

YOUR TITLE GOES HERE

A Dissertation

Presented to the Faculty of the Graduate School
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in Partial Fulfillment of the Requirements for the Degree of
Doctor of Philosophy

by

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Cornell University 2012

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BIOGRAPHICAL SKETCH

Scott Clark grew up in Tigard, Oregon and graduated from Central Catholic High School in Portland, Oregon in 2004. He recieved Bachelor of Science degrees in Mathematics, Computational Physics and Physics (Magna Cum Laude) from Oregon State University in 2008.

In 2008 Scott was awarded a Department of Energy Computational Science Graduate Fellowship (CSGF) supporting his doctoral work at Cornell University Center for Applied Mathematics (CAM). He plans to move to San Francisco after graduation and has accepted a position at Yelp Inc.

This document is dedicated to my family.
Your constant, unconditional love and support at every stage of my education
made this possible.

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Part I

ALE: Assembly Likelihood Evaluation

CHAPTER 1

ALE INTRODUCTION

Recent advances in metagenomics have enabled the study of the microbes directly from complex communities implicated in environment and health Tringe, 2005. DNA extracted from microbial communities can be investigated either by 16S rDNA sequencing to explore their phylogenetic diversity Costello 2009;, or by whole metagenome shotgun sequencing to understand their full genetic constituents Venter 2004; Tringe 2005;Qin 2010;Yooseph 2010; Hess 2011. With the unprecedented amount of data obtained from next generation high-throughput sequencing (NGS), individual genomes can be directly assembled from a mixture of thousands of genomes, without the need to isolate single genomes through laboratory cultivation or single cell sorting Hess, 2011. The ability to assemble a metagenome to resolve the genomes of individual species, or at least the abundant ones from a complex community, is crucial to understanding their community structure and dynamics and to exploring inter-species interactions, thereby providing deeper insights into the function of the community.

Assembly of individual genomes from metagenomics datasets generated by NGS poses significant informatics challenges. Many of these challenges, including short read length, noisy data and large data volume, are also faced in the assembly of single large genomes from short reads (reviewed in Lin 2011; Li 2010). Beyond those faced in assembling single genomes, there are also several challenges unique to metagenome assembly. First, unlike in single genome assembly where the sequence depth for the target genome is expected to be uniform, the sequencing depth of genomes in a metagenome usually vary greatly. Sec-

ond, most genome assemblers have difficulties in resolving repetitive regions within a single genome, and this problem is exacerbated in metagenome assembly because conserved genomic regions and lateral gene transfer have greatly increased the portion of the repetitive genomic regions. Finally, although there are quite a few single genome assemblers such as Velvet Zerbino and Birney 2008, ABySS Simpson et al 2009, soapDenovo Li 2010 and All-Path-LG Gnerre et al 2010 that are capable of assembling large genomes, there is no metagenome specific assembler yet. Instead, assemblers designed for single genomes are being applied to metagenome data without significant modifications Qin 2010; Hess 2011. The impact of using an assembler developed to assemble single genome has not yet been systematically evaluated for metagenome assembly, especially in how well it addresses challenges like variable sequencing depth and closely related species that are unique to metagenomes. Quantitative measurement of the quality of a metagenome assembly, as well as the ability to compare the results of different assemblers from the same data set, are so far impossible. Many current studies either use only the overall size of assembly (N50), which ignores accuracy, or maps the resulting assembly onto some known reference genomes obtained independently to estimate the accuracy Hess 2011, but such references are not available in most cases. In this work we focus on the accuracy of the proposed genome using only the proposed assembly and the reads used to create it. This allows us to pinpoint localized errors instead getting bogged down trying to quantify the completeness of an entire metagenome.

Quality measurements of a single genome assembly have been derived by using a basic statistical framework integrating several metrics Lin 2011; . These metrics in general include the completeness (the total assembled bases), the contiguity (N50), and the accuracy (how well the assembly is supported by the

reads and mate pairs) Li 2010. The first two often improve as the sequencing depth increases, and the accuracy at the base level is also correlated with sequence depth. However, accuracy at the contig/scaffold level is often independent of sequence depth, as chimeras can form by mis-joins and repeats regions can be misplaced and miscounted, which requires additional assessments. Such assessments can be derived from the original reads that formed the assembly, for example, by mapping the reads back to the proposed assembly Zhong, Rob: REF? Maybe bowtie?. Good assemblies require mate pairs to map to the same loci, insert length to be normally distributed around the mean, and most reads to map onto the assembly Zhong, Rob: REF? Or common knowledge?. Additionally they require that when reads are mapped onto the assembly their coverage, or depth, must be consistent with the Poisson distribution, which follows from a random shearing process Lander 1988. Unfortunately these requirements may not be directly applied to evaluate metagenome assembly quality. For example, single genome assemblies require all read pairs to be oriented consistently by the assumption a single genome, a constraint not followed when dealing with metagenome assemblies because read pairs can map to similar regions on different genomes.

In this work we aim to provide a comprehensive integrated framework for evaluating the quality of single genome and metagenome assemblies. In related work, Phillipy 2008 also proposed a method for evaluating the quality of a whole single genome, but the method proposed is a pipeline of conceptually separate techniques for evaluating the different aspects of genome quality. Choi 2008 also combined evidence from several conceptually separate measures of genome quality to identify mis-assemblies. In the previous literature, those works that use a single statistical framework tend to focus on only a single as-

pect of genome quality: Zimin 2008 introduced a metric (CE statistic) for finding gaps in an assembly by comparing to the genome of a related organism; Meader 2010 developed a statistical method for estimating the rate of erroneous insertions and deletions present in an assembly by comparison to an assembly of a closely related species; Olson 2009 uses mate pair information and a reference genome from a similar organism to identify assembly errors and structural variation; Kelly 2010 introduced a method that detects false segmental duplication using mate pair and coverage information. All of these previous approaches contrast with the current work, which is an integrated method for validating several aspects of genome and metagenome assembly quality simultaneously based on a single statistical model. Like the current work, Laserson 2011 also used a single statistical model to assign a likelihood score to assemblies, focusing specifically on the metagenomic case, but the statistical model used ignores the role of mate pairs in assessing assembly quality, which are becoming more prevalent with NGS technologies such as Illumina and PacBio strobe reads..

In this work, we measure the overall quality of an assembly in a mathematically rigorous way, using a probabilistic model for the way that reads are generated from a genome. Using Bayesian statistics, we give explicit expressions for the probability that an assembly is correct, and computational methods based on these expressions. These mathematical methods avoid the pitfalls of summary statistics like N50 score, which only capture one dimension of assembly quality. The methods provided may be used in a number of ways. First, they are useful as a tool for comparing different assemblies of the same genome or metagenome, and can be used to show how much more likely one assembly is than another of being correct. Two assemblies with roughly equal likelihood of correctness can be considered as having roughly equal quality, while if one

assembly has a likelihood that is much lower, then we may safely discard it as inferior. Second, when considering a single assembly in isolation, these methods can also be used to give an absolute score that indicates the quality of this assembly, and how this quality compares to the quality of other assemblies. Third, these methods can be used to examine a single assembly and identify errors and their location, which is particularly useful when finishing the assembly.

CHAPTER 2

ALE METHODS

2.1 The ALE Score and the likelihood of an assembly

The ALE framework is founded upon a statistical model that describes how reads are generated from an assembly. Given a proposed assembly (a set of scaffolds or contigs), S , and a set of reads R , this probabilistic model gives the likelihood of observing this set of reads if the proposed assembly were correct. We write this likelihood, $P(R|S)$, and its calculation includes information about read quality, agreement between the mapped reads and the proposed assembly, mate pair orientation, insert length (for paired end reads), and sequencing depth. This statistical model also provides a Bayesian prior probability distribution $P(S)$ describing how likely an assembly S would be, if we were unable to observe any read information. This prior probability is computed using the k-mer distribution of the assembly.

The ALE score is computed from these two values, and it is proportional to the probability that the assembly S is correct. We write this probability as $P(S|R)$. Bayes rule tells us that this probability is

$$P(S|R) = \frac{P(R|S) P(S)}{Z} \quad (2.1)$$

where Z is a proportionality constant that ensures that $P(S|R)$ is a probability distribution. We see $P(S|R)$ as a statistical measure of the overall quality of an assembly S . As is typical in large-scale applications of Bayesian statistics, it is computationally intractable to compute the constant Z exactly. The ALE score is computed by replacing the constant Z with an approximation described in the

Methods section.

Although the ALE score can be reported as a standalone value, and understood as an approximation to $P(R=S)$, it is most useful for comparing two different assemblies of the same genome, using the same set of reads to evaluate them. As shown in the Methods section, the assembly with the higher ALE score is then also the one with the larger probability of being correct. Moreover, we show that the difference between two assemblies ALE scores describes their relative probabilities of correctness. If one assembly's ALE score is larger than the others, with a difference of x between their ALE scores, then the assembly with the larger ALE score is more likely to be correct by a multiplicative factor of e^x . Below, we refer to the ALE score more precisely as the total ALE score, to differentiate it from the sub-scores (described below) used to construct it.

Figure 1 shows the pipeline used to compute the total ALE score. Given a set of reads and a proposed assembly, ALE first takes as input the alignments of the reads onto the assembly in the form of a SAM or BAM file (Li and Durbin 2009), which can be produced by a third-party alignment algorithm such as bowtie (Langmead et al. 2009) or bwa (Li et al. 2009). ALE then determines the probabilistic placement of each read and a corresponding placement sub-score for each mapped base, which describes how well the read agrees with the assembly. In the case of paired end reads, ALE also calculates an insert sub-score for all mapped bases of the assembly from the read pair, which describes how well the distance between the mapped reads matches the distribution of lengths that we would expect from the library. ALE also calculates a depth sub-score, which describes the quality of the sequencing depth accounting for the GC bias prevalent in some NGS techniques. The placement, insert and depth scores together

determine $P(R|S)$. Independently, with only the assembly and not the reads, ALE calculates the k-mer sub-score and $P(S)$. Each sub-score is calculated for each scaffold or contig within an assembly independently, allowing for variations commonly found in metagenomes. The four sub-scores are then combined to form the total ALE score. The constituent calculations in this pipeline are described in the Methods section.

In addition, these four sub-scores are reported by ALE as a function of position within the assembly, and can be visualized with the included plotting package or imported in table form to another package such as the Integrative Genomics Viewer (IGV) (Nicol et al. 2009), or the UCSC genome browser (Kent et al. 2002). When used in this way, these sub-scores can be used to locate specific errors in an assembly.

2.2 Probabilistic ingredients of the total ALE score

We can combine the two probabilities, $P(R|S)$ and $P(S)$, to provide an expression for the probability of the assembly given the reads, $P(S|R)$. While this combined expression is too computationally expensive to compute exactly, ALE provides a summary measure of quality called the total ALE score that is proportional to $P(S|R)$ and can be used compare assemblies.

Below, we first describe how $P(R|S)$ and $P(S)$ are computed from a set of reads R and a given assembly S . We then describe how they are combined to compute the ALE score, and how the ALE score can be used to compare the qualities of different assemblies. We first provide an overview of how $P(R|S)$ and $P(S)$ are defined and computed, beginning with $P(R|S)$ and then discussing

$P(S)$.

The statistical model from which $P(R|S)$ is calculated supposes that each paired read is generated at random from the genome or collection of genomes according to the following process. First, the distance between the two paired read ends, and their orientation, is chosen at random from a distribution that is specific to the library used to generate them. Second, the locations of the mate pairs on that genome are chosen at random, potentially with a consistent GC bias. Third and finally, the content of each of the two paired ends are generated by taking the genomes true base pairs at the chosen locations and then copying these base pairs into the reported read, with a given probability of error, insertion, or deletion for each base pair given by the sequencers quality score.

The likelihood $P(R|S)$ that results from this process can be factored into three components

$$P(R|S) = P_{placement}(R|S)P_{insert}(R|S)P_{depth}(R|S) \quad (2.2)$$

The first component, $P_{placement}(R|S)$ describes how well the reads contents match the assembly at the locations to which they are mapped. The second component, $P_{insert}(R|S)$, describes how well the distances and orientations between each paired read match the distances and orientations that we would expect from the library. The third component $P_{depth}(R|S)$ describes how well the depth at each location agrees with the depth that we would expect given the GC content at that location. Contributions to these three quantities, as a function of position in the assembly, are used to produce the placement, insert and depth sub-scores.

Together with the likelihood of the reads R given the assembly S , $P(R|S)$, the

ALE framework also depends upon a Bayesian prior probability distribution over assemblies, written $P(S)$. $P(S)$ describes how likely we would believe the assembly S to be, if we did not have any read information. In this prior probability distribution, we encode the belief that within a single genome, each k-mer has a unique k-mer frequency. This is the frequency of any set of k base pairs appearing in order in the genome. This defines a 4^k dimensional vector that is conserved across a genome and can help discover when different genomes have been mistakenly combined in a metagenome setting (Teeling et al. 2004; Woyke et al. 2006). Because $P(S)$ is determined by k-mer frequencies, we use the notation $P_{kmer}(S)$ rather than the more generic $P(S)$ when referring to this probability distribution. Contributions to $P_{kmer}(S)$ as a function of position in the genome is referred to as the k-mer sub-score.

2.2.1 Placement sub-score

$P_{placement}(R|S)$ quantifies the likelihood of observing a read r_i , or set of reads R , given an assembly S . It includes information about how the read maps onto the assembly, the quality score of each base and orientation.

We assume that every paired read is independent of all other pairs of reads, which allows us to write $P_{placement}(R|S)$ as

$$P_{placement}(R|S) = \prod_{r_i \in R} P_{placement}(r_i|S), \quad (2.3)$$

where $P_{placement}(r_i|S)$ describes how well the contents of a single read r_i match the assembly at the locations to which they are mapped, as well as how well the distance and orientation between that reads paired ends match the distance and orientation that we expect from the library. We assume independence of these

distributions, allowing us to write this as

$$P_{placement}(r_i|S) = P_{matches}(r_i|S) P_{orientation}(r_i|S). \quad (2.4)$$

$P_{matches}(r_i|S)$ measures how well the read matches the section of the assembly to which it maps. Making the assumption that each base j of the read is correctly called by the sequencer independently with a probability equal to the bases quality score Q_j , we can write this as

$$P_{matches}(r_i|S) = \prod_{base_j \in r_i} P(base_j|S) \quad (2.5)$$

where

$$P(base_j|S) = Q_j \quad (2.6)$$

when the base j correctly matches the assembly and

$$P(base_j|S) = (1 - Q_j)/4 \quad (2.7)$$

when it does not. This expression follows from our modeling assumption that all 4 possible errors that the sequencer could have reported at that base (three different substitutions and deletion) are equally likely when the read does not match the sequence. This symmetry requires each of the four possible reported errors (a base not equal to the assembly or a deletion) to have equal probability. An insertion, which does not have a corresponding base in the assembly, is modeled similarly, with the 4 in the denominator representing the uniform likelihood of observing any of the 4 possible bases on the assembly at that position. The product across all bases in a read is then equal to the total probability of observing that particular read at the given location in the assembly.

If the assembly has an unknown base at the location (denoted by an N) then we set

$$P(base_j|S) = 1/4 \quad (2.8)$$

modeling the fact that there is no information about the correct base at that location with a uniform distribution over all 4 possible bases. If an ambiguity code is reported by the sequencer then the above expression is modified to account for a distribution over the possible bases encoded by the corresponding code.

Each read is only allowed to be placed at a single position in the assembly. If the aligner placed a particular read at more than one position we choose a single position at random, weighted by $P_{placement}(r_j|S)$ score for each proposed position of the read on the assembly. This allows for repeat regions to be properly represented with the correct number of reads in expectation. A further explanation can be found in the section Placing Reads

The orientation likelihood, $P_{orientation}(r_i|S)$, is calculated by first counting the number of times that each orientation occurs in each library from the mapping information. The probability that a particular read from a particular library has a particular orientation is then modeled as that orientations empirical frequency in the library (this can be overridden with user-specified values for the probabilities). The likelihood $P_{orientation}(r_i|S)$ is then the empirical frequency of the observed orientation of the read r_i in the library from which r_i belongs.

After combining these two independent probabilities we are left with the total placement score $P_{placement}(R|S)$ for a given read. Below, we use this when calculating the probability that an assembly is correct given the reads, as well as the overall total ALE score. We also use it to calculate per-base placement scores at particular positions in the assembly. The placement sub-score at a particular position is given as the geometric mean of $P(r_j|S)$ of all r_j covering that specific position,

$$\left[\prod_R P(R|S) \right]^{1/N} \quad (2.9)$$

where the product is over all reads R covering the given position, and N is the number of such reads.

2.2.2 Insert sub-score

The insert likelihood, $P_{insert}(r_i|S)$, is determined by first observing all insert lengths from all mappings of all reads and calculating the population mean, μ , and standard deviation, σ^2 of these lengths (the mean and standard deviation can also be set by the user, if they are known). This step only needs to be done once. Once completed, we calculate the insert likelihood for each read r_i by assuming that the corresponding observed insert length L_i is distributed normally with this mean and variance, so that

$$P_{insert}(r_i|S) = Normal(L_i; \mu, \sigma^2) \quad (2.10)$$

In this expression, the insert length L_i is computed from the read r_i and its mapping to the assembly S . Similar to the placement score we can calculate the geometric mean of insert scores at a given position to come up with the insert sub-score. This can be useful for determining areas of constriction or expansion within a proposed assembly.

2.2.3 Depth sub-score

$P_{coverage}(R|S)$ describes how well the depth at each location agrees with the depth that we would expect given the GC content at that location (which is ideally Poisson-distributed (Lander and Waterman 1988)).

For each read, the GC content is the proportion of bases that are either G or C. Modern sequencers and library preparation techniques can bias GC-rich areas of a genome (Aird et al. 2011) This bias affects the observed depth of reads mapping onto specific areas of an assembly. To correct for this bias we first calculate for each of the following 100 ranges of GC content over the average read length, 0% to 1%, 1% to 2%, ..., 99% to 100%, the average observed depth for positions in each contig in the assembly with a GC content in this range. Call $\mu_{depth(X_i)}$ the observed average depth of all reads with a GC content falling in the same range as the GC content percentage X_i . We set the minimum expected depth to be 10, discounting regions of exceptionally low average depth.

We model the depths to be Poisson distributed about a mean drawn from a Gamma distribution centered at the expected depth for that position given its GC content. This models the dependence of the expected depth on more than just the GC content at that position, such as the presence of hard stops, and the GC content at nearby positions. It results in an infinite mixture of Poissons that is equivalent to a Negative Binomial distribution. For simplicity and computational convenience, we make an independence assumption when computing this component. This causes the expected coverage at a location to depend only upon the GC content at that position, and not the GC content at nearby positions.

Then, at any given position the depth sub-score is

$$\begin{aligned}
& P_{depth}(d_j | S, X_i) \\
&= \text{Poisson}(d_j; Y_i], Y_i \sim \text{Gamma}(\max(10, \mu_{depth(X_i)}), 1) \\
&= \text{NegBinom}(d_j; \max(10, \mu_{depth(X_i)}), 1/2)
\end{aligned} \tag{2.11}$$

where the depth is d_i and where the GC content percentage X_i is averaged across

all reads that map (in the placement step) to that position.

2.2.4 k-mer sub-score

$P_{kmer}(S) \propto P(S)$, the k-mer sub-score, describes the likelihood of the assembly S , in the absence of any read information. Within this prior probability distribution, we encode the belief that within a single genome, each k-mer (a permutation of k base pairs, where k is a fixed user defined number initially set to 4) has a unique k-mer frequency. This is the frequency with which the k-mer appears in the genome. The 4^k dimensional vector giving this frequency for each k-mer is conserved across a genome and can help determine if two different genomes have been mistakenly combined (Teeling et al. 2004; Woyke et al. 2006). Let K be the set of all possible unique k-mers, so $|K| = 4^k$, and for each i in K let n_i be the number of times this k-mer appears in a contig in the assembly. Then, the frequency f_i of a particular k-mer i within a contig is

$$f_i = \frac{n_i}{\sum_{j \in K} n_j} \quad (2.12)$$

The k-mer score is the product of this frequency over each k-mer appearing in each contig of the assembly S , which can be written as

$$P_{kmer}(S) = \prod_{i \in K} f_i^{n_i} \quad (2.13)$$

This is equivalent to assuming each k-mer in the assembly is drawn independently with identical distributions from a multinomial distribution with probabilities empirically estimated from the assembly.

The k-mer sub-score of a base at any given position in the assembly is the (geometric) average of $P_{kmer}(S)$ of all k-mers that cover that position. In calcu-

lating this average, the very first base in the genome only has one contributing k-mer, the second has two, up to k contributing k-mers after $k - 1$ bases.

2.3 Approximating Z

Bayes rule tells us that the probability that the assembly S is correct is

$$P(S|R) = \frac{P(R|S)P(S)}{Z} \quad (2.14)$$

where Z is a proportionality constant that ensures that $P(S|R)$ is a probability distribution, where Z is found by summing over all possible assemblies S' ,

$$Z = \sum_{S'} P(R|S')P(S') \quad (2.15)$$

Z cannot be explicitly computed because the space of all possible assemblies is far too large (4^L where L is the length of the assembly).

Instead we compute below an approximation \hat{Z} to Z . This provides an approximation to $P(S|R)$,

$$P(S|R) \approx \frac{P(R|S)P(S)}{\hat{Z}} \quad (2.16)$$

We can compare two assemblies generated from the same library of reads without calculating Z , the denominator in our Bayesian likelihood framework, because it cancels when taking the ratio of the likelihoods of the two assemblies. To determine a total ALE score for a single assembly, however, we must calculate or approximate Z . Our goal in approximating Z is to use a quantity that does not depend on the assembly S (or only depends weakly through some empirically estimated quantities included as parameters in the overarching statistical model), and is approximately of the same order of magnitude as the exact value

of Z . In this section, we refer to our approximate Z as \hat{Z} , and define it as a product of terms,

$$\hat{Z} = \hat{Z}_{placement} \hat{Z}_{insert} \hat{Z}_{depth} \hat{Z}_{kmer}. \quad (2.17)$$

We define each term in this product separately.

2.3.1 Approximating $Z_{placement}$

$\hat{Z}_{placement}$ is defined as

$$\hat{Z}_{placement} = \prod_{r \in R} \hat{Z}_{placement}(r|S). \quad (2.18)$$

In this expression R is the set of reads actually observed, r is one read in this set of reads, and $\hat{Z}_{placement}(r|S)$ is defined as

$$\begin{aligned} \hat{Z}_{placement}(r|S) &= \mathbb{E} [P_{placement}(r')|S] \\ &= \sum_{r' \in R'} [P_{placement}(r'|S)]^2 \\ &= \sum_{matches} \sum_{orientations} (P_{matches}(r'|S) P_{orientations}(r'|S))^2 \end{aligned} \quad (2.19)$$

In this expression R' is the set of all possible reads of the length given by r , and we sum over all possible matches and orientations, which is analogous to summing over all possible reads. Although S appears in this expression, its value does not depend on S because of permutation symmetry. This symmetry allows us to calculate this expression analytically, without enumerating over R' . In addition to its lack of dependence of S and its ease of computation, this choice for $P_{placement}(r)$ is motivated by the belief that this quantity scales roughly like

$$P_{placement}(r) = \sum_{S'} P_{placement}(r|S') P(S'), \quad (2.20)$$

which is a quantity identical in form to Z , but restricted to the placement probability of a particular read.

2.3.2 Approximating Z_{insert}

We define

$$\begin{aligned}\hat{Z}_{placement}(r|S) &= \mathbb{E}[P_{insert}(r')|S] \\ &= \sum_{r' \in R'} [P_{insert}(r'|S)]^2 \\ &= \sum_{insert} (P_{insert}(r'|S))^2\end{aligned}\tag{2.21}$$

Where again, in this expression R' is the set of all possible reads of the length given by r , and we sum over all possible insert lengths.

2.3.3 Approximating Z_{depth}

We define \hat{Z}_{depth} as,

$$\hat{Z}_{depth} = \prod_{base_i \in S} \hat{Z}_{depth}(X_i|S)\tag{2.22}$$

where

$$\hat{Z}_{depth}(X_i|S) = \mathbb{E}[P_{depth}(X_i|S)|S] = \sum_{d=0}^{\infty} (P_{depth}(d|X_i, S))^2,\tag{2.23}$$

where P_{depth} is defined as before. Although S appears in this expression, its value does not depend on S . We can calculate this expression analytically using a hyper-geometric function, see implementation.

2.3.4 Approximating Z_{kmer}

We define \hat{Z}_{kmer} as the expected kmer score,

$$\hat{Z}_{kmer} = \mathbb{E}[P_{kmer}(S)] = \left(\sum_{i \in K} f_i^2 \right)^N\tag{2.24}$$

where f_i , K and n_i are defined as before. This method finds the expected k-mer score for a uniform random k-mer and applies that score N times. Although

\hat{Z}_{kmer} depends on S through the empirically determined f_i , which may be undesirable, this dependence follows naturally from our statistical model because the f_i are considered parameters, which are estimated from data and then treated as known by the model.

The preceding calculations allow us to approximate Z and find an absolute likelihood score for a given assembly without comparing it to another with the same library and alignment.

2.4 Relationship of the difference of total ALE scores to probability of correctness

Here we derive an expression described in the Results section for the difference of two total ALE scores in terms of the probability that an assembly is correct. Suppose we have two assemblies, S_1 and S_2 . Call A_1 the total ALE score of the first assembly, and A_2 the total ALE score of the second assembly both generated from the same set of reads R . The difference of these scores is then

$$\begin{aligned}
A_1 - A_2 &= \log(P(R|S_1)) + \log(P(S_1)) - \log(\hat{Z}) + \log(P(R|S_2)) + \log(P(S_2)) + \log(\hat{Z}) \\
&\approx \log(P(R|S_1)) + \log(P(S_1)) - \log(Z) + \log(P(R|S_2)) + \log(P(S_2)) + \log(Z) \\
&= \log\left(\frac{P(R|S_1)P(S_1)}{P(R|S_2)P(S_2)}\right)
\end{aligned} \tag{2.25}$$

2.5 Placing reads

In this writeup we compare two different policies for sampling “reads” from a distribution. Each read $x \in \{1, \dots, N\}$ has a “hidden position” $m_x \in \{1, \dots, L\}$ and a function $f_x(n)$ such that

$$\arg \max_x f_x(n) = m_x \quad \forall x$$

and

$$0 \leq f_x(n) \leq 1 \quad \text{and} \quad f_x(m_x) = 1 \quad \forall x, n$$

For each position $p \in \{1, \dots, L\}$ we would like to find all reads that have that position as their hidden position. $f_x(n)$ will represent how “similar” a read is too that position and is proportional to the probability that it is the hidden position.

At each step we will track each read i ’s a_i , “assumed hidden position,” which will be defined by

$$a_x = \arg \max_{n \text{ sampled}} f_x(n) \quad \forall x$$

and

$$A_x = f_x(a_x)$$

This is our best guess for the hidden position of the read.

2.5.1 The Policies

Threshold Policy

The first policy, the Threshold Policy, will order reads by $f_x(a_x) = A_x$, which is to say reads will low probability that their $a_x = m_x$ will be placed first. This is because $f_x(n)$ is proportional to the probability that it is the hidden position and a_x is the current candidate for that reads hidden position. The policy will then sample the bottom M such reads for the given position.

Random Sample Policy

The second policy, the Random Sample Policy, will randomly sample reads with probability

$$P(x = x_{n+1}) = \frac{1 - f_x(a_x)}{\sum_x f_x(a_x)} = \frac{1 - A_x}{\sum_x A_x}$$

This will have the effect of sampling reads with low probability that their $a_x = m_x$ at a higher rate. The main advantage over the threshold policy is that it will not always get stuck by certain pathological cases.

2.5.2 The Set Up

We create N reads with hidden positions randomly distributed among L possible positions. We then draw the function $f_x(n)$ randomly from a distribution (currently using a Beta(2,5) and Uniform(0,1)) for each x and each n . We then artificially set $f_x(m_x) = 1$ for each x . We then choose starting assumed hidden positions a_x randomly distributed among the L possible positions and set $A_x = 1/L$

until it is first sampled.

2.5.3 The Run Through

For each position t we sample M reads, updating their a_x and A_x as we go. Both policies have the property that when $f_x(a_x) = A_x$ is high the likelihood that it will be sampled decreases, and when $f_x(a_x) = 1$ we know $a_x = m_x$ and this read x will no longer be sampled at all.

2.5.4 The Metrics

High Score

We want to maximize the quantity

$$\sum_x f_x(n_{\text{sampled}})$$

This is a measure of how likely we think all of our hidden position guesses are in aggregate. A score of x would mean we got all of them correct. A score of $0.99x$ would mean that on average we were 99 percent sure we had the right hidden value for a given read.

Accuracy

We also want to maximize this quantity

$$\sum_x \delta_{a_x, m_x}$$

Where $\delta_{x,y}$ is the Kronecker delta with the property of $\delta_{x,y} = 1 \iff x = y$. This is a measure of how many hidden positions we actually correctly identified. A score of x is perfect and means we got them all right. A score of b means only b hidden positions were correctly identified.

Results

We test the two policies against the two metrics and average them over 1000 runs of $N = 40, L = 10, M = \{1, \dots, 40\}, N = 80, L = 20, M = \{2, 4, \dots, 80\}$ for both Beta(2,5) and Uniform(0,1). The clear winner is the Threshold Policy. Although I contend that it will still be beat in a pathological case. In fact, the final graphs are the min values of each metric, rather than the average, but alas the set of pathological cases is too few! Threshold wins again. At the very end is uniform, where there is a slighter difference, albeit a consistent one.

INSERT FIGURES

2.6 Thresholding the total ALE score

In the plotting program distributed with ALE we use a thresholding algorithm to highlight potential areas of poor assembly quality using the per-base ALE scores. We do this by averaging scores within windows, allowing for the discovery of large errors in the assembly while smoothing out the noise. By the

Central Limit Theorem, when we average many independent and identically distributed random variables the result is approximately normally distributed. This allows us to create a threshold for which to delineate good scores from bad and pinpoint problematic regions. This is represented by a solid black line in the figures labeled 5σ . This line is calculated by assuming that the individual scores at each position in the assembly are drawn from a mixture of two normal distributions: one for high accuracy and another for low accuracy. We use maximum likelihood to determine the mean and variance of the two underlying distributions. The threshold is set as five standard deviations from the mean of the high accuracy distribution. This allows us to readily find areas of inaccuracy that are unlikely to be drawn from an accurate region. Five standard deviations corresponds to 1 false positive in 2 million positions if the joint normal distribution assumptions hold. The number of standard deviations at which the black line is drawn can be set from the command line by the user.

A black bar is drawn on the plot if the likelihood falls below the threshold at a significant fraction of the positions in any contiguous region with a given length (this fraction and length are user defined, and are initially set to 0.01% and 1000bp respectively) see figure XXX. These red bars correspond to regions of potential inaccuracy in the assembly that should be examined further. The plotter outputs these regions in a tab delineated text file for easy input into genome viewing software programs like IGV.

2.7 Influence of alignment input

ALE takes as input a proposed assembly and a SAM/BAM (Li 2009) file of alignments of reads onto this proposed assembly. This allows ALE to calculate the probability of observing the assembly given the reads. ALE assumes that this mapping will include, if not all possible mappings, at least the “best” mapping for each read in the library (if such a mapping exists). For assemblies with many repeat regions (>100) or libraries with large insert sizes, this can be difficult to obtain due to the bias introduced using default parameters of standard aligners. While an extensive review of alignment packages and their optimization is beyond the scope of this paper a review can be found in (Li and Homer 2010). If an assembly has many repeats and the aligner bias causes the reporting of reads only mapping to a fraction of possible regions, then ALE will see the unmapped regions as having 0 depth (no supporting reads) which will result in artificially low depth sub-scores. The robustness of ALE will still allow for comparison between assemblies with similar biases, but should be taken into account if the input to ALE is biased for only certain assemblies. To avoid this bias some mappers must be explicitly forced to search for all possible placements (-a in bowtie).

In summary, ALE determines the likelihood of an assembly given the reads and an accurate, unbiased alignment of those reads onto the assembly, without which the model assumptions are violated. These preconditions are usually met except for certain pathological genomes, and even in these cases can be readily corrected for by changing the parameters of the aligner used to make ALEs input.

CHAPTER 3
ALE RESULTS

CHAPTER 4

ALE IMPLEMENTATION

4.1 Depth Z normalization

When calculating \hat{Z}_{depth} at a specific position analytically,

$$\hat{Z}_{depth}(r, k) = \sum_{k=0}^{\infty} \left(\text{nbPMF} \left(k, r, \frac{1}{2} \right) \right)^2 = \frac{1}{4^r} {}_2F_1 \left(r, r; 1; \frac{1}{4} \right) \quad (4.1)$$

where r is the depth, k is the expected depth, ${}_2F_1$ is a hyper geometric function,

$${}_2F_1 \left(r, r; 1; \frac{1}{4} \right) = \sum_{n=0}^{\infty} \frac{(r)_n^2}{4^n n! (1)_n} \quad (4.2)$$

where

$$(r)_n = \frac{\Gamma(r+n)}{\Gamma(r)} \quad (4.3)$$

and nbPMF is the negative binomial probability mass function

$$\text{nbPMF}(k, r, p) = \binom{k+r-1}{k} (1-p)^r p^k \quad (4.4)$$

We note that numerically evaluating this function results in precision errors for large r due to the fact that we are multiplying a very small number by a very large number. If we move the fraction into the hyper-geometric function and take the exponential of the log we get

$$\hat{Z}_{depth}(r) = \sum_{n=0}^{\infty} \exp(2S(r+n) - 2S(r) - 2S(n+1) - (r+n)\log(4)) \quad (4.5)$$

where

$$S(x) = \log(\Gamma(x)) \quad (4.6)$$

and we can use Stirling's approximation,

$$S(x) = \log\left(x - \frac{1}{2}\right) \log(x) - x + \log(2\pi) + \frac{1}{12x} - \frac{1}{360x^3} + \frac{1}{1260x^5} - \frac{1}{1680x^7} + O\left(\frac{1}{x^9}\right) \quad (4.7)$$

to estimate this value. The sum is calculated in practice from $n = 0$ until the resulting contribution is less than machine precision (10^{-16} for doubles) due to the fact that the interior function is monotonically decreasing. This is pre-computed in python for common values of r (0 to 2048) for constant time lookup. Other values are computed in real time as needed.

This allows us to numerically calculate \hat{Z}_{depth} with high precision.

Part II

EPI: Expected Parallel Improvement

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EPI INTRODUCTION

CHAPTER 6
EPI METHODS

CHAPTER 7
EPI RESULTS

CHAPTER 8

EPI IMPLEMENTATION

Part III

Velvetrobe

Velvetropo: a parallel, bitwise algorithm for finding homologous regions within sequences

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Abstract

Existing methods for recognizing common patterns in sequence data streams do not scale well. This scaling problem becomes critical for problems that are driven by large-scale sequencing, such as metagenomics and cancer genomics. Restricting comparisons to exact identities of amino acids between a single test sequence and a set of test sequences allows many efficiencies to be realized, including bitwise parallel operation and low-order scaling.

We introduce an algorithm based on global and local densities of matches at the amino-acid level that finds areas of high commonality across a set of sequences. It produces results that are intermediate between local and multiple sequence alignment and can address questions that other approaches cannot address. The speed of the algorithm is superior to BLASTX and HMMER v3, and the scaling is $O(N)$ where N is the total length of the sequences being compared.

CHAPTER 9

VELVETROPE INTRODUCTION

Finding shared elements of sequence among possibly-related genes is a fundamental operation that underlies most of the analytical methods of molecular biology, including local sequence alignment, gene matching, multiple sequence alignment, phylogenetic tree calculation, and taxonomic assignments. The earliest approaches to finding this homology between sequences was derived from pairwise sequence alignment algorithms such as Needleman-Wunsch [?] or Smith-Waterman [?] both of which employ dynamic programming and are computationally expensive, in the sense that it does not scale linearly with the size of the data. A second approach employs hidden-Markov model (HMM) algorithms such as HMMer [?]. The HMM may be local or non-local in nature, is built up by training from a curated data set, and is also generally computationally expensive. A third approach relies upon exact or near-exact matches between short solid patterns (k -mers for a length k) before also resorting to dynamic programming. The k -mer approach underlies many algorithms such as the widely-used pairwise aligner and gene matcher BLAST [?] and its relatives [?, ?, ?]. k -mers also are the first pass in the widely used multiple-sequence aligners MUSCLE [?] and DIALIGN-TX [?]. Though the k -mer approach can be made quite computationally efficient, especially as k is made large, detecting distant homologies requires use of short values of k and it is easy to construct pathological cases where commonality will not be detected even for the limiting value of $k = 1$.

The importance of computational efficiency and scaling is made paramount by the recent advances and demands of data-driven projects in fields such as

shotgun metagenomic sequencing and cancer genomics. Such projects routinely create data sets exceeding 10 Gbp (10^{10} bp) and will soon extend to the Tbp (10^{12} bp) region as new sequencing technologies come online. Speed and scaling, especially at the early steps of analysis, is critical to make advances in these fields tractable.

Velvetropo was conceived to enable finding sequence homology with an algorithm that was simple, scalable and parallel from the start. Our approach is based on finding areas of high densities of shared identities (Amino Acid or DNA) in local (adjustable) regions between sequences, rather than finding k -mers. This allows for rapid bitwise operations between sequences, computeable in parallel. These areas are found by performing first a global, then local filter on the shared identities. By omitting the k -mer step we allow Velvetropo to access homology information between evolutionarily distant sequences otherwise inaccessible by other methods.

While areas of high sequence identity density are qualitatively similar to local alignments, they are significantly different from the outputs of traditional pairwise-local or global alignment algorithms. These regions do correspond to areas of high probability to be in a standard alignment as they represent areas of high local homology. Rather than explicitly calling these regions alignments we refer to them as “in the club,” thus giving rise to the name, ‘Velvetropo’ the traditional barrier between those in and out of a club.

Velvetropo is a quick and simple and highly parallelizable method (we present both a serial and parallel implementation) that finds areas of high similarity between many sequences in a pairwise fashion, never performing a k -mer based step and independent of order. This allows for it to quickly find areas of

high local homology, including areas that these other methods may ignore like proteins with transposed domains.

CHAPTER 10

VELVETROPE METHODS

To find the areas of high local homology between sequences we employ a two-part filtering system that first finds offsets (sets of positions) where two sequences share a higher than expected amount of identity (global filter), and then filters these sets of positions to find areas with higher than expected identity within them (local filter).

Velvetropes filtering system implements only bitwise operations on a sequence of interest S compared against a possibly large set of other test sequences T . The first step is a global filter and works by taking the sequence of interest and comparing it using DNA or Amino Acid translations (up to 6 frames). For the motivating examples we will assume we are in a coding region and use a Amino Acid translation. We can compare the sequence S against each sequence in the set of sequences to be compared against $T \in \mathbf{T}$ using simple AND operations. To track the sequence identities within these offsets we construct a binary concordance matrix M that keeps track of all matches (sequence identities) across all possible offsets of the two sequences.

The aggregate number of matches for every offset found is compared to what would be expected if the test sequence were randomly rearranged at that offset; if the number of matches is above some threshold then this offset is saved as having a possible area of high local homology, this is the global filter. All possible offsets up to the length of the proposed sequence are checked in this fashion. By looking at all possible offsets between the two sequences we can allow the areas being compared to shift across the two sequences, even becoming transposed if need be. This can be done in parallel for all sequences in \mathbf{T} and even

across different offset sets within a particular test sequence.

The next filter is local and works by looking over a fixed-bit window in each of the possible offsets proposed by the first step. The window keeps a running average of the number of matches within it, correcting for the expected number of random matches and keeping track of only the difference between the number of matches were actually found and what is expected. When there is a large spike in this value then the window has shifted over an area with a large number of possibly non-random matches, an area of high sequence identity density. The region is then saved as an area of high local homology between the two sequences.

10.1 Construction of the Concordance Matrix M

We construct the concordance matrix M by comparing a sequence of interest S against each test sequence $T \in \mathbf{T}$ aligned so residue 1 in the sequence of interest (S_1) is being compared to residue 1 of the test sequence (T_1), residue 2 compared against residue 2 (S_2, T_2), etc. The first row of the bit-matrix is then constructed as follows: if the residue in the sequence of interest matches the residue it is lined up against in the test sequence then we give that position a value of 1, otherwise we give it a 0. We note that the row has length $\min(L_S, L_T)$, where L_S is the length of the sequence of interest S and L_T is the length of the test sequence T . The test sequence is then shifted so that now residue 2 of the test sequence (T_2) lines up with residue 1 of the sequence of interest (S_1), residue 3 compared against residue 2 etc. (T_3, S_2). This corresponds to offset 2. The second row is then constructed as before. We define some minimum window size w (user defined, initialized to 20), all $L_S + L_T - 2w$ possible offsets of overlap

greater than or equal to w are tested. In general

$$M_{ij} = \begin{cases} 1 & \text{if } S_j = T_{i+j} \\ 0 & \text{otherwise} \end{cases}, \quad (10.1)$$

for all

$$1 \leq i \leq L_S + L_T - 2w \quad (10.2)$$

and

$$\max(1, L_T - (w + i)) \leq j \leq \min(L_S, L_T + i - w). \quad (10.3)$$

This creates a banded $(L_S + L_T - 2w) \times (\min(L_S, L_T))$ matrix M that contains all pairwise comparisons between all possible offsets of size at least w between the sequence of interest S and the test sequence T . If every amino acid in T were randomly distributed and there were equal frequencies of every amino acid we would have (inside the band of the matrix that actually contains information)

$$E[M_{ij}] = \frac{1}{20}. \quad (10.4)$$

This is not always true, and the algorithm takes local expectation into account, but this can be used as an approximation for motivation purposes. This is to say, long linear stretches of ones in this matrix should be rare and possibly contain useful information about areas of high similarity.

For example purposes we will compare the RNA Polymerase Beta Subunit between *E. Coli* and *Bacillus subtilis* (available in the supplementary material or [?]) for the rest of the implementation section. We can see the row sum of the concordance matrix that these two genes imply compared against the expectation in Figure 1.

[FIGURE 1 HERE]

10.2 First filter: Global

Now that we have this $(L_S + L_T - 2w) \times (\min(L_S, L_T))$ binary matrix M , we want to find what offsets result in abnormal quantities of matches. We want to find the rows in the matrix that have a higher than expected number of ones in them. To do this we take the sum of each row and compare it to the expectation of the number of matches based on amino acid frequency between that offset of the test sequence and the sequence of interest using a random model. If the sum of the ones is higher than some predetermined multiple of standard deviations away from the mean then it is marked as having a possible alignment. A default value of 3.5 assures that false positives should be extremely rare. We mark a row i if,

$$\sum_j M_{ij} > E\left(\sum_j A_{ij}\right) + \alpha \sqrt{E\left(\sum_j A_{ij}\right)}. \quad (10.5)$$

where $E(X)$ is the expectation of X , $A_{i\cdot}$ is a random vector constructed from sequences with the same amino acid composition, α is a parameter and is set to 3.5 by default and the square root represents the standard deviation (we assume a Poisson distribution). The value of 3.5 ensures a false positive rate of less than 0.1% and we only look at one side distribution, offsets with higher than expected matches. The value of the mean and expectation is calculated analytically by combinatorially looking at all possible permutations of the test sequence. See figure 2.

We note that as the lengths of the sequences grow large the signal can become lost in the noise. Even a k -mer of length 1Kbp would be lost when comparing a 3Gbp sequence using this method. To account for this and also to make easier use of the Graphics Processing Unit (GPU) implementation of this algorithm, which enforces strict memory constraints, we break up the sequences

into chunks of length 1000 before forming the matrix M . This not only ensures that the noise will not overwhelm the signal, but also allows for much faster, parallel implementations. Areas of similarity that extend over a separation are rejoined in the recompilation step. By only looking over a linear number of offsets in the length of the test sequences we achieve scaling of $O(N)$ where N is the total length of the sequences being compared. This is far less computationally complex than the alternative dynamic programming and HMM based methods.

[FIGURE 2 HERE]

10.3 Second filter: Local

We now have the set of offsets that have a significant number of ones in them. The next goal is to quickly find where the areas of high density are in these vectors, if such areas exist, as these would be areas of high homology between the sequences. This is done by taking a running sum of each vector from its start, at each point we subtract off the expectation based on the amino acid frequency of the two sequences for each position. This has an effect of calculating how many ones have been found at or before that position above the number that would be expected. We know that this value must increase at some point in the vector because at the end there needs to be some extra number of ones equal to some number of standard deviations away from the mean, based on it passing the global step. Where this value peaks is where the club starts (is has a significant jump in the running sum over some window). When the value flattens out again that part of the sequence is no longer in the club. See Figure 3.

Two parameters are used here (combined with the one from the global filter

they represent all three parameters of the model), the width of the block used for approximating the derivative and how many matches above the expectation are needed to trigger the start of the region. We can get the quick, bitwise location of the high density region in the vector, which corresponds to our in the club region. A useful side effect of this filter is that if there is no region of high density, if we have just accidentally found an outlier from the global filter that just happens to have a lot of sparse matches, then it will not trigger and we will not get a false positive from the result of the global step.

[FIGURE 3 HERE]

10.4 Recompilation

Now we have the regions where we have reason to believe that there are local alignments between the two sequences, our in club areas. We can see where they lie on their respective sequences and how their densities compare with each other and the sequences as a whole. This can be important information because the shifting of conserved regions and possible transposition events can represent evolutionary distance between the sequences. If we consider the conserved regions to be fixed by natural selection then their relative drift away from each other should be related to when they originally diverged. We can see an example of this in Figure 4 where there is a difference in the sequence length between conserved areas of sequence.

[FIGURE 4 HERE]

CHAPTER 11

VELVETROPE RESULTS

11.1 Multiple Sequence Alignment

Multi-domain proteins have traditionally been cumbersome to Multiple Sequence Alignment (MSA) algorithms like MUSCLE [?] and DIALIGN-TX [?] like the 31 multi-domain lectin proteins in Reference 8 of BALiBASE v3 [?]. The two domains for lectin are transposed for 4 of the organisms and are ordered “correctly” for the other 27 in the reference database (See figure 5). Because Velvetrope works independent of order it allows us to find transposed domains from within a protein such as this with relative ease and compute a probable, non-traditional MSA.

Comparing a sequence of interest against a large set of test sequences allows Velvetrope to find the areas within the sequence of interest that are homologous to multiple test sequences. By combining this information across many sequences (as in figure 6) we make a histogram of which residues were matches and in the club across many test sequences. We are able to discern areas of possible multiple alignment from within the sequence of interest in this fashion. By looking at the areas within the sequence of interest which are consistently identical to test sequences or in the club we can generate regular expressions of sequence that can be readily re-mapped onto the sequence of interest, representing a non-traditional multiple alignment. This allows us to find a probable MSA and because Velvetrope only compares a single sequence of interest against a larger set we can use this to quickly append a new sequence to a multiple alignment multiple orders of magnitude faster than traditional methods

which would have to recalculate the entire MSA for every appended sequence.

Traditional methods, like those in BALiBASE, have to be prompted with domain information to make sense of a multi-domain protein at all. Even with this information they only align the prompted domain and merely append the other domain(s) around the domain of interest. This results in a MSA that does not represent the true alignment between the proteins. Velvetrope is able to produce a shorter MSA with all domains represented without any prior information. In Figure 7 we look at two MSAs in which BALiBASE was prompted with the two lectin domains and it generates a non-intuitive alignment. While using just a single sequence of interest we are able to find both domains and re-map them onto that sequence and generate a much more compact and representative probable MSA very quickly.

[FIGURE 5,6,7 HERE]

Local alignment comparison

While Velvetrope does not perform a local alignment in the traditional sense it is able to find areas of high local homology between sequences, regardless of order or k -mer density, that are highly probable areas of local alignment. Velvetrope compares well at a visual level to standard algorithms like BLAST [?] and HMMer [?] and the C/CUDA implementation executes at the same order of magnitude or faster than these methods. Velvetrope is very susceptible to high indel rates within a conserved region (shifts the offsets) but has been shown to equal or outperform these other methods in areas of low indel rate especially when there are only short k -mers within the homologous region between the

two sequences.

CHAPTER 12

VELVETROPE IMPLEMENTATION

Velvetrope is able to find areas of sequence homology quickly and efficiently across multiple sequences. It finds these areas of high shared identity density in a way that allows it to locate areas otherwise missed by k -mer based or position dependent methods. It is able to correctly find probable alignments in multi-domain proteins and pairwise local areas of similarity between distant homologies. Its low order of computational complexity, $O(N)$ where N is the total length of the sequences being compared, allows for it to scale with the data intensive challenges that fields like metagenomics and cancer genomics present.

We also present a freely available, open source implementation (both serial and parallel; in Python, C and CUDA) with easy to navigate HTML output similar to MEME [?]. The API and documentation make it easily extendable and able to adapt to the future computationally intensive problems it is designed to address.

12.1 Availability and requirements

- **Project name:** Velvetrope
- **Project home page:** velvetrope.sourceforge.net
- **Operating systems:** Linux 32/64-bit, Mac OSX, Windows (Cygwin)
- **Programming languages:** Python, C, CUDA, HTML/CSS
- **Other requirements:** Some python packages, see documentation
- **License:** GPL v2.01

APPENDIX A
CHAPTER 1 OF APPENDIX

Appendix chapter 1 text goes here