title

2024-11-10

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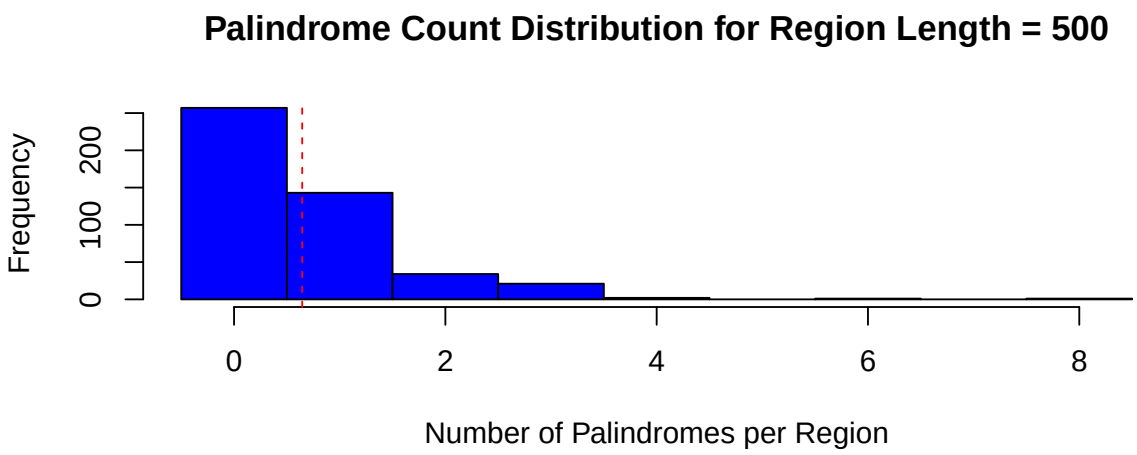
2.3 Palindrome Counts

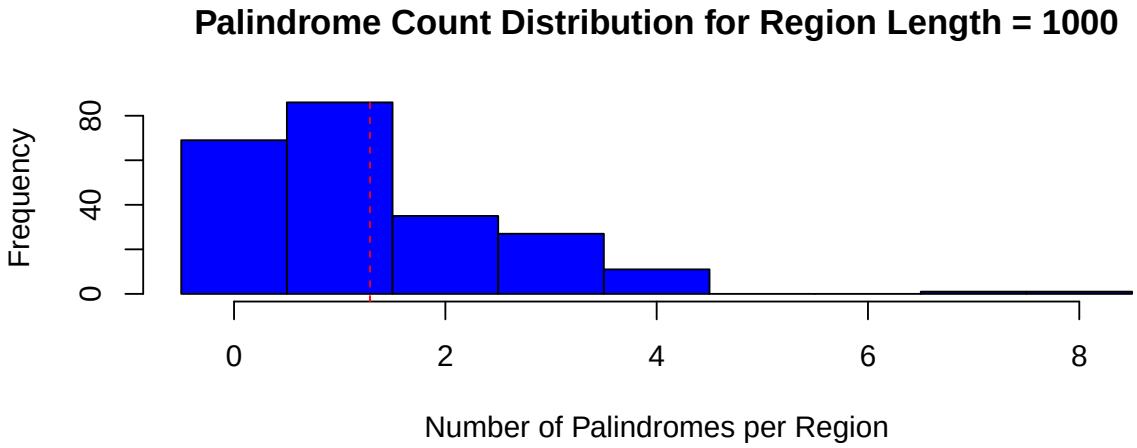
2.3.1 Methods

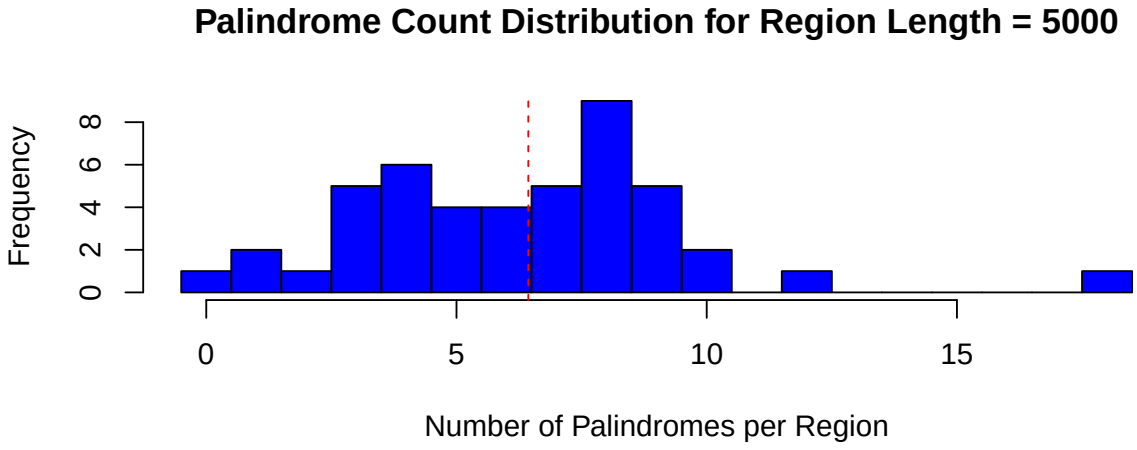
To examine palindrome counts in different regions of DNA, we split the DNA sequence into equal-length, non-overlapping regions, counted the palindromic sequences in each, and compared these counts to those expected from a uniform random scatter. To visualize the results, we graphed histograms to visualize the distribution of palindrome counts across regions. We then used Chi-Square Goodness of Fit Tests to compare observed palindrome counts to expected counts, testing the hypothesis of a uniform random distribution of palindromic sequences across regions.

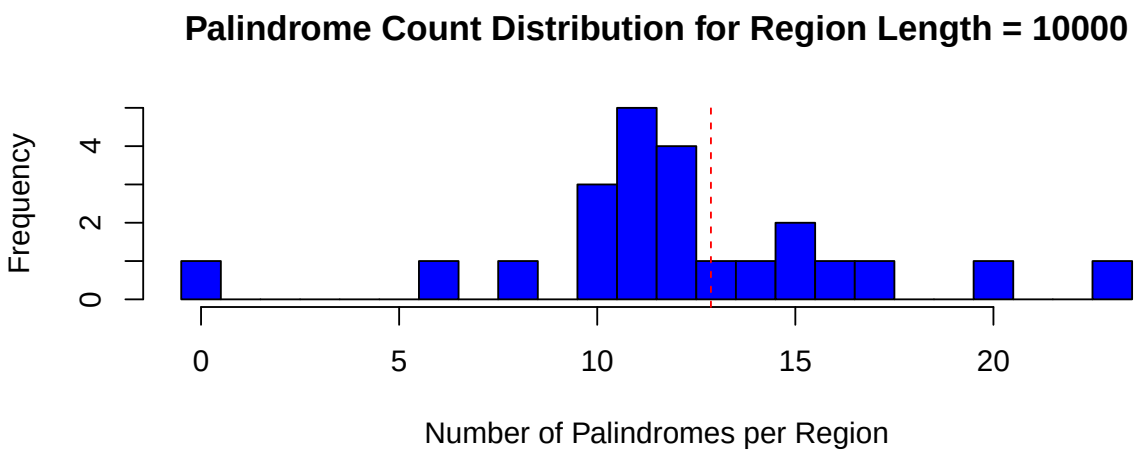
2.3.2 Analysis

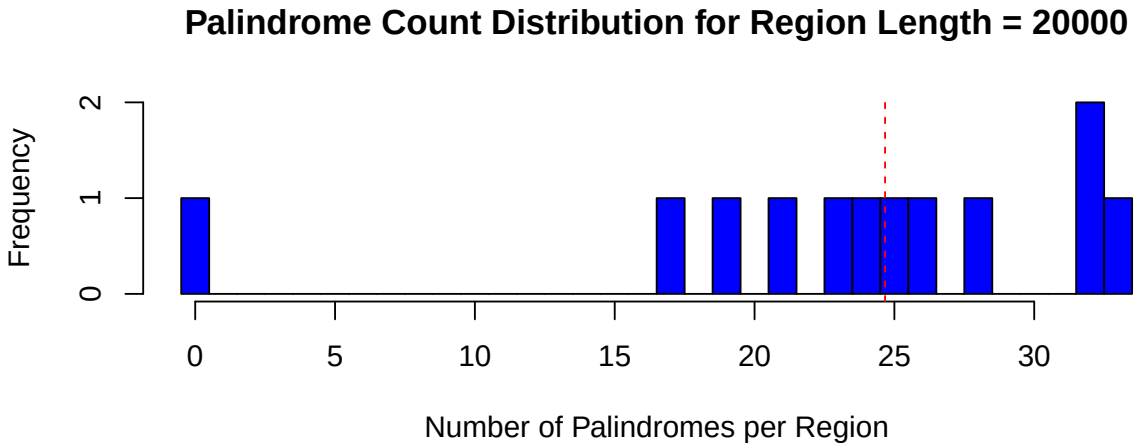
The histograms and Chi-Square Test results are shown below.


Palindrome Count Distribution for Region Length = 500
Frequency
0
100
200
0
2
4
6
8
Number of Palindromes per Region


Palindrome Count Distribution for Region Length = 1000
Frequency
0
40
80
0
2
4
6
8
Number of Palindromes per Region


Palindrome Count Distribution for Region Length = 5000
Frequency
0
2
4
6
8
0
5
10
15
Number of Palindromes per Region





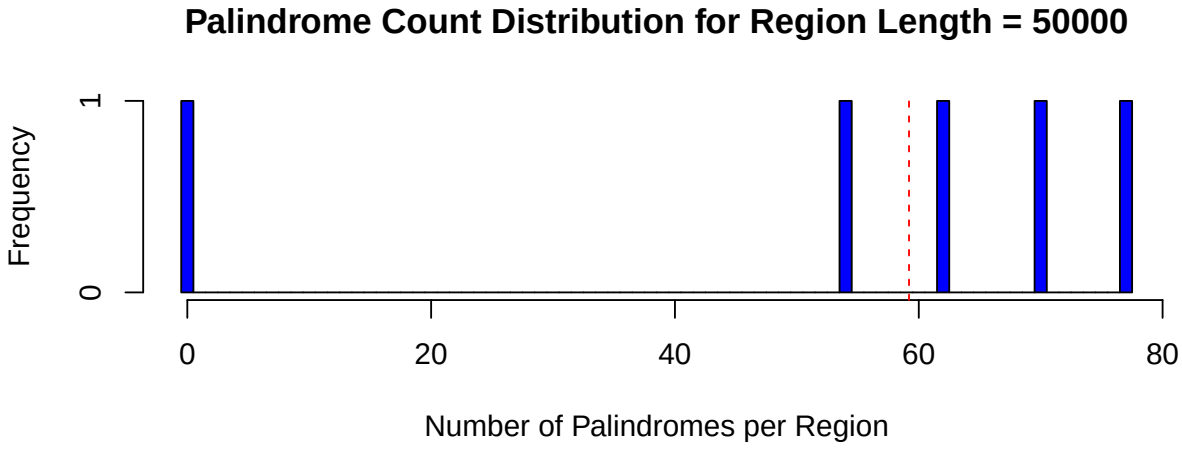


Table 1: Chi-Square Test Results

	Region.Length	Chi.Square.Statistic	p.value	Interpretation
X-squared	500	634.40541	0.0004998	Significant
X-squared1	1000	292.98649	0.0069965	Not Significant
X-squared2	5000	74.70242	0.0069965	Not Significant
X-squared3	10000	37.89286	0.0179910	Not Significant
X-squared4	20000	37.91429	0.0004998	Significant
X-squared5	50000	71.39163	0.0004998	Significant

2.3.3 Conclusion

The histograms of palindrome counts revealed that the smaller the region length, the more right skewed the count histogram was, which indicates that shorter regions have a higher frequency of intervals with low or zero palindrome counts, while a few regions have unusually high counts. This is consistent with the idea that smaller regions are more susceptible to variability in palindrome counts. Using a cut-off value of 0.001, the chi-square tests yield significant p-values for very small and very high region lengths, but insignificant p-values for middle region lengths. The significant result at region length 500 suggests that palindromic sequences are clustered in certain small regions rather than being uniformly scattered across the DNA. The non-significant results at the intermediate scales (region lengths 1,000, 5,000, and 10,000) imply that, when viewed at these sizes, the distribution of palindromic sequences appears more uniform. At these lengths, local clusters of palindromic sequences are likely averaged out, resulting in counts that are more consistent with a uniform random distribution. The significant results at region lengths 20,000 and 50,000 indicate that there are larger-scale structural or organizational patterns in the distribution of palindromic sequences across broad DNA segments.

2.4 The Biggest Cluster

2.4.1 Methods

We now want to investigate whether the interval with the highest number of palindromic sequences in a DNA sequence could suggest a potential origin of replication. To do this, we determined if a high-count palindrome cluster deviates significantly from a random scatter and whether such clusters align with features characteristic of origins of replication. Based on prior analysis, region lengths were selected to avoid both overly large and overly small intervals. Small intervals risk splitting clusters across adjacent regions, while large intervals may obscure tight clusters. For each interval, the number of palindromic sequences was counted, yielding a distribution of palindrome counts across intervals and the interval with the highest count of palindromic sequences was identified. Finally, Chi-square goodness of fit tests were applied to determine if the palindrome count in the highest-count interval deviates significantly from expected counts under a random distribution. Histograms were generated to visualize palindrome counts across intervals.

2.4.2 Analysis

The results of the Chi-Square Tests across different region lengths is shown below.

Table 2: Chi-Square Test Results

Region.Length	Max.Count	Max.Interval	Expected.Count	Chi.Square.p.value	Interpretation
500	8	186	0.6462882	0.0004998	Significant
1000	8	93	1.2925764	0.0024988	Not Significant
5000	18	19	6.5777778	0.0199900	Not Significant
10000	23	10	13.4545455	0.2773613	Not Significant

20000	33	5	26.9090909	0.3253373	Not Significant
50000	77	2	74.0000000	0.1949025	Not Significant

2.4.3 Conclusion

As shown in the table above, only the smallest region length (500) showed a significant p-value, while the larger region lengths (1000, 5000, 10000, 20000, and 50000) did not. This suggests that clustering of palindromic sequences exists on a small scale but not over broader intervals. The presence of a high number of palindromic sequences within an interval suggests non-random clustering, which may signal biological importance. Since the statistical analysis shows that the count in this interval is significantly higher than expected by chance, this could imply functional relevance, such as a replication origin.

2.5

2.5.1 Methods

2.5.2 Analysis

2.5.3 Conclusion

3. Advanced Analysis

3.1 Methods

3.2 Analysis

3.3 Conclusion

4. Discussion