Towards building an automated bioinformatician: more accurate transcript assembly via parameter advising

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Abstract

Computational tools used for genomic analyses are becoming increasingly sophisticated and complex. While these applications often provide more accurate results than their predecessors, a new problem is emerging in that these pieces of software have a large number of tunable parameters. Choosing the wrong parameter values for an application may lead to significant results being overlooked or false results being reported. We take some first steps towards generating a truly automated genomic analysis pipeline by developing a method for automatically choosing input-specific parameter values for reference-based transcript assembly. We extend the parameter advising framework, first developed for multiple sequence alignment, to optimize parameter choices for the `Scallop` transcript assembler. In doing so, we provide the first method for finding advisor sets for applications with large numbers of tunable parameters. By choosing parameter values for each input, the area under the curve (AUC) when comparing assembled transcripts to a reference transcriptome is increased by 28.9% over using only the default parameter choices on 1595 RNA-Seq samples in the Sequence Read Archive. This approach is general, and when applied to `StringTie` it increases AUC by 13.1% on a set of 65 RNA-Seq experiments from ENCODE. Parameter advisors for both `Scallop` and `StringTie` are available on Github[1].

1 Introduction

As the field of computational biology has matured, there has been a significant increase in the amount of data that needs to be processed and the reliance of users without computational expertise on the highly complicated programs that perform the analyses. At the same time, the number and sophistication of such tools has also increased. While the accuracy of such applications is constantly improving, a new problem has emerged: the sometimes overwhelming number of tunable parameters that each of these sophisticated pieces of software brings with them. Changing an application's parameter settings can have a large impact on the quality of the results produced. When incorrect or non-ideal parameter choices are used, significant results may be overlooked or false conclusions may be reported.

The default parameter choices that most users rely on for these programs are typically optimized by the the algorithm designer to maximize performance on the average case. This can be a problem since the most interesting experiments are often not "average."

[1] https://github.com/Kingsford-Group/scallopadvising

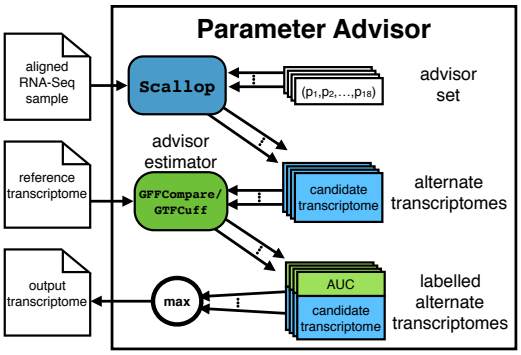


Figure 1: The `Scallop` parameter advisior. The advisor's input mirrors that of `Scallop` (an RNA-Seq sample that has been aligned to the reference genome). A set of candidate assemblies is created by running `Scallop` on each parameter vector in the advisor set. The advisor then returns the assembly with the highest AUC value, obtained by running `GFFCompare` and `GTFCuff`.

Manually tuning the parameter settings of an application often produces more accurate results, but it is very time consuming. The tuning process can be accelerated for users with domain and/or algorithmic knowledge, as these experts can make more informed decisions about the correct direction to proceed when altering parameter values. But tuning the parameter choices to increase accuracy for one input does not imply that the results will be improved for all inputs. This means that, for optimum performance, tuning must be repeated for each new piece of data. In the case of high-throughput genomic analysis, this manual procedure is utterly infeasible. For these applications, without some sort of automatic parameter choice system, the defaults must be used.

To address the automated parameter choice problem for multiple sequence alignment (MSA) DeBlasio and Kececioglu [1] have defined a framework to automatically select the parameter values for an input. This process, called "parameter advising," has been shown to greatly increase accuracy of MSA without sacrificing wall-clock running time in most cases, and it can readily be applied to new domains. A parameter advisor, depicted in Figure 1, has two components: (1) a set of parameter vectors – assignments of a value to each of the tunable parameters for the application, called an "advisor set"; and (2) an assessment criteria – a method to rank the quality of multiple solutions, called an "advisor estimator". The advisor selects the appropriate parameter vector by first running the application on the input using each parameter vector in the set, and selecting the parameter vector that produces the best result according to the accuracy estimator. Parameter advising for a given application is fast in practice. The instantiations of the application being tuned are independent processes that can be executed in parallel. Assuming that the number of processors available is at least the number of parameter vectors in the advisor set, the only additional wall time is the assessment of the results using the accuracy estimator (which can also be performed in parallel) and the comparison of these values, both of which are negligible compared to the running time of the application in most cases.

Parameter advising is an example of *a posteriori* parameter selection — it examines an application's output to select a parameter setting. In contrast, separate work has been done in other fields on *a priori* selection, where the parameters are chosen in advance by looking at the raw input. This includes work such as `SATZilla` [2] for choosing from a collection of SAT solvers, or `ParamILS` [3] which finds optimal settings for the `CPLEX` computational optimization tool. More information is available when performing *a posteriori* assessment since the full final solution can be examined, but *a priori* prediction is necessary in cases when it is not feasible to apply multiple configurations.

In this work we improve the performance of reference-based transcriptome assembly by extending parameter advising. Transcriptome assembly takes an RNA-Seq sample and reference genome as input and reconstructs the set of transcripts that are present. Common tools for reference-based transcript assembly include `Scallop` [4], `Cufflinks` [5], `StringTie` [6], and `TranscComb` [7].

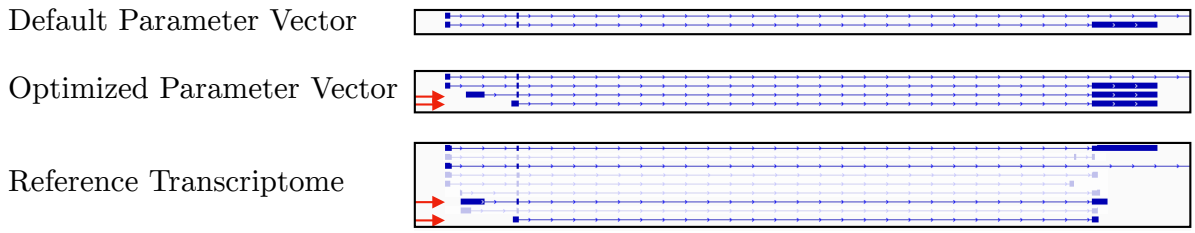


Figure 2: Impact of parameter choice on the produced transcriptome. The 3 transcriptomes are those assembled using `Scallop`'s default parameter vector, an optimized parameter vector, and the reference transcriptome for positions 30231125 to 30260786 on Chromosome 2 in `SRR543291/HISAT`. The red arrows highlight the two transcripts from the reference that are not recovered using the default parameter vector.

The assembler first aligns reads to the reference genome using a tool such as `HISAT` [8], `STAR` [9], `TopHat` [10], or `SpliceMap` [11]. Using the read splice locations (the positions where a read maps to non-neighboring locations on a genome) the assembler constructs the exons of each transcript. The produced transcriptome consists of a combination of transcripts that can be mapped to ones we already know and transcripts that are unique to the sample that was provided. These transcriptomes are used to perform analyses such as gene quantification [12] and differential expression [13].

Figure 2 shows an example of just how much impact using non-optimal parameter vectors can have on a transcriptome assembly. If the default parameters had been used, two transcripts at this location alone would not have been identified; both of these transcripts are present in the reference transcriptome and supported by the sequencing reads.

Transcript assembly using `Scallop` has a larger number of tunable parameters than previous targets of parameter advising. Because of the high-dimensionality of the parameter space, the existing methods for finding advisor sets are not viable. However, there are certain properties of the interaction between parameter choices and accuracy that can be exploited for some applications. If the accuracy landscape when adjusting these parameters does not contain many non-global local maxima, iterative optimization techniques can be used to find an advising set. We describe the requirements an application domain must meet in order for these optimization techniques to be used, and we show that transcriptome assembly with `Scallop` appears to satisfy these requirements.

Contributions The contributions of this work are threefold: first, we show for the first time that sets of alternative parameter vectors in certain domains can be found using methods other than exhaustive enumeration; second, we take some of the first steps towards producing a fully automated genomic analysis pipeline by automating sample-specific parameter selection; and third, we show that even with its drawbacks AUC is a better measure to use for parameter optimization in reference-based transcript assembly than existing *de novo* metrics.

We show that by applying the parameter advising framework, we can greatly increase the quality of the transcriptomes produced using the `Scallop` assembly tool. Using our new tool to construct reference-based transcriptomes, the area under the curve shows a median increased of 8.7% over using only the default parameter vector on a set of 10 RNA-Seq experiments contained in the ENCODE database that are commonly used for benchmarking. The median improvement is even larger, 28.9% higher AUC than the default parameter vector in a high-throughput pipeline applied to over 1500 samples from the Sequence Read Archive.

We also confirm that this method can increase AUC for other programs by applying it to `StringTie`. For a set of 65 examples from the ENCODE database, we are able to increase its accuracy by 13.1% over using only the default parameter vectors.

2 Developing a parameter advisor for transcript assembly

Constructing a `Scallop` parameter advisor is expedited because we can use AUC as the "advisor estimator", but finding an advisor set is especially challenging. `Scallop` has 18 tunable parameters compared to approximately 5 for multiple sequence alignment. This means the previously developed method of enumerating a parameter vector universe then using combinatorial optimization to find an advisor set is infeasible. The `Scallop` transcript assembler generates a transcriptome from a set of reads that have been aligned to a reference genome. It first splits the genome into regions of non-overlapping reads, which are called bundles. These bundles can be thought of as genes or groups of overlapping genes. Then, within each bundle a splice graph is constructed based on the split reads that define possible exon boundaries. Paths through the splice graph define potential transcripts, and the final set of transcripts is formed by decomposing the splice graphs into paths while trying to respect as many of the read mappings as possible. The 18 tunable parameters of `Scallop` govern various stages of this process and are: maximum dynamic programming table size (DP), maximum edit distance (ED), maximum intron contamination coverage (ICC), maximum number of exons (NE), minimum bundle gap (BG), minimum exon length (EL), minimum flank length (FL), minimum mapping quality (MQ), minimum number of hits in a bundle (NH), minimum router count (RC), minimum splice boundary hits (SBH), minimum subregion gap (SG), minimum subregion length (SL), minimum subregion overlap (SO), minimum transcript length, base (TLB), minimum transcript length, increase (TLI), uniquely mapped reads only (UM), and whether to the secondary alignment (US).

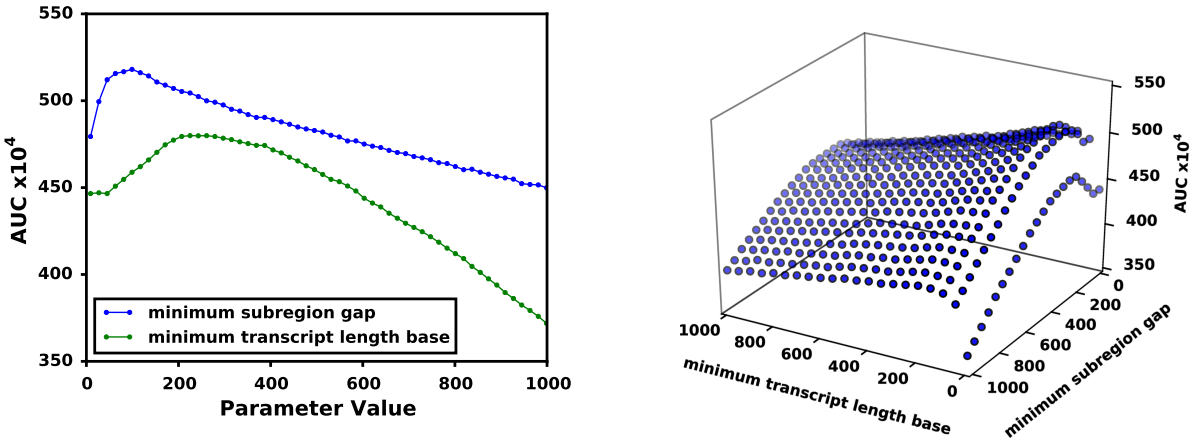
In this work, as opposed to [4], we choose to not separately evaluate multi-exon transcripts and single-exon transcripts but rather maximize a combined AUC. This was done by not having `Scallop` filter its output based on minimum transcript coverage (the average number of reads that are aligned to each position along the transcript's length) then allowing the tools `GFFCompare`[2] and `GTFCuff`[3] to calculate an AUC by thresholding this value after the fact.

2.1 Analyzing parameter behavior

Iterative optimization strategies such as gradient ascent [14], simulated annealing [15], and coordinate ascent [16, sec. 5.4.3], work by systematically searching high-dimensional spaces based on a specific optimization criteria. But, for these methods to work well the parameter landscape should be free from a large number of local maxima as well as large discontinuities.

To determine the behavior of the parameters of `Scallop`, we calculate the AUC of the assemblies produced when varying a single parameter's value and keeping the remaining parameters at the default. Figure 3a shows the effect of varying the "minimum subregion gap" and "minimum transcript length, base" parameters. Figure 3b shows the shape when varying both. Note that throughout

[2] urlhttps://github.com/gpertea/gffcompare
[3] https://github.com/Kingsford-Group/rnaseqtools



(a) Single Parameter Behaviour

(b) Paired Parameter Behaviour

Figure 3: AUC for various values of the "minimum subregion gap" and "minimum transcript length base" parameters. The points in the plot show the area under the curve (vertical axis) for the transcriptome produced by changing the value each of the parameters either (a) alone or (b) together leaving all other parameters their default values on SRR534291/`HISAT` from `ENCODE10`.

this work, we multiply area under the curve values by 10^4 for ease of comparison. AUC is a value in the range $[0, 1]$, but generally for transcript assembly the value is very small, typically < 0.1.

We examined these curves for several experiments from the ENCODE database, and found that the shape of the curves for all 16 continuous parameters and all of the pairs tested contained only one visible local maximum. These tests suggest that there may be very few local maxima in the high-dimensional parameter space.

2.2 Finding an advisor set using coordinate ascent

The greedy coordinate-ascent-based procedure we use here starts at the default parameter vector. Then one dimension (parameter) at a time, we examine the AUC of the parameter vector with that parameter changed by one step in each direction and update our current vector if we see an improvement. We continue tuning one dimension until no more improvements are made. Our procedure is deterministic meaning we would never take a step that decreases (or maintains) AUC, unlike many implementations. Taking inspiration from simulated annealing, we use a decreasing step size for each dimension. We start with large step sizes in each dimension, and any time we interrogate the whole set of parameters without making any change we decrease all of the step sizes by a factor of $\frac{1}{4}$ and repeat the process. This continues until all of the step sizes are small (1 for integer parameters and 0.01 for real numbers) and no more changes to the parameter vector are made. For the tunable parameters in `Scallop` that accept only binary input, the same rules as integer parameters are applied but with an initial step size to 1 and limiting the range to 0 and 1 ('false' and 'true').

Figure 4 shows the trajectory of three coordinate ascent training sessions. The large increases in AUC in the initial iterations are likely the procedure moving away from the multi-exon optimized parameter vector. As the sessions continue, the increase in AUC becomes smaller because the procedure is narrowing in on the apparent true maximum and the decreases in step size.

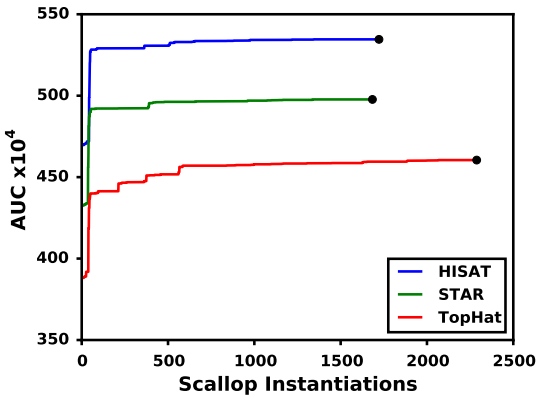


Figure 4: Area under the curve for each step of the coordinate ascent procedure for SRR534291 from `ENCODE10` using all 3 aligners. Each curve in the plot shows the progress of the coordinate ascent landscape exploration for one of `HISAT`, `STAR`, and `TopHat`. Across the horizontal axis is the number of exploratory steps taken in the search and the vertical shows the area under the curve for the current best parameter vector.

Coordinate ascent will find higher-AUC parameter vectors for an input, but it is slow so it is not a viable candidate for finding input-specific parameter choices in practice. Instead, we can explore the parameter landscape in order to develop the advisor sets we need. These sets are computed in advance so as long as the the training set is diverse, meaning it represents the range of possible inputs, they can be reused for any new input.

2.3 Data

We use 3 sets to train and validate parameter advising:

- `ENCODE10` contains a collection of 10 RNA-Seq experiments from the ENCODE database [17] that were used to benchmark `Scallop` and have been extensively used to evaluate transcriptome assembly tools [6, 7]. 30 examples were produced by aligning each sample to the human reference genome (GRCh38) using three tools: `HISAT`, `STAR`, and `TopHat`. (Command line arguments are listed in Supplemental Table 3, Experiment identifiers in Supplemental Table 6.) A subset of these examples was used to find the `Scallop` default parameter vector.
- `ENCODE65` contains a collection of 65 RNA-Seq experiments, also from ENCODE, that were not included in `ENCODE10` and that had preexisting alignments in the database. These alignments are produced using an aligner selected by the group that submitted the sample and are mapped to either GRCh37 or GRCh38. (Experiment identifiers in Supplemental Table 7.)
- `SRA` contains a collection of 1595 RNA-Seq experiments from the Sequence Read Archive [18] that have been filtered for quality. We eliminate any sample that contained very few reads unaligned ($<$ 1GB sequence file) or aligned ($<$ 1GB alignment file). All remaining samples were aligned using `STAR` to GRCh38. (Experiment identifiers in Supplemental Tables 8-18.)

3 Validating the transcript assembly parameter advisor

3.1 Finding a `Scallop` advisor set

The `ENCODE10` dataset is ideal for training because it is highly diverse and will produce parameter vectors that should generalize. It contains samples that are widely accepted as benchmarks and has examples that have been generated using a collection of commonly used aligners. The coordinate ascent procedure described in Section 2.2 was used to find improved parameters for each sample. The parameter vectors found are in Supplemental Table 1.

Most of the parameters values deviate quite far from each other, meaning there is unlikely to be one parameter choice that works well for all of the training examples. The deviation of the parameter vectors from the default is not surprising given that in this work we are optimizing AUC on all transcripts, rather than only multi-exon ones as was done previously. When single-exon transcripts are evaluated in concert with multi-exon transcripts, a new default parameter setting could be recommended for some single parameters, such as in the case of "minimum mapping quality" where almost all samples used a value of 11 rather then the default of 1, and "minimum transcript length increase" where most samples found improvement by selecting values that are much smaller than the default. In fact, we find that the parameter vector found for SRR545723/`TopHat` had higher AUC for all of the samples in the test set and would be the best vector to use as the default.

In reduced resource environments (when 31 processors are not available), it may be desirable to run fewer parameter settings to keep the number of parallel processes smaller than the number of available threads. We used the oracle set-finding method described by DeBlasio and Kececioglu [1, 19] to find a subset of parameter vectors that maximizes the average AUC for advising.

Advisor subsets are found using an integer linear program that has two sets of binary variables: one variable for each parameter vector, and one for each example. Where an example is a parameter vector used to assemble a sample. Constraints are used to ensure that only one example for each sample is chosen, and that the associated parameter setting is also chosen. The objective is then to maximize the sum of the accuracies of the chosen examples while only selecting a predefined number of parameter vectors. Using the samples in `ENCODE10`, we found advising subsets of 1, 2, 4, and 8 parameter vectors. The subsets induce an assembly tool that can be run in reduced resource environments, such as on an individual desktop. The advising subset choices are shown in the right most columns of Supplemental Table 1. Note that an advising set of size 1 is equivalent to finding a new default parameter vector since it maximizes the average accuracy across the training examples.

3.1.1 Advising on the training set

Figure 5 shows the AUC for all of the samples from `ENCODE10`. For each example (a sample combined with an aligner) there are two values shown: the AUC of the parameter vector produced as a result of coordinate ascent, and the AUC of the leave-one-out advising parameter vector. For the leave-one-out experiment, advising was limited to the 18 parameter vectors that were learned on examples produced using the 2 aligners and 9 samples that were different from the example being tested. This test is used to show the robustness of the advising set.

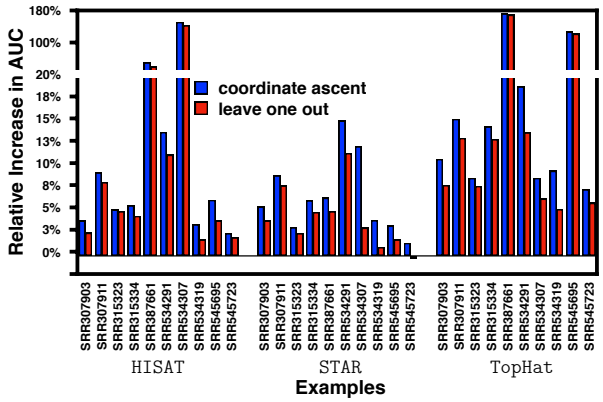


Figure 5: Increase in AUC for examples in `ENCODE10`. Each of the 30 examples is listed on the horizontal axis. Each bar's height is the normalized difference between the default AUC and that of the assembly produced using either coordinate ascent (blue) or leave-one-out (red).

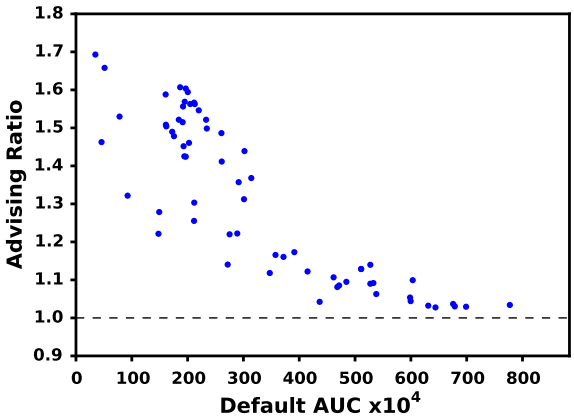


Figure 6: AUC improvement for `ENCODE65`. Each point is a single experiment positioned by the AUC of the default `Scallop` parameters (horizontal axis) and the ratio of the advised AUC over the default (vertical). A value above 1.0 indicates an improvement.

3.2 Assessing the generality of learned parameter vector

3.2.1 `ENCODE65`

The `ENCODE65` dataset is used to show that on a large number of samples from a range of aligners (possibly using non-default parameter settings) advising for `Scallop` provides a higher AUC transcriptome. Figure 6 shows the increase in AUC for all 65 examples in `ENCODE65`. The figure indicates, as expected, that the higher the default AUC, the less room there is for improvement and thus the smaller the advising ratio (the AUC of the transcript assembly produced by the advised parameter vector normalized by that of the default parameters). Using advising on this highly diverse set of samples increases the AUC of each transcriptome by a median of 31.2%. When using the resource limited sets, the median increase remains 18.2%, 19.0% and 24.4% for sets of 2, 4, and 8 parameter settings respectively. Even with these small sets, there is a large increase in AUC.

Random Advisor Sets. To confirm that the increase in accuracy is due to our advisor set construction method and not an artifact of having multiple choices of parameter vectors, a collection of random parameter vectors were generated and used for parameter advising. A range was defined for each tunable parameter by examining all of the values that provided an increase in AUC for any example at any stage in coordinate ascent. A random vector was then constructed by selecting parameter values for each parameter uniformly at random. In total 30 such parameter vectors were generated to match the advisor set size developed using coordinate ascent. This randomization procedure was then replicated 100 times to ensure stability of the average.

Figure 7 shows the AUC achieved by parameter advising on `Scallop` using the the coordinate ascent derived advising set versus the AUC of advising using the random advisor sets. Note that the default parameter vector was left out of the all advising sets. Because of this, many of the randomly generated advisor sets (29 of 65) had a decrease in accuracy relative to the default. On

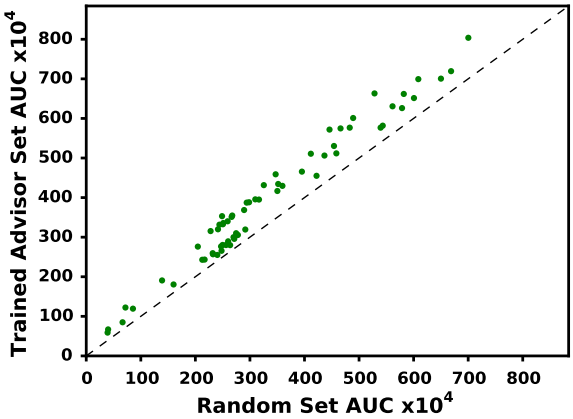


Figure 7: Comparison to randomly generated advisor sets. Each point in the chart represents one example from ENCODE65 positioned by the AUC value of using a randomly generated advisor set (horizontal axis) or the trained advisor set (vertical axis) averaged over 100 random replications. Points above the diagonal line show an improvement of training over random.

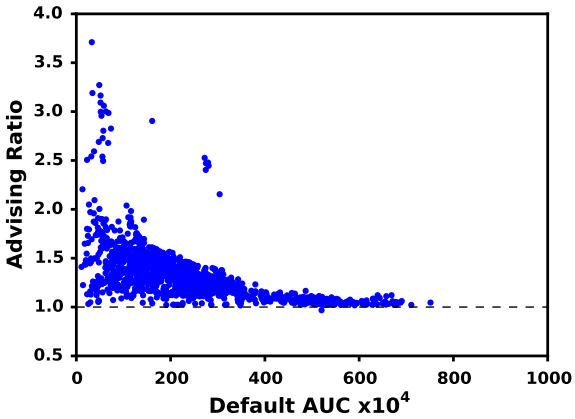


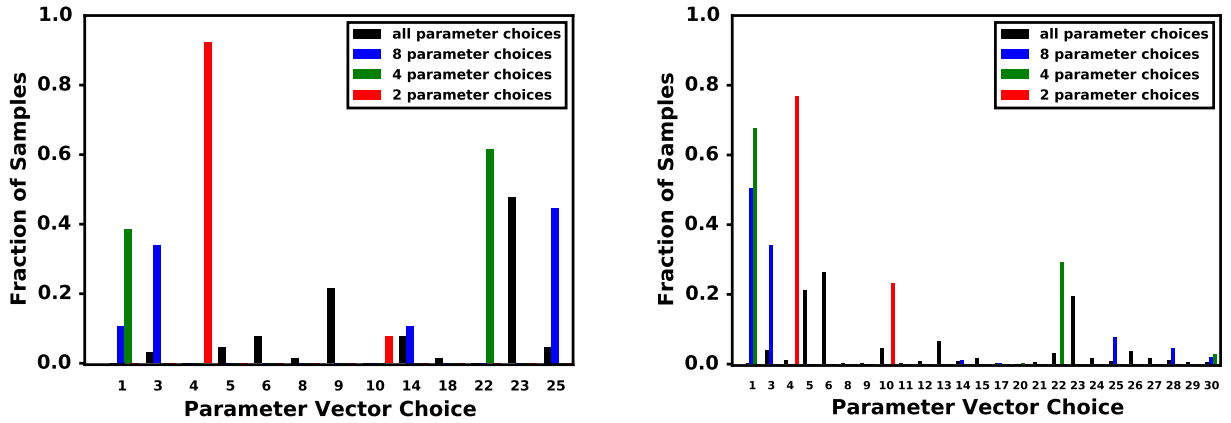
Figure 8: AUC improvement the SRA assemblies. Each point is a single experiment positioned by the AUC of the default Scallop parameters (horizontal axis) and the ratio of the advised AUC over the default (vertical). A value above 1.0 indicates an improvement. For this test the default was excluded from the advising set, but can be included in practice to ensure the AUC is never reduced.

some examples the performance is similar between the two sets, but the average increase in AUC is much higher for the coordinate ascent advisor set (median AUC increase of 31.23 versus 5.59). In all of the 65 examples, the coordinate ascent sets outperform the random ones.

Figure 9a shows the frequency with which each of the 31, 8, 4, and 2 parameter vectors provides the maximum AUC when running parameter advising on the ENCODE65 set. Not all 31 parameter vectors are used, but more parameter settings are used when they are available. Only 4 of the set of 8 are used, as well as only 2 of the 4.

3.2.2 SRA

Our SRA dataset gives some insight into the improvement that can be gained in a high-throughput environment. It contains a large number of samples that have all been preprocessed in the same way with respect to the aligner. The advising ratio for the 1595 samples in SRA is shown in Figure 8 compared with the area under the curve for the transcriptome produced using the Scallop default parameter settings. Because, in general, the samples in SRA have a smaller initial area under the curve than those in Figure 6 (AUC values of 241.3 and 325.0 respectively), the median improvement is higher at 28.9%. For several samples in the set the AUC increases by more than a factor of 3. These improvements are also seen for the resource-limited advisor sets where the median improvement is 25.6%, 24.1% and 24.3% with 2, 4, and 8 parameter vectors, respectively. Notice that the increase in AUC actually goes down slightly when increasing the size from 2 to 4. This is likely an artifact of the reduced advisor sets not being subsets of each other. This means that the parameter vectors and sets may be slightly overfit to the training data.



(a) ENCODE65

(b) SRA

Figure 9: The horizontal axis shows labels of the parameter vectors from Supplemental Table 1 that produced the highest AUC transcriptome for any sample in the dataset. The vertical axis is the fraction of samples that have that parameter vector as the maximum. The four groups of bars show the use in the full set of 30 parameter vectors and the reduced sets of 2, 4, and 8 parameter vectors.

Figure 9b shows the frequency with which each of the 31, 8, 4, and 2 parameter vectors provides the maximum AUC when running parameter advising on the SRA set. More parameter vectors are used than were for ENCODE65, which is expected because the set of samples is larger, but because all of the examples in SRA were aligned using the same aligner many of the choices are maximal more frequently. Surprisingly, even though all of the examples are aligned using STAR, many of the higher-frequency parameter vectors were optimized for examples that were aligned using TopHat (IDs 1–10). Ties, if any existed, would be resolved in alphabetical order of the experiment name then aligner but no ties for the maximum AUC were found in SRA or ENCODE65.

3.3 Running time

As alluded to earlier, the wall time of running coordinate ascent is much larger than the running time of any single instance of Scallop. For the 30 examples from ENCODE10, running coordinate ascent took between about 40 hours and over 22 days. Since running Scallop using the default parameter vector for the same input takes between about 7 minutes and 1 hour, even if no parallelization was possible parameter advising would be able to run in a fraction of the time of running coordinate ascent.

3.4 Advising for StringTie

In order to show the generalizability of the method, we also applied it to the StringTie transcript assembler. As before, we ran coordinate ascent on the 10 experiments in ENCODE10, now using StringTie. We then show the utility of using the 30 parameter vectors to perform parameter advising on ENCODE65. Since StringTie has only 9 tunable parameters, the coordinate ascent time was much shorter, but the increase in accuracy was still observed. For the 30 coordinate ascent

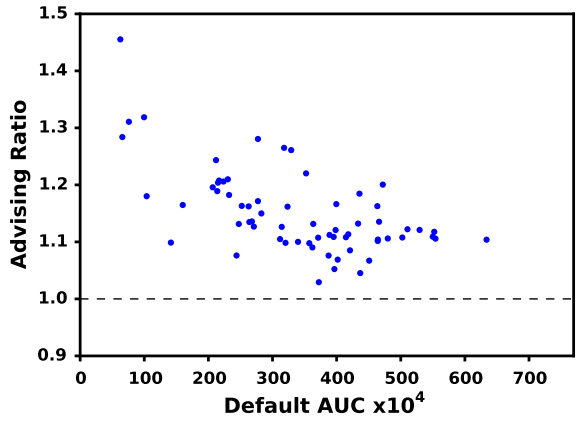


Figure 10: AUC improvement the ENCODE65 assemblies using StringTie. Each point is a single experiment positioned by the AUC of the default Scallop parameters (horizontal axis) and the ratio of the advised AUC over the default (vertical). A value above 1.0 indicates an improvement.

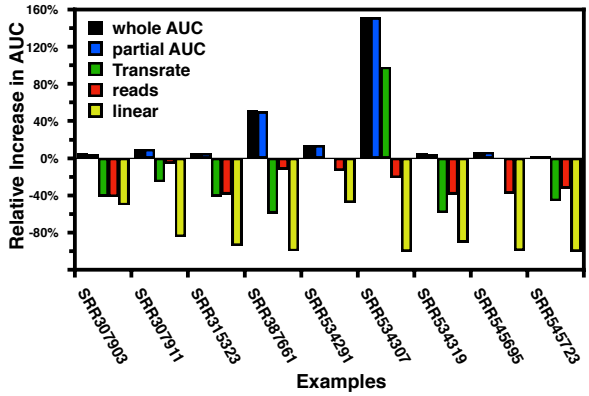


Figure 11: Relative increase in accuracy over default of using various transcript assembly metrics for coordinate ascent. The bars represent the difference in AUC between the optimal parameter choice for each metric and the defaults, normalized by the default AUC for each of the examples from ENCODE10.

runs, we saw a median increase in AUC of 12.2%. We also saw 10.0% increase in AUC on the similar leave-one-out experiments as those performed above. (StringTie parameter vectors and individual ENCODE10 AUC values are shown in Supplemental Tables 4 and 5 respectively.)

Figure 10 shows the advising ratio for the 65 RNA-Seq samples from ENCODE65. For these examples the median gain in AUC is 13.1% over using only the default parameter vectors. For the StringTie assembler, samples with lower AUC using the default parameter vectors still generally have higher advising ratios but this correlation is not as strong as with Scallop.

3.5 Justification on using AUC as the metric

AUC has been widely used to benchmark reference-based assemblers. However, the performance of AUC is theoretically bounded by the completeness of the reference transcriptome. By definition, all transcripts in a sample that do not map to the reference provide a reduction of AUC, even those that represent true novelty. To understand just how much novelty is being lost by using AUC as an optimization metric, we constructed a simulated dataset using the samples in ENCODE10. We restricted the "reference" transcriptome to be the collection of correctly annotated transcripts seen at any accepted parameter choice in coordinate ascent (we call this the "whole reference" which produces a "whole AUC"). Then, using a holdout set to simulate the reality where we do not know some of the transcripts, we produced a smaller subset of this reference (we call this the "partial reference" and in turn we can optimize the "partial AUC").

To determine the ideal metric for comparative transcriptome analysis, we systematically test several metrics and their ability to improve the assembly when being optimized. Since the true novelty in biological reads cannot be confirmed without biological verification, our approach is to create a new reference transcriptome ("partial reference") to be used in optimization from a collection of

transcripts that we know to be present in an experiment ("whole reference"). The whole reference is prepared by first running coordinate ascent and collecting every annotated transcript across parameter settings. From this, we sample transcripts with different probabilities, set according to their frequencies, to be maintained in the partial reference. Transcripts that are observed more often across parameters are more likely to be remained in the partial reference. The resulting partial reference closely resembles the actual reference transcriptome in a sense that it contains the majority of frequently encountered transcripts, while missing some that are rare. To measure and compare the quality of the optimal assemblies under different metrics, we provide only the partial reference in optimization, and check for the improvement by calculating AUC against whole reference (whole AUC). Metrics that we consider include a de-novo transcriptome assembly quality analysis tool (`TransRate` [20]), linear combination of feature functions that mainly capture coverage consistency and transcript confidence with learned weights using SVM (Linear Sum), and the number of reads mapped to the assembly (Num Reads).

Figure 11 shows the improvement of the parameter vectors found using coordinate ascent when optimizing whole AUC, partial AUC, and several *de novo* assembly metrics (which do not use the reference transcriptome) compared to the default `Scallop` parameter vector. The *de novo* metrics are `Transrate` [20], "number of reads" mapped to the transcriptome using `Salmon`, and a linear combination of the features from `Transrate`, number of reads, and other novel features combined as a weighted sum (labeled as "linear"). Whole AUC in this scenario is the ground truth since the method for construction guarantees that the selected reference contains all of the possible transcripts in the experiment and nothing else. Optimizing on partial AUC always finds parameter choices that recover more of the ground truth than the default. Notice that the amount improved by optimizing on whole AUC highlights the room for possible improvements, and partial AUC optimization reaches a value close to that maximum in all samples. For the other metrics, we see that after optimization there is often a decrease in accuracy with respect to the default. They are being lead astray by not incorporating the knowledge contained in the reference transcriptome.

4 Discussion

Our results show that sample-specific parameter vectors are essential to developing any strong genomic pipeline that includes transcriptome assembly as a step. In this work, we begin to answer the question of how to produce transcriptome assemblies effectively for any input without sacrificing quality or manpower. This is done using a combination of parameter tuning though exploration using coordinate ascent and the established method of parameter advising. Two key points that made this merger viable and distinguish transcriptome assembly from other domains are: (1) the insight that because the parameter landscape likely has few maxima, finding a suitable parameter set can be achieved by coordinate ascent rather than exhaustive enumeration, and (2) that a small, but representative, number of training examples is sufficient to provide a large increase in AUC over the default parameter setting.

One drawback of using a single example to find each parameter vector in the set is that coordinate ascent is going to overfit to the training examples. We have shown that even with this potential issue, we are able to greatly improve the quality of the transcripts produced according to the AUC measure. One extension to this method that could possibly improve the generalizability would be to perform coordinate ascent simultaneously on more than one sample.

Acknowledgements

The authors would like to thank the members of the Kingsford Group for their helpful comments through out this project, in particular Mingfu Shao, Jonathan King, Heewook Lee, and Guillaume Marçais.

Funding

This research is funded in part by the Gordon and Betty Moore Foundation's Data-Driven Discovery Initiative through Grant GBMF4554 to C.K., by the US National Institutes of Health (R01HG007104 and R01GM122935). This work was partially funded by The Shurl and Kay Curci Foundation and by the generosity of Eric and Wendy Schmidt by recommendation of the Schmidt Futures program.

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