Research Article

Exploratory Bioinformatics Study of IncRNAs in Alzheimer’s Disease mRNA Sequences with Application to Drug Development

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Long noncoding RNA (lncRNA) within mRNA sequences of Alzheimer’s disease genes, namely, APP, APOE, PSEN1, and PSEN2, has been analyzed using fractal dimension (FD) computation and correlation analysis. We examined lncRNA by comparing mRNA FD to corresponding coding DNA sequences (CDSs) FD. APP, APOE, and PSEN1 CDSs select slightly higher FDs compared to the mRNA, while PSEN2 CDSs FDs are lower. The correlation coefficient for these sequences is 0.969. A comparative study of differentially expressed MAPK signaling pathway lncRNAs in pancreatic cancer cells shows a correlation of 0.771. Selection of higher FD CDSs could indicate interaction of Alzheimer’s gene products APP, APOE, and PSEN1. Including hypocretin sequences (where all CDSs have higher fractal dimensions than mRNA) in the APP, APOE, and PSEN1 sequence analyses improves correlation, but the inclusion of erythropoietin (where all CDSs have higher FD than mRNA) would suppress correlation, suggesting that HCRT, a hypothalamus neurotransmitter related to the wake/sleep cycle, might be better when compared to EPO, a glycoprotein hormone, for targeting Alzheimer’s disease drug development. Fractal dimension and entropy correlation have provided supporting evidence, consistent with evolutionary studies, for using a zebrafish model together with a mouse model, in HCRT drug development.

1. Introduction

The instructions of a genetic sequence are carried by the fluctuations or variations in the nucleotide bases along the sequence. The bioinformatics of a sequence can be studied if the sequence is modeled as a series based on the nucleotide atomic number of the nucleotides A, T, C, and G. A recent study on such fluctuation in the FOXP2 gene pathway has been reported [1]. The fractal dimension and the Shannon entropy were found to have a negative correlation ($R^2 = 0.85, N = 12$) for the FOXP2 regulated "accelerated conserved-non-coding" sequences in human fetal brain. In general, fractal dimension and the Shannon entropy generate a 2D map representing a set of genetic sequences. For example, using the human Y chromosome, which contains 429 genetic sequences according to the http://ncbi.nlm.nih.gov/mapview/ database, the listed sequences have fractal dimension values from 1.92 to 2.06 and the Shannon dinucleotide entropy from 3.0 to 3.8 bits per base. Fractal dimension, being a nucleotide position sensitive measure, would be related to the richness in the embedded informatics associated with the sequence. In terms of transcription and translation, fractal dimension may be related to a docking energy parameter with similarity to the concept of roughness in a zipper and assembly traffic analogy for the docking interactions. In addition to CDS, mRNA sequences are often embedded with intronic regions. Noncoding RNA sequence with more than 200 base pair in length has been used to label a long non-coding RNA (lncRNA) regardless of intronic or intergenic in origin. This project uses fractal dimension of mRNA and coding DNA sequences (CDS) to probe the IncRNAs within the mRNAs (but not the CDS) in Alzheimer’s disease genes, namely, APP or AD1, APOE or AD2, PSEN1 or AD3, and PSEN2
or AD4. The IncRNA sequences have been shown to be involved in significant regulatory functions. The IncRNA SPRY4-IT1 sequence was reported to have migrated to the cytoplasm, and upregulation was observed in melanoma cells [2]. Differential expressions in IncRNA upon radiation of HeLa and MCF-7 cells and in glioblastoma pathogenesis have been reported [3, 4]. The IncRNA relationship to cellular genetic stability has been reported in the mouse model [5]. Microarray data analysis linked IncRNA to Huntington's disease [6], and the IncRNA role in neurological disorders and cancers has been reviewed [7, 8]. The IncRNAs becoming a new cancer diagnostic and therapeutic gold mine have been postulated [9]. Despite all these activities, only a few computation analysis results on the IncRNAs have been reported to our knowledge. A comparative study of IncRNAs with 3′ untranslated regions (3′ UTRs) in protein coding RNA sequences has revealed parallel structure in the studied sequences, consistent with the presence of similar evolutionary constraints [10].

This project focuses on the study of disease related genetic sequences. The IncRNAs within the mRNAs sequences in Alzheimer’s disease genes, namely, APP or AD1, APOE or AD2, PSEN1 or AD3, and PSEN2 or AD4, have been analyzed in terms of fractal dimension computation and correlation analysis. The exploratory hypothesis that the IncRNA sequences embedded in a transcribed mRNA sequence would exhibit correlation in Alzheimer’s disease genes has been studied in a comparative fractal dimension model of mRNA sequences versus coding DNA sequences (CDSs), which do not include the IncRNA sequences.

2. Materials and Methods

The data used in this study was downloaded from GenBank according to the following Gen-ID numbers. The studied human genes are APP-Gen-ID-351 containing 10 mRNA variants, APOE-Gen-ID-348, PSEN1-Gen-ID-5663 having 2 mRNA variants, PSEN2-Gen-ID-5664 having two mRNA variants, HCRT-Gen-ID-3060, HCRTR1-Gen-ID-3061 (HCRT Receptor-1), HCRTR2-Gen-ID-3062 (HCRT Receptor-2), EPO-Gen-ID-2056, and EPOR-Gen-ID-2057. The MAPK signaling pathway gene accession numbers have been listed in the report of differential expression of long non-coding intronic RNAs in pancreatic cancer cells [11]. The Allen Brain Atlas database has been accessed at http://brain-map.org.

A sequence with a relatively low nucleotide variety would have low Shannon’s entropy (more constraints) in terms of the set of 16 possible dinucleotide pairs. A sequence’s entropy can be computed as the sum of $p_i \log(p_i)$ over all states $i$, and the probability $p_i$ can be obtained from the empirical histogram of the 16 di-nucleotide pairs. The maximum entropy is 4 binary bits per pair for 16 possibilities ($2^4$). For mono-nucleotide consideration, the maximum entropy is two bits per mononucleotide with four possibilities ($2^2$). In general, the monoentropy is proportional to di-nucleotide entropy with $R^2 > 0.75$ for the reported sequences in the paper.

Roughly speaking, fractal dimension measures the complexity of a self-similar sequence. For a 1D sequence such as a DNA sequence, a fractal dimension near 2 indicates great complexity, while one closer to 1 would indicate little complexity, variety, or information. Among the various fractal dimension methods, the Higuchi fractal method is well suited for studying signal fluctuation [12]. A random spatial series with equal spatial steps can be modeled as a brightness signal in time such that the time series analysis tools can be used for spatial series analysis. The spatial intensity (Int) random series with equal intervals could be used to generate a difference series $(\text{Int}(j) - \text{Int}(i))$ for different lags in the spatial variable. The nonnormalized apparent length of the spatial series curve is simply $L(k) = \Sigma(\text{Int}(j) - \text{Int}(i))$ where the sum is for all pairs where $j-i = k$. The number of terms in a $k$-series varies, and normalization must be used to get the series length. If the Int$(i)$ is a fractal function, then the $\log(L(k))$ versus $\log(1/k)$ should be a straight line with the slope equal to the fractal dimension. Higuchi incorporated a calibration division step such that the maximum theoretical value is calibrated to the topological value of 2. The details of the calculation method are given in the literature [12]. Numerical examples of the fractal dimension computation can be found in our earlier reports [13, 14]. For clarity, a Matlab implementation of the algorithm we used is listed below. “data” is an array loaded with the input sequences (one in each column), “width” is the number of sequences loaded in the data array. “max K” is cutoff for the maximum distance between $j-i$ pairs. A max K of 7 was used for this paper, although other values for max K gave very similar results.

Consider

- % calculate Length vectors for each column
- $L = \text{zeros}(\text{max } K, \text{width});$
- for $k = 1 : \text{max } K,$
- data2 = circshift(data, k);
- data2 = abs(data2 – data);
- data2 (1 : k ; :) = 0; % remove end effects
- $L(k,:) = \text{sum}(\text{data2})/k/k \ast (\text{height} - 1)/(\text{height} - k);$  
- end

- % calculate slopes (FDs)
- slope = zeros(1, width);
- for $i = 1 : \text{width},$
- temp = 1 : 1 : \text{max } K;
- $\log k = \log (1./\text{temp})’;$
- $X = [\text{ones(size(log } k)) \log k] ;$
- $Y = \log(L(:,i));$
- $a = X \setminus Y;$
- $\text{FD}(i) = a(2);$  
- End
The sequence GenBank accession numbers have been listed in [11].

The correlation with $y$ Series1). The correlation resultssuggestahypothesiswhereHCRT, a neurotransmitter only produced in the hypothalamus and carriers, an accepted hallmark for Alzheimer's disease [16]. The inclusion of hypocretin sequences (where all CDSs have higher fractal dimension values than mRNAs in HCRT, HCRT-R1, and HCRT-R2) in the APP, APOE, and PSEN1 sequence analysis would improve the correlation ($R^2 = 0.985, N = 16$) as shown in Figure 3. Erythropoietin EPO has been shown to have interaction with dopamine pathways [17–19] and offer protection for neuronal injury [20, 21]. The inclusion of erythropoietin (where all CDSs have higher dimension than mRNA in EPO and EPOR) in the correlation of APP, APOE, and PSEN1 would suppress the correlation ($R^2 = 0.953, N = 15$).

Figure 1: The fractal dimension correlation of the APP, APOE, PSEN1, and PSEN2 CDSs versus mRNAs in Alzheimer’s disease is displayed with $R^2$ of 0.969 ($N = 15$ Series1). The y-axis represents the fractal dimension (FD) of the CDSs, and the x-axis represents the FD of the mRNAs. Deletion of PSEN2 Variant 1 (1.9793, 1.9748) and Variant 2 (1.9791, 1.9743) where CDSs have lower fractal dimension values as compared to the mRNA sequences, which would give $R^2$ of 0.979, $N = 13$.

Figure 2: The fractal dimension correlation of the differentially expressed MAPK signaling pathway long non-coding intronic RNA in pancreatic cancer cells is displayed in Figure 2 with a correlation of $R^2 = 0.78$ in the studied Alzheimer’s disease sequences. An negative ratio of CDS length to mRNA length ranges from 0.23 to 3. Results of Fractal Analysis in pancreatic cancer cells with a correlation of expressed MAPK signaling pathway long non-coding intronic RNA

$\text{CDSs could be indicative of certain characteristic interaction of the Alzheimer’s gene products APP, APOE, and PSEN1 where a correlation with } R^2 \text{ of } 0.979 \text{ (} N = 13 \text{)} \text{ was obtained. Hypocretin (orexin) loss in Alzheimer’s disease patients has been reported [15]. A brain scan study on a group of young adults has revealed } 1/3 \text{ of them are PSEN1 E280A mutation carriers, an accepted hallmark for Alzheimer's disease [16]. The inclusion of hypocretin sequences (where all CDSs have higher fractal dimension values than mRNAs in HCRT, HCRT-R1, and HCRT-R2) in the APP, APOE, and PSEN1 sequence analysis would improve the correlation (} R^2 = 0.985, N = 16 \text{) as shown in Figure 3. Erythropoietin EPO has been shown to have interaction with dopamine pathways [17–19] and offer protection for neuronal injury [20, 21]. The inclusion of erythropoietin (where all CDSs have higher dimension than mRNA in EPO and EPOR) in the correlation of APP, APOE, and PSEN1 would suppress the correlation (} R^2 = 0.953, N = 15 \text{).}

4. Discussion

The regression intercepts in Figures 1, 2, and 3 are negative, while the slopes are all greater than 1. This indicates selection pressure driving up CDS fractal dimension or a selection pressure against high FD in lncRNA. Whether the negative intercept value would suggest a minimum fractal dimension threshold in mRNA for containing a functional CDS in the studied set of Alzheimer’s disease genes needs further investigation. The exploratory hypothesis that the lncRNA sequences embedded in the transcribed mRNAs would exhibit correlation in Alzheimer’s disease genes receives supporting evidence in a comparative fractal dimension model of mRNA sequences versus coding DNA sequences (CDSs).

The correlation results suggest a hypothesis where HCRT, a neurotransmitter only produced in the hypothalamus and related to the wake/sleep cycle, could be a relatively more...
Figure 3: The fractal dimension correlation of the APP, APOE, PSEN1, HCRT, HCRT-R1, and HCRT-R2 CDSs versus mRNAs in Alzheimer’s disease is displayed with $R^2$ of 0.985 ($N = 16$ Series1). The $y$-axis represents the fractal dimension (FD) of the CDSs, and the $x$-axis represents the FD of the mRNAs.

Figure 4: HCRT Receptor-2 expression level distribution in the brain regions (168 regions for each patient) using the 4-patient data from Allen Brain Atlas. The expression level $z$-score values are displayed in the $x$-axis. The displayed line is used as a visual guide. The Skewness of the distribution has been computed to be $= 0.91$.

Figure 5: EPO Receptor expression level distribution in the brain regions (168 regions for each patient) using the 4-patient data from Allen Brain Atlas. The expression level $z$-score values are displayed in the $x$-axis. The displayed line is used as a visual guide. The Skewness of the distribution has been computed to be $= 0.04$.

Figure 6: HCRT expression level distribution in the brain regions (168 regions for each patient) using the 4-patient data from Allen Brain Atlas. The expression level $z$-score values are displayed in the $x$-axis. The displayed line is used as a visual guide. The Skewness of the distribution has been computed to be $= 2.2$.

Figure 7: EPO expression level distribution in the brain regions (168 regions for each patient) using the 4-patient data from Allen Brain Atlas. The expression level $z$-score values are displayed in the $x$-axis. The displayed line is used as a visual guide. The Skewness of the distribution has been computed to be $= 1.1$.

important candidate as a blocker or promoter when compared to EPO, a glycoprotein hormone produced by kidney and liver, for targeting drug development with application to Alzheimer’s disease clinical trials. The HCRT hypothesis would be consistent with MRI brain scans (168 regions) containing microarray array expression level data from the Allen Brain Atlas database. The brain scan data analysis has showed higher Skewness value in HCRT Receptor-2 expression level distribution (Figure 4) in the brain as compared to EPO Receptor distribution (Figure 5). The reasoning follows the fact that hypocretin Receptor expression level distribution would have a positive long tail representing high expression level and high demand for HCRT in the brain as compared to EPO receptor expression level distribution. The Skewness value would be 0.91 for HCRT Receptor-2 (Figure 4) versus 0.04 for EPO Receptor (Figure 5), a factor difference of about 20. The HCRT and EPO expression level distributions in the brain are displayed in Figures 6 and 7, respectively. The Skewness value would be 2.2 for HCRT (Figure 6) versus 1.1 for EPO (Figure 7), a factor difference of about 2. The large factor difference in receptor expression level in the brain would influence the selection of targeted receptors in drug development.
Mouse model has become a popular choice in drug development since evolution has been a cornerstone for the understanding of biology. A plot of fractal dimension versus entropy for HCRT CDSs in human, mouse, and zebrafish is displayed in Figure 8 with an adjusted $R^2$ of 0.9996, and rat HCRT CDS would be viewed as an outlier (square) from the regression analysis of human (lowest fractal dimension), mouse and zebrafish (highest fractal dimension). GenBank information: mouse Mus musculus HCRT has Gen-ID-15171, rat Rattus norvegicus HCRT has Gen-ID-25723, and zebrafish Danio rerio HCRT has Gen-ID-613239.

Could serve as a starting platform with UV Circular Dichroism and Synchrotron based X-ray absorption spectroscopy structural data [22]. In any event, when a fractal dimension entropy map is used as a tool for evolutionary pressure study beyond simple classification, a strong correlation would lend quantitative support to the choice of mouse model and zebrafish model in HCRT drug development. Extension of fractal dimension computation and correlation analysis to the recently published dataset of expressed lncRNAs in zebrafish embryogenesis would help HCRT drug development [23].

Recently the R47H variant of TREM2 was reported to be associated with Late-onset Alzheimer’s disease (LOAD) [24, 25]. The human TREM2 is known as an innate immune receptor and signals through TYROBP (agonist with 4 mRNA variants and 4 CDS variants) to clear the damaged tissue and reduce inflammation. The fractal dimension computation and correlation is displayed in Figure 10 with $R^2 = 0.999, N = 5$. The BLASTN comparison of TREM2 (lowest left corner data point in Figure 10) shows $E = 0.11$, given a CDS of 693-nucleotide sequence versus a 366-nucleotide sequence within the mRNA obtained by adding the beginning and ending non-coding region together. Similar BLASTN comparison of TYROBP Variant 1 (uppermost right corner data point in Figure 10) had returned a null result, given a CDS of 342-nucleotide sequence versus a 266-nucleotide sequence within the mRNA obtained as described.
Variants 1

Variant 1 has the highest fractal dimension and TYROBP-Variant TREM2, and APOE would give similar correlation analysis on the mouse and Bos taurus TYROBP, 0.9993 on set Alzheimer’s disease.

The fractal dimension is represented on the $x$-axis, and the TREM2 CDSs involved in Late-onset Alzheimer’s disease in human. The fractal dimension is represented on the $y$-axis. TYROBP-Variant 1 has the highest fractal dimension and TYROBP-Variant 2 has the second lowest fractal dimension, and TREM2 has the lowest fractal dimension. Inclusion of APOE (2.0382, 1.8673) would suppress $R^2$ to 0.32.

As [24] pointed out, the apolipoprotein E (APOE) malfunction still remains as the most important sequence variant that would be risk of Late-onset Alzheimer’s disease. The inclusion of APOE in Figure 10 would give $R^2$ of 0.9993 ($N = 6$), suggesting a very stringent regulation in selecting CDSs from mRNAs in the studied LOAD sequences. For comparison, similar correlation analysis on the mouse and Bos taurus TYROBP, TREM2, and APOE would give $R^2$ values of 0.89 ($N = 3$), and 0.45 ($N = 3$) respectively. The BLASTN comparison of human APOE had returned $E = 0.11$, given a CDS of 954-nucleotide sequence versus a 269-nucleotide sequence within the mRNA obtained by adding the beginning and ending non-coding regions together. The inclusion of HCRT and EPO informatics would suppress the correlation to $R^2$ values of 0.973 ($N = 9$) and 0.927 ($N = 8$), respectively, suggesting that HCRT drugs could be a better choice for treating Late-onset Alzheimer’s disease as compared to EPO drugs. The inclusion of APOE would give $R^2$ of 0.32 in the entropy versus fractal dimension graph in Figure 11. The APOE sequence has the lowest entropy among the studied sequences, and all CDSs have lower entropy than mRNAs in the Late-onset Alzheimer’s disease studied sequences. The APOE mononucleotide entropy of 1.8673 would suppress very slightly the mono-nucleotide correlation of mRNA versus CDS in Late-onset Alzheimer’s disease studied sequences from $R^2$ of 0.9948 ($N = 5$) to 0.9944 ($N = 6$). The Late-onset Alzheimer’s disease studied mRNAs and CDSs show very high correlation in fractal dimension ($R^2$ of 0.999) and entropy ($R^2$ of 0.994), consistent with a Late-onset Alzheimer’s disease IncRNA hypothesis of high fractal dimension satisfied by low entropy in CDSs selection by deleting the IncRNAs with low entropy values about 1.91 except for TREM2 IncRNA having 1.995 bits per nucleotide type.

High correlation results are also observed in two other neurodegenerative disease involving TYROBP. The Nasu-Hakola disease, a disorder affecting both brain and bone, is known to be related to the malfunctioning of TREM2 or TYROBP [26]. The CSF1R (a microglial receptor) where malfunctioning is associated with a corticobasal syndrome called hereditary diffuse leukoencephalopathy with spheroids was reported to be cosignaling with TYROBP [27]. The addition of CSF1R in Figure 10 would reduce the correlation from 0.999 ($N = 5$) to 0.992 ($N = 6$). The exploratory study of noncoding RNA by comparing mRNA versus CDS informatics has revealed regularity. An examination of Figure 1 with $R^2 0.969$ ($N = 15$) and Figure 10 with $R^2 0.999$ ($N = 6$ including APOE) would suggest that the noncoding RNA assembly process in Late-onset Alzheimer’s disease would involve relatively highly systematic process or
processes as compared to familial early-onset Alzheimer’s disease with APP, PSEN1, PSEN2, and APOE. The project has used $R^2$ differences in the order of 0.02 to be the demarcation in the lncRNA investigation by comparing mRNAs versus CDSs in a cluster of disease related sequences. The mRNA versus CDS informatics comparative method could be a supplement to the well-accepted BLAST method. Further investigations using fractal analysis for neurodegenerative disease sequences and currently targeted receptors would be productive.

5. Conclusions

The long noncoding RNAs (lncRNAs) within the mRNA sequences in Alzheimer’s disease genes, namely, APP, APOE, PSEN1, and PSEN2, have been analyzed in terms of fractal dimension computation and correlation analysis. The results show that APP, APOE, and PSEN1 CDSs select slightly higher fractal dimensions as compared to the mRNA sequences with a pattern evidenced by correlation coefficient of $R^2 = 0.979$ ($N = 13$ including variants). Inclusion of the 2 variants in PSEN2 where CDSs have lower fractal dimension values than mRNAs would yield $R^2$ of 0.969 ($N = 15$). The systematic selection of higher fractal dimension CDSs could be indicative of characteristic interaction of Alzheimer’s gene products APP, APOE, and PSEN1. The inclusion of hypocretin sequences would improve the correlation ($R^2 = 0.985$, $N = 16$) but inclusion of erythropoietin would suppress the correlation ($R^2 = 0.953$, $N = 15$), suggesting that HCRT could be a relatively more important candidate as a blocker or promoter when compared to EPO for targeting in drug development with application to Alzheimer’s disease clinical trials. The HCRT hypothesis would be consistent with MRI brain scan containing microarray expression level data from the Allen Brain Atlas database that shows higher Skewness value in HCRT receptor expression level distribution as compared to EPO receptor expression level distribution in the brain. Study of sequence fractal dimension and entropy correlation has provided quantitative supporting evidence, consistent with evolutionary studies, for using zebrafish model together with mouse model, in HCRT drug development. The TREM2 and TYROBP mRNAs reported recently in Late-onset Alzheimer’s disease also yield a correlation of $R^2$ of 0.999 ($N = 6$) using similar informatics analysis, but HCRT informatics inclusion would suppress the correlation slightly as compared to the EPO informatics inclusion.

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