## Lecture No. 6 Information Theory

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- Information: Knowledge or intelligence communicated, received or gained.
- Information Theory: Indication of number of possible choice.
- Information theory deals with transmission of messages.
- Sequence data can be thought of as messages.
- Bits units: From information theory, a bit denotes the amount of information required to distinguish between two likely possibilities.
- Bit, the minimal amount of structural complexity needed to encode a given piece of information.
- The number of bits of information, $N$ required to convey a message that has $M$ possibilities is:

$$
\log _{2} M=N \text { bits }
$$

- Consider a number 1224 an equivalent 12 digit binary number made of $\{0,1\}$ is 010011001000
$0+1024+0+0+128+64+0+0+$ $8+0+0+0$
Here each residue is one bit of information.
- A sequence of 0's and 1's or any sequence of any alphabet or symbols need not represent a number. It may just be a code that needs to be translated into some action.
- How many bits of information there are in a sequence of given length composed of symbols drawn from a chosen alphabet. E.g., $\{A, G, C, T\}$.
- A number of bits of information in a sequence of length 12 with symbol $\{0,1\}$ is exactly 12.
- The RNA alphabet is $\{A, G, C, U\}$. There are $4^{12}$ words of length 12 that can be formed from these 4 letter alphabet.
- On the assumption each letter occurs in nature with equal probability ( $p=0.25$ ), the information content associated with such a word
$\log _{2}\left(4^{12}\right)=\log _{2}\left(2^{24}\right)=24$ bits
- Actual genetic instructions arise from the 20-letter amino acid code, each letter of which is associated with an ordered triple from the RNA alphabet.
- Since there are $4^{3}=64$ residue triples from the alphabet $\{\mathrm{A}, \mathrm{G}, \mathrm{C}, \mathrm{U}\}$.Information in an amino acid gene word of length 4 is

$$
\log _{2}\left(20^{4}\right)=17.3
$$

This is only true if each of the letter occurs with equal probability ( $p=1 / 20$ ), which they do not. There are reasons for this:
1). Some amino acids are coded for by more triples than others.
2). Some amino acids are biologically more important than others.

- In a perfect world every symbol in a alphabet occurs with equal probability. In this way the information content is maximized.
1). Example Suppose two sequence symbols $\{0,1\}$ with equal probability for each symbol to occur, i.e., $P_{0}=P_{1}=.5$. In this case each residue is one bit. Thus equal probability yield one bit/residuemaximum.
2). Example Suppose $P_{0}=1$ and $P_{1}=0$ The information for each residue in this case is zero bit.
Probabilities of 0's and 1 yield zero bits/residue-minimum.
5). What if $p_{0}=0.8$ and $p_{1}=0.2$. In this case number of bits/residue is between one and zero. In particular it is:
$-\left[0.8 \log _{2}(0.8)+0.2 \log _{2}(0.2)\right]=0.722$
- The information/residue of $n$ letters alphabet, such that the probability that the ith letter will appear in any given residue is $p_{i}$ is:

$$
H=-\sum_{i=1}^{n} P_{i} \log _{2} p_{i}
$$

Where $H=$ Entropy
It is a measure of disorder.

- Example: If all the $p_{i}$ 's are the same, i.e., $P_{i}=1 / n$ for $i=1,2, \ldots, n$, then

$$
\begin{aligned}
H & =-\sum_{i=1}^{n} 1 / n \log _{2}(1 / n) \\
& =-\log _{2}(1 / n) \\
& =\log _{2} n
\end{aligned}
$$

- Example: The nucleotide alphabet contains 4 symbols with probability $1 / 4$, has Entropy

$$
H=\log _{2} 4=2
$$

i.e., average information content $=2$ for random DNA.
i.e., the bits/residue is 2 . We need to ask two (yes/no) questions to determine a base $A$ or $G$ to match the column to a position in a test sequence.
A nucleotide string of length 900 is equivalent to 1800 bits which can code for $4^{900}=2^{1800}$.

- Calculating log base 2

$$
\log _{2} a=\frac{\log _{z} a}{\log _{z} 2}
$$

where $z=$ any base

$$
\begin{aligned}
\log _{2} a & =\frac{\log _{1} 0 a}{\log _{10} a} \\
\log _{2} a & =3.32 \log _{10} a
\end{aligned}
$$

- How does the amount of information change after we have more information? This is considered a decrease in uncertainty.

$$
\text { Information }=H_{\text {before }}-H_{\text {after }}
$$

$$
\text { Random DNA }=H_{\text {before }}
$$

$$
=2
$$

- Example: If we note that one region has $P_{A}=0.7, p_{G}=0.4$ then

$$
\begin{aligned}
H_{\text {after }} & =-.7 \log _{2} .7-.3 \log _{2} .3 \\
& =0.88 \text { bits } \\
\text { Information } & =2-0.88 \\
& =1.12 \text { bits }
\end{aligned}
$$

This is an increase in information content.

