to the true Jaccard than the classic approach. The mean and variance of the classic min hash approach on this data was $0.004861 \pm 0.001629 whileusingthecontainmentapproach, thisimprovedto 0.002042 \pm 0.000011$.

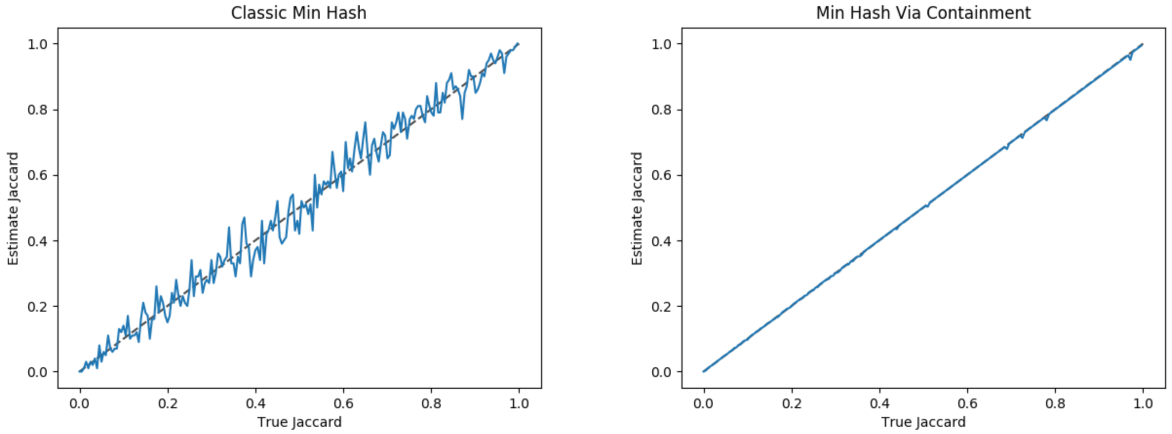

Figure 1. Comparison of containment min hashto the classical min hash estimate of the Jaccard index on synthetic data. Each method utilized the 100 smallest hashes of the murmer3 hash function on the 11-mers of two randomly generated strings with sizes 10,000 and 15 respectively after appending a common substring of increasing size. a) Classical min hash estimate of the Jaccard index. b) The proposed containment min hashon the same data.

3.2. Simulated biological data.

3.3. Real biological data.

4. Discussion