Methods

- Explain about MSAT and the correction for msat by adding expected energies.

- Explain procedures for calculating correlation between abortive probabilities and RNA/DNA bond

- Procedure for calculating DNA/DNA bond and RNA/DNA+DNA/DNA bond.

- Procedure for correlating AP values to RNA/DNA bonds.

- Procedure for correlating AP values to NOTE: DNA/DNA bonds.

Results

DNA/DNA bonds

- DNA/DNA bond does not explain PY values (show lack of correlation for increasing ITR length for both physical and unphysical model).

RNA/DNA bonds

- Correlation exists between RNA/DNA bond of ITR and PY

- Correlation increases almost monotonically with increasing ITR-length.

  - The more information we have, the more we can explain

- Although correlation non-significant below nt 10, the near-monotinical increase is highly significant (probability of similar increase pattern occuring with random sequences is XXX)

- A 20nt RNA/DNA bond is unphysical. Calculation with physical RNA/DNA model (1,2), (1,3),..,(1,8/9),(2,9/10)..(11/12,20) revealed a similar correlation pattern.

- One plot of data with standard deviations. Suggestion: the best full ITR with E(energy) added after msat.

- Effect of outliers. N25/A1 big outlier. The rest not so bad.

- Correlation between purines and binding energy, show ladder. Show mean and stadard deviation for 43 runs of random sequences with normal distribution figure :).

RNA/DNA+DNA/DNA

- Elongation models use a sum of RNA/DNA and DNA/DNA energies (++). A kinetic model of translation initiaton did the same. No correlation is found with both unphysical and physical methods.

Abortive probabilities

- AP values in general do not correlate with RNA/DNA values

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- However, looking at max/min AP, correlation was found.

Discussion

- Hopothesis that DNA/DNA energies control abortive initiation. No role was found.

- Hypothesis that AP-values can be predicted. In general no, except for the most extreme.

- Intrestingly results are in some cases better without correcting for msat, but within the standard deviation as calculated by putting random sequences after msat.

- Outliers: N25/A1 a naturally evolved promoter.

- Correlation found for max/min AP. Could be a result of large experimental errors, thus the incentive for max/min values.

- Argue that the energy-purine correlation is nothing outside what would be expected from random sequences. This shows that the string (0.77) purine-PY correlation in the data acts through a mechanism different from RNA/DNA bonds. What would have been the case if the RNA-purine link had been significantly larger/smaller than 0.31????