

Lecture - 12a
Hydrophobicity profiles

In this lecture, we will mainly discuss about the construction of hydrophobicity profiles and the applications. Earlier we discussed all different types of applications of these amino acid sequences. So, what are the various parameters or features or properties we discussed in the previous class?

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Refresh

Amino acid occurrence

Composition

Molecular weight

Residue pair preference

Applications

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Student: So, amino acid composition.

Amino acid occurrence, amino acid composition.

Student: Molecular weight.

Molecular weight, pair preference and so on. So, what is amino acid occurrence?

Student: So, number of time.

It is essentially.

Student: Occurrence.

Number of times each amino acid occurs in a protein sequence, then composition.

Student: Normalized

Normalized with the chain length. So, a difference between amino acid occurrence and composition is normalization with the number of residues in a sequence. Then we discussed about molecular weight. So, you can calculate the molecular weight?

Student: Hm.

By substituting appropriate weight for each amino acid residues and subtracted with.

Student: water.

The water molecules, $18(N-1)$ water molecules, because when you form peptide bonds, it's elimination of one water molecule. Then we discussed about the pair preference, how far the residues occur next to each other: A with A, A with D and so on. Then we will discuss about couple more applications. One major application we discussed, is how to distinguish between different types of proteins. We have proteins, with different functions, we have different structures. So, whether it is possible to distinguish between these 2 types of proteins based on the amino acid sequence information.

So, we discussed based on the parameter or based on the property, amino acid composition, we used amino acid composition for the 2 sets of proteins and for unknown ones, we compared with the known ones, and then we decide depending upon the deviation. We can also do with the correlation the also we can use different properties. So, also we discussed about the amino acid properties for a average property for any given sequence, each amino acid have the unique values. So, add up together normalized with the chain length, that will give the average amino acid property values.

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Hydrophobicity profile

Hydrophobicity profile is simply the plot of the hydrophobicity indices of the residues against their sequence numbers.

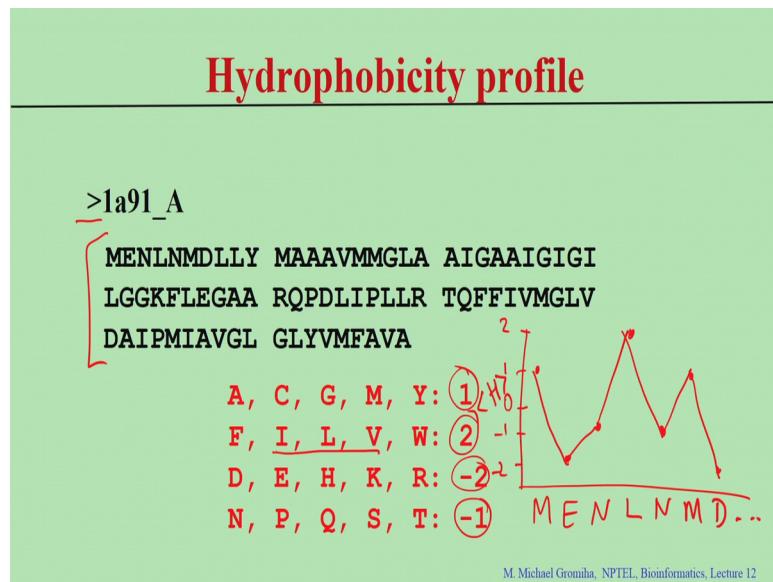
E.g. SAMPLEDATAWITHHYDINDICES

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So, now what is hydrophobicity profile? Because name itself tells, it is the plot of the hydrophobicity indices versus amino acid sequence. For example, if you take any protein sequence. So, we can make a 2D pot. So, X axis, we give about the amino acid sequence. Y axis - you write the hydrophobicity. Each amino acid has a value, depending upon the hydrophobic character of the residues.

So, depending among the amino acid sequence, the residues in the sequence, we can make a plot for each value. When you connect then we will get a plot. So, we will see how to construct a plot with an example.

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We have the sequence, for example; this is the amino acid sequence in which format?

Student: Fasta format.

Fasta format because you can say they started with the > symbol, here we have the amino acid sequence. So, I made some numbers for the 20 amino acid residues, based upon their hydrophobic behavior. For example, if you take the highly hydrophobic residues like isoleucine, valine, leucine, phenylalanine, I put value of 2 and less hydrophobic, I put the value of 1, and the polar residues I give -1 and the charge residues I give value of -2.

So, now you take the amino acid residues versus these hydrophobic indices, what is a hydrophobicity profile? It is a plot connecting?

Student: Sequence.

A sequence versus the values right. So, here what is the sequence?

Student: M.

M.

Student: E.

E.

Student: N.

NL.

Student: N.

N M D and so on right. So, here you can put the hydrophobicity value. So, first one is M, what is the value for M?

Student: 1.

1. So, you can conclude here this is 0. So, here you can put 1, 2 -1 -2. So, M equal to 1. So, I plot here and the second one is E, what is the value of E?

Student: -2.

-2 here and N.

Student: -1.

N -1, L +2, this N -1, M +1, D -2 and so on. Then we connect. We connected. So, when you construct a plot, we can see some sort of patterns. This hydrophobicity profile will provide you a specific pattern which will be helpful to identify some secondary structures, or you can see any specific motifs, or you can see any segments which traverse the membrane and so on.

So, there are various software available to make a plot right. So, one of this is available in the literature, that is called 3DInsight, this will consider various properties, it will take the hydrophobicity values along with other properties to make a graph. X axis is the amino acid index and Y axis is a hydrophobicity profile or any different properties. In this slide, when I made this profile, I use a value of 1 2 -2 -1. Actually all the 20 amino acid residues contain specific values right.

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Sample data			
Nozaki-Tanford-Jones (H_t)			
A: 0.87	D: 0.66	C: 1.52	E: 0.67
F: 2.87	G: 0.10	H: 0.87	I: 3.15
K: 1.64	L: 2.17	M: 1.67	N: 0.09
P: 2.77	Q: .00	R: 0.85	S: 0.07
T: 0.07	V: 1.87	W: 3.77	Y: 2.67

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So, I give couple of examples, one is the Nozaki-Tanford-Jones scale this is the first scale derived for the 20 different amino acids, you see experimentally. Directly we cannot calculate the hydrophobicity values, so they did indirect way, that is a relative solubility of each amino acid residues in water as well as in ethanol. So, they did the relative solubility and converted the solubilities into hydrophobicity. So, if you look into this 20 different amino acid residues we can see specific residues which are high values and some of them may have less values.

So, if you see this one can you name few residues, which are highly hydrophobic?

Student: isoleucine, tryptophan.

Right tryptophan, isoleucine.

Student: Phenylalanine.

Right phenylalanine right. So, these residues are hydrophobic because they contain aliphatic groups or aromatic groups. So, they are hydrophobic. So, in the partition coefficient, even the relative solubility, they also showed that these residues are highly hydrophobic. On the other hand, if you look into the charged residues or polar residues for example, you have a serine or you have aspartic acid or you have the glutamic acid, you can see that the values are less, compared to the hydrophobic residues.

So, if you make an average value. So, you can easily discriminate the hydrophobic and hydrophilic residues with these numbers. This is one example which you obtain experimentally. Likewise there are several scales available, I show another example.

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Sample data							
Ponnuswamy-Gromiha (H_{gm})							
A: 13.85	D: 11.61	C: 15.37	E: 11.38				
F: 13.93	G: 13.34	H: 13.82	I: 15.28				
K: 11.58	L: 14.13	M: 13.86	N: 13.02				
P: 12.35	Q: 12.61	R: 13.10	S: 13.39				
T: 12.70	V: 14.56	W: 15.48	Y: 13.88				

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This we obtain from computation analysis. What we did here? Here we considered different dataset of proteins and assign the values for each residue which are influenced with the neighboring residues. They identified the residues which are occurring within the limit of any specific radius and then see; what are the residues which are within this limit. And they assigned the experimental value and then finally, they derived these final scales, but I will explain about the development of the scale in later classes, fine.

So, if you see in this scale here also you can see the real situation. As we discussed earlier, they have some of the hydrophobic residues, see like cysteine, tryptophan, isoleucine they are highly hydrophobic and several polar residues and the charge residues like lysine and you can see the case of aspartic acid and glutamic acid and these residues, they are polar in nature. And major difference you find from these 2 scales, that is mainly proline, proline they did the relative solubility, proline as a ring. So, you can see this is hydrophobic in this case, but if you look into the location of this proline, it is mainly surrounded with polar residues, this is the reason why proline is polar in this scale. Many scales, they assign proline as polar residues.

So, you can see some differences and similarities and most of the scales, currently we have more than 100 indices available. So, they have qualitatively, they have similar behavior. So, I show one example where we can construct the plot.

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Amino Acid Analysis [1prc]

Chain ID : oC oL oM oH oALL

Amino Acid Table :

- q31: size (chothia,1974) average volume of buried residue (a3)
- q32: relative mutability/100 (dayhoff, p.347, 1978)
- q33: aa composition in average percent (dayhoff, p.363,1978)
- q34: pk-n (sober,1970)
- q35: pk-c (sober,1970)
- q36: melting point/10 (sober,1970)
- q37: specific rotation alpha-d/10 (sober,1970)
- q38: dihedral angle between four successive c-atoms levitt,1976
- q39: point mutation data *100 (dayhoff, p.347, 1978)
- q40: residue accessibility in tripeptide (chothia, jmb 105,1,1976)
- q41: av accessibility in folded protein (janin, jmb 125,357,1978)
- q42: hydrophobicity (eisenberg et al, pnas 81:140,1984)
- q43: hydrophobicity,hydrophathy(kyte & doolittle,jmb 157,105,1982)
- q44: surrounding hydrophobicity (ponnuswamy & gromiha,jpr 42:326,1993)
- q45: solvent accessible surface (denatured) (prog.biophys.molec.biol.59,237,1993)
- q46: solvent accessible surface (native)(prog.biophys.molec.biol.59,237,1993)
- q47: solvent accessible surface (unfolding)(prog.biophys.molec.biol.59,237,1993)
- q48: gibbs free energy of hydration (unfolding)(prog.biophys.molec.biol.59,237,1993)
- q49: gibbs free energy of hydration (denatured)(prog.biophys.molec.biol.59,237,1993)
- q50: gibbs free energy of hydration (native)(prog.biophys.molec.biol.59,237,1993)

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So, here is a list of several properties and here we have several hydrophobicity values for example, the hydrophobicity values given with Eisenberg also the Kyte and Doolittle scale, they developed in 1982 then this is the hydrophobicity scale. So, you have different scales, if you want to make a plot, you first you take the PDB code or amino acid sequence, this is the PDB code and here we take the L chain.

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So, we selected this hydrophobicity scale and if you click, then we will get the plot.
What is the X axis?

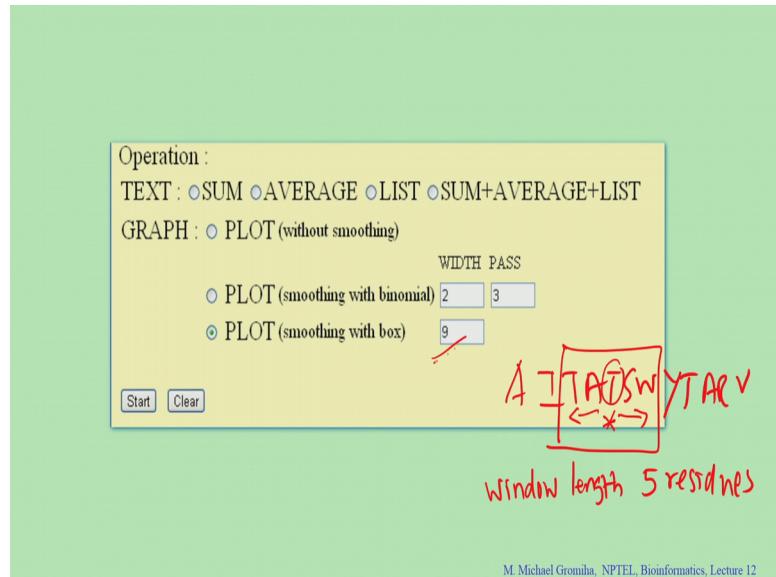
Student: Chains.

Amino acid sequence, what is the Y axis?

Student: Hydro.

Hydrophobicity value right. So, you can see the plot connecting the sequence and the plot. Some cases you can infer the information, some cases, it is not. If you see here, it is kind of clusters. So, we can see the zigzag positions, up and down on this case. So, if you cannot infer anything from the single residue plot, most of the cases, you can find some patterns, then you can also try to get some window average.

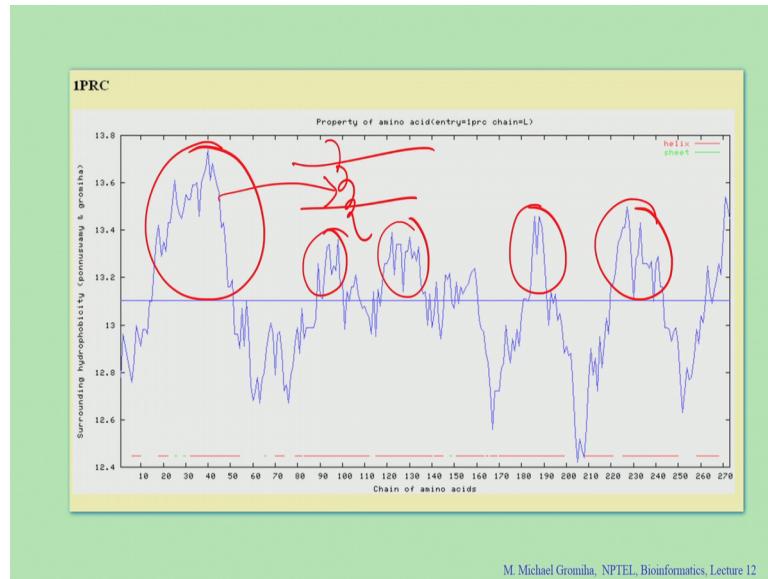
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In this case it is this possible to get the average. So, for example, if you click on the plot with smoothing with box, in this case you can smooth for any window length, for example, if you can amino acid sequence like this.

So, if you take the single residue plot, they plot for each residue. For each residue they have the hydrophobicity value, they plot. We carry window length for example, any residue if you take a window length of 5 residues for example, window length 5. So, what they do? So, they make a window, considering 5 residues, 2 from left side, 2 from right side, where this is the central one. So, they have made a window 5. So, what they do? They calculate the average value and plot for the central one. For the first residue we do not have the left side residues. First 2, if you have a window length of 5, and all other residues take a 5 residues length.

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So, now if you do this for example, if we take the smoothing box of 9, then will get the plot like this. Now can you see the difference between the previous plot and this plot? Yes. Here you can easily identify some regions which are highly hydrophobic in nature and some regions which are less hydrophobic in nature for example, if you see here all the residues are highly hydrophobic and you can see somewhere here, someplace here, someplace here, and someplace here, here you can see these completely polar charged residues or polar residues.

So, will you have this one, this will tell you that there is a stretch of residues, but there highly hydrophobic in nature with one or 2 polar residues in between. Because of that one or 2 residues, in the first plot we can see a zigzag, look at that polar residues has less hydrophobic is down. Here because of the average, that compensates maybe somewhere here, the residues are highly hydrophobic and interestingly if you see this protein, is a membrane protein as I discussed earlier, the proteins which are embedded in membranes right.

So, these residues, they span in a membrane, if you see there is a membrane. So, here this is the protein right. So, the region is a membrane. So, this response resembles this one. So, you can use you can make a plot. This plot has some applications to identify the regions, which are inserted in the membrane right. So, if you can use this hydrophobicity profiles to get several other information.

So, this is another behavior which are related with hydrophobicity, there is called amphipathic character.

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Amphipathicity

- Amphipathic character of amino acid residues is the **periodicities in the polar/nonpolar character of the amino acid sequence** in a protein.
- This has been examined by assigning a numerical hydrophobicity to each residue and searching for periodicity in the resulting one-dimensional function.

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What is a meaning of amphipathic?

Student: has both charge.

Both right. 2. *Amphi-* means 2 right. So, where this is high or low. So, this will give you the information regarding periodicities of the polar and non-polar characteristics of sequence. How do get that? You have the numerical hydrophobicity values, we assign the values and then we see if there are there any periodicity in one dimensional plot. How to do this? For example, if we take alpha helical segment. How many residues per turn?

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Amphipathicity: α -helices

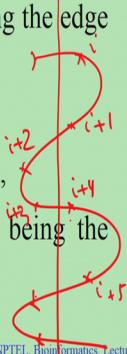
The residues of an α -helical segment are considered on four adjacent edges along the direction of the helical axis. The average hydrophobicity of the residues constituting the edge i ($i = 1, 4$) is given by

$$\alpha_i = (\Sigma h_{i+j})/n,$$

where n is the total number of residues in the edge,

j increases at an interval of 4 from 0 to m , m being the number of residues in the helix;

h is the hydrophobic index of the residue.



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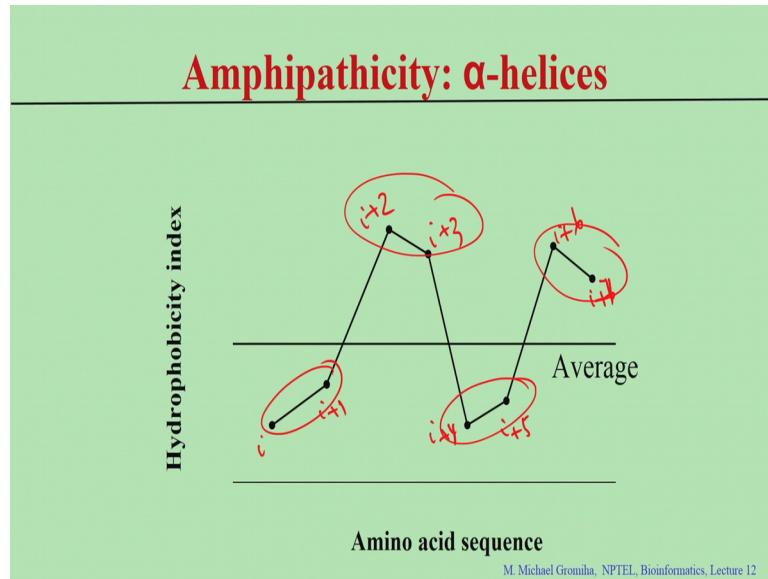
Student: 3.6.

3.6 residues per turn. So, if you have a helix, it starts from here right. So, one turn is up to here, this way and this way right. So, you have a helical axis, you can put the residues 1 2 3 4, the same way 1 2 3 4. So, you can make it. So, in this case you can see the 2 residues are on side and 2 residues on the other side. So, they show a periodicity of these residues at different positions, this is i , for this is i , this is $i+1$, $i+2$, $i+3$, $i+4$. So, you can see the periodicity $i+5$. So, between this i and $i+4$.

So, these 1 2 3 4 and this 5. 1 and 5, there would be on the same place, likewise you can see the 2 and 6. So, if you have a helical segment, you can make on 4 adjacent edges you can put 1 2 3 4 in the direction of the helical axis, then you can calculate the average hydrophobicity of each edge for example, we take this, these plus same is here, same is here.

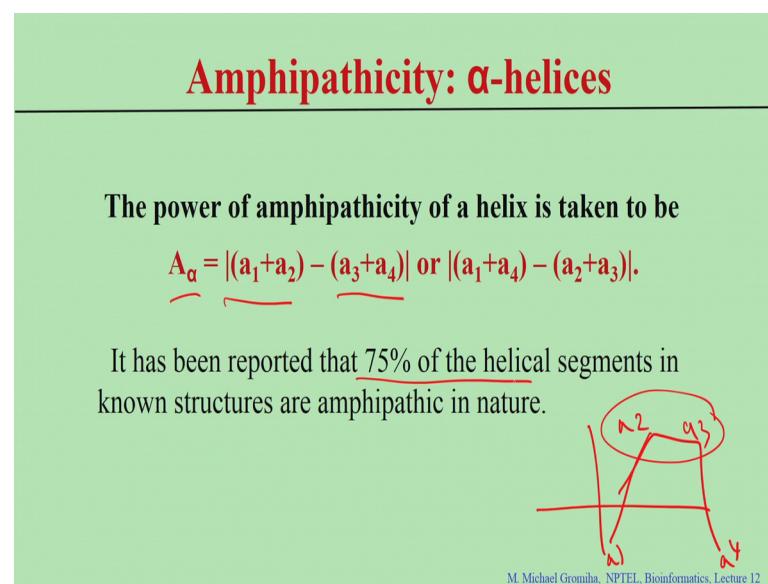
So, you can see $i+j$ with the interval of 4, and see how many residues in that particular place.

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So, for example, if you see this periodicity this is i , this $i+1$, $i+2$, $i+3$, $i+4$ and $i+5$. You can see a periodicity, 2 residues are less hydrophobic here and 2 residues have high hydrophobicity and then again 2 less and 2 high. So, if you have this type of patterns, then we can say these residues are part of alpha helix, or these residues can suit alpha helix right. So, if you have a sequence and if you make a plot with hydrophobicity and if you see any of these patterns, then you can say that these residues can form alpha helix. Then the second is, how to calculate the power of amphipathicity. For example if you have 2 helices, they are amphipathic and which one is more amphipathic.

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For in this case, you can calculate the power of amphipathicity alpha.

So, if 1 and 2 are high and 3 and 4 are less then take the first 2 and the second, third and forth and get the absolute difference. In this case, here take these numbers as 1 and these numbers as 2, this is $i+6$ and this is $i+7$. So, then take the difference, this will give you the power of amphipathicity, you can see the A_α , either $a_1 - (a_3 + a_4)$ or if $a_1 a_4 - (a_2 + a_3)$, this is in this case for example, if it is like this right.

So, this is 1 2 3 4; $a_1 a_2 a_3 a_4$, if this is the case, this will come together $a_2 + a_3$ and this will come together, you can see difference. So, from this one, we can see whether they are amphipathic or not, but if you look in to the literature about 75% of the helical sequence of known structures were amphipathic in nature. This case, if you use this type of profiles, we are able to predict to some level of acquires at least to 70, 65 to 70% of accuracy in any sequence. This is for alpha helix. How about in the case of beta sheets? In the case of beta strands right.

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Amphipathicity: β -strands

A β -strand segment is considered to have two faces and the average hydrophobicity of residues constituting the face i ($i = 1, 2$) is given by

$$\beta_i = \frac{\sum h_{i+j}}{n},$$

where n is the total number of residues in the face; j increases at an interval of 2 from 0 to m , m being the number of residues in the strand;

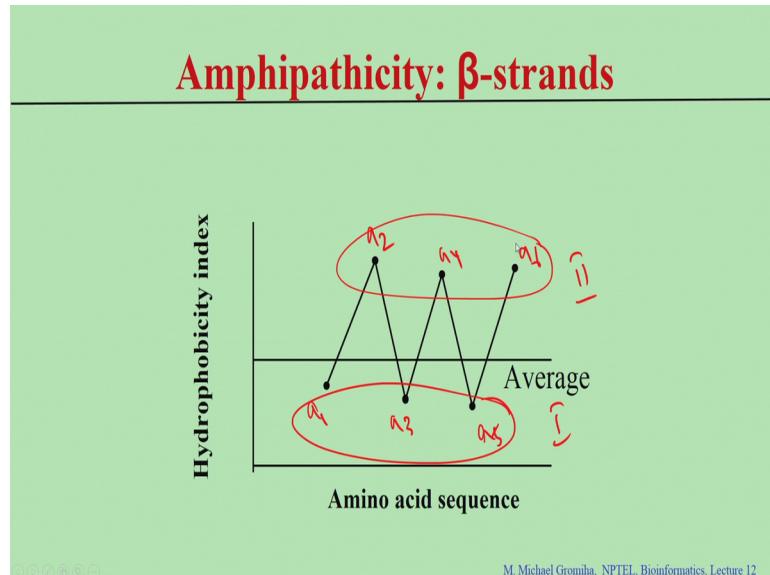


So, you can see there are 2 faces; you have 2 faces, one is here, one is here. The alternate faces. So, one is having high, another is low hydrophobicity.

So, in this case you can calculate β_i , this is a summation h_{i+j} by n , where here these intervals of 2, the helix we have interval of 4, in the beta sheet interval of 2, with up to n ,

where n is the number of residues in the strand. So, the calculate the β_i is equal to $\sum h_{i+j}$ divided by n , for n is the number of residues in each face, either here or here.

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So, now we have the patterns, you can see the X axis is amino acid sequence, Y axis hydrophobicity index. So, here these are the hydrophobic values of different amino acids. So, this is the average value. So, this $a_1, a_2, a_3, a_4, a_5, a_6$. So, if you see the power of amphipathicity, you can calculate, may be this is one side, this is another side, this is one face, second face, then add up all these together, take the average and add here everything together, and take the average finally, you can get the values right.

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Amphipathicity: β -strands

The amphipathicity index of a strand is computed using the equation,

$$A_{\beta} = |\beta_1 - \beta_2|.$$

The structural analysis showed that about 65% of the β -strands possess amphipathic character.

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You can get $\beta_1 - \beta_2$. So, they get the amphipathic behavior of this particular beta sheet.

So, the structural analysis also showed that about 65 percent of the beta sheets, they possess amphipathic in nature. If you take the all the beta sheets in the known structures and construct the plots and you can see about 65 percent, they are amphipathic in nature. So, now, what are other applications of this hydrophobicity profiles, here we discuss 2 cases, one is the alpha helices. What is periodicity in alpha helix?

Student: 1 + 4.

Yeah 2 on one side, and 2 on other side. What is the periodicity in beta sheets?

Student: 2 1 1 2.

1 1, you have the alternate high and low hydrophobicity patterns.

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Patterns

Identify the pattern of hydrophobic residues for membrane spanning helical proteins

E.g. AILVGYWFFVVA

Amino acid sequence

Membrane helix

Average

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So, some cases for example if you get the hydrophobic behavior, this is the average value. For example, this is the average value if you take, and all the residues are highly hydrophobic, For example, I put this sequence, A is hydrophobic, I is hydrophobic, L is hydrophobic. So, all residues are hydrophobic. So, we have the pattern of highly hydrophobic residues. If this is the case, this will resemble a type of protein, a type of segment, which type of segment?

Student: (Refer Time: 19:49).

This is membrane spanning alpha helices right. So, this is membrane spanning alpha helices. So, if you plot, make a plot, you can get some information from primary sequences right. So, without having any information, if this character provides a specific information, at least you can develop from that point of view. So, constructing hydrophobicity profiles, will give some information from the sequence.

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Patterns

Amphiphatic character of β -strands by alternative hydrophobic-hydrophilic residues

E.g. AKINIHVTFKIKLP

Amino acid sequence

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This is another pattern, just I discussed earlier which is the beta sheets, amphiphatic character. So, because you can see the red one, is the hydrophobic, and the black one is the hydrophilic. So, you can say alternating hydrophobicity. So, this will give the pattern for the beta strands.

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Pattern Definition

1 2 4 5 6 7 8 10 14 16 17
[LIVM]-[VIC]-x(2)-G-[DENQTA]-x-[GAC]-x(2)-[LIVMFY](4)-x(2)-G

1. Use capital letters for amino acid residues
2. Use "[...]" for a choice of multiple amino acids in a particular position. [LIVM] means that L, I, V, or M can be in the first position

D R Y G X X G

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So, now in the amino acid sequence, it is also possible to identify any specific motifs or patterns. In this case we define a specific definition for defining patterns for example, you take any sequence like for example, 5 residue segments or 10 residue segments

whether they possess any specific patterns. So, in some cases we discussed earlier about conservation. So, what is conservation?

Student: Residues conserved

Yeah may position a particular residue occupies the same position in all the homologous sequences. In this case that residue is said to be conserved, if your residue is certainly conserved then you have to keep that particular residue in all the positions for example, if you have specific motifs GXXG motif, or any specific motif, DRY motif, this is for something for the GPCR, this is for a disulphide bridge forming enzymes. So, if they have some specific motifs then we can search any specific motifs in the whole database and see whether there is any characteristic pattern for that particular set of proteins.

So, in this case we define patterns using some sort of notations. So, here we show one sequence, we use some residue names for example, here this means the residue glycine is conserved at that particular position, that maintains the same residue at the particular position. So, we cannot change this, for this place as well as this place. They put x, what is the meaning of x?

Student: Any residues.

Any residues. You can put all the 20 amino acid residues, any residue is allowed at this particular position, then we have these numbers. Number means?

Student: 2 time.

Number of times, with 2 means 2 times. So, we can follow the same notation. Then we use the square brackets for example, if here we put L I V M, this will give you the choice of amino acids, any of these 4 residues. Among these 4, either L or I or V or M, any residue can accommodate at the position number one.

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Pattern Definition

3. Use "{...}" to exclude amino acids. CF means C and F should not be in that particular position
4. Use "x" or "X" for a position that can be any amino acid.
5. Use "(n)", where n is a number, for multiple positions; x(3) is the same as "xxx"

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Then we have this curly brackets, if this is brackets.

Student: exclude.

This is excluded, that this is not allowed for example, if you put CF, C and F should not be in that particular position, they give the exception that these are not allowed. Then you put x for any amino acid, n means number of times. If I show this one, how many amino acids in this pattern? This is 1 2, here 2, 2 plus 2, 4 5 6 7 8 10 14 16 17; 17 amino acids in this pattern.

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PIR: Pattern Definition

V V VVG Q P A IA LMFV AA G
[LIVM]-[VIC]-x(2)-G-[DENQTA]-x-[GAC]-x(2)-[LYVMFY](4)-x(2)-G

Illustrates a 17 amino acid peptide that has:
L, I, V, or M at position 1;
V, I, or C at position 2;
any residue at positions 3 and 4;
G at position 5 and so on

So, how to write a pattern in this case, if you take this one? So, position number 1, which residue can come in position number 1?

Student: Anything

Anything, for example I put V, for the second position again we put V, third and forth?

Student: Anything

Anything, you can put a 2 times V again. And this position?

Student: GG.

G because here we cannot do anything. So, you have to use G because G is conserved. And in this here?

Student: N

NQ you can put Q. So, where is x, x we can put P right. So, here.

Student: A.

A then 2, any residues?

Student: 2 3.

I, A, I A and here.

Student: L.

L.

Student: M.

M.

Student: F.

F.

Student: V.

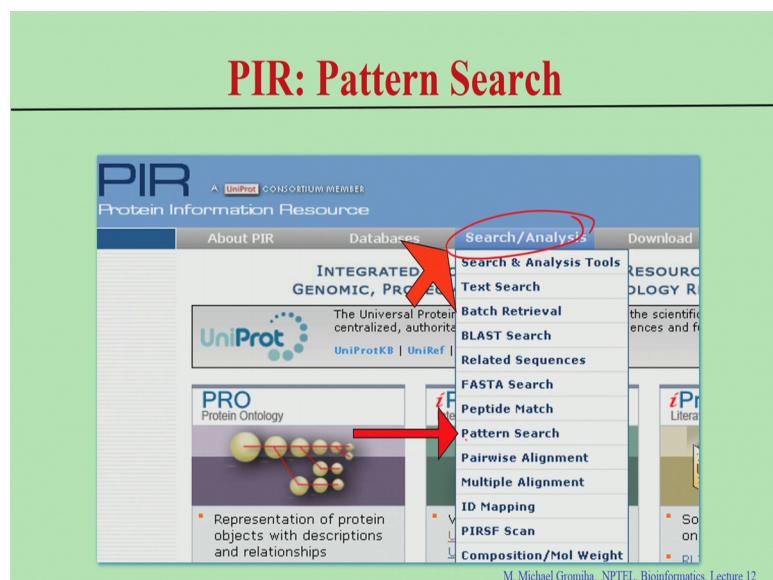
V. So, because L is allowed, M is allowed and F is allowed and V is allowed 4 times because 4 times you put 4, then 2x, AA and finally, G. So, we can write a pattern and then we can use this pattern to see whether you can see this type of patterns in all the sequences of particular type. I will explain one with an example.

So, now this we can write a code to get the pattern, and also this tool is available in the PIR; what is PIR?

Student: protein information resource

Protein information resource, as they first initially developed for the protein sequences right.

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And then they develop some tools for analyzing sequences and here, if you go the search analysis, there is a tool called this pattern match.

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PIR: Pattern Search

Pattern Search Forms

Search a query pattern against a UniProt database

1. Select a database: UniProtKB (or restricted by organism/taxon group)
 UniRef100

2. Insert a user-defined pattern below:
[LIVM]-[VIC]-x(2)-G-[DENQTA]-x-[GAC]-x(2)-[LIVMFY](4)-x(2)-G
Or, alternatively, enter a valid PROSITE code for a query pattern:

Submit Reset Example: PS00888 (annotated output)

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So, we go with this pattern match. So, we can give the pattern, I give a same pattern here LIVM same, and if you submit.

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[LIVM]-[VIC]-x(2)-G-[DENQTA]-x-[GAC]-x(2)-[LIVMFY](4)-x(2)-G

Pattern Search Result (UniProtKB)

1 selected 0 unselected

Protein AC/ID	Protein Name	Length	Organism Name	PIRSF ID	Match Range
Q96777/Q96777_1HEV	Cyclic nucleotide and voltage-activated ion channel	678	<i>Heliotropium vesicatum</i> (Tobacco hornworm)	PIRSF004669	477-493;
Q97119/Q97119_LMP01	Cyclic nucleotide-gated ion channel LNCN1	900	<i>Umrulus polyphemus</i> (Atlantic horseshoe crab)	PIRSF004669	532-548;
POA117/POAQ_SALTY	Surface presentation of antigens protein spaQ	86	<i>Salmonella typhimurium</i>	PIRSF004669	4-20;
POA118/POAQ_SALT1	Surface presentation of antigens protein spaQ	86	<i>Salmonella typhi</i>	PIRSF004669	4-20;
POA119/POAQ_SALDE	Surface presentation of antigens protein spaQ	86	<i>Salmonella senftenberg</i>	PIRSF004669	4-20;
POA119/POAQ_SALTP	Surface presentation of antigens protein spaQ	86	<i>Salmonella typhimurium</i>	PIRSF004669	4-20;
POA038/CRP_ECOLI	Catabolite gene activator; (Alternate: Full=cAMP receptor protein; Altname: Full=cAMP regulatory protein)	210	<i>Escherichia coli</i> (strain K12)	PIRSF003151	30-46;
POA039/CRP_ECOL6	Catabolite gene activator; (Alternate: Full=cAMP receptor protein; Altname: Full=cAMP regulatory protein)	210	<i>Escherichia coli</i> O6	PIRSF003151	30-46;
POA040/CRP_ECOL9	Catabolite gene activator; (Alternate: Full=cAMP receptor protein; Altname: Full=cAMP regulatory protein)	210	<i>Escherichia coli</i> O147:H7	PIRSF003151	30-46;
P29973/CNGA1_HUMAN	cGMP-gated cation channel alpha-1; (Alternate: Full=cNG channel alpha-1; Short=cNG-1; Short=cNG1; Altname: Full=Cyclic nucleotide-gated channel alpha-1; Altname: Full=Cyclic nucleotide-gated channel, photoreceptor; Altname: Full=Cyclic nucleotide-gated channel alpha-1; Altname: Full=Cyclic nucleotide-gated channel, photoreceptor alpha-1)	690	<i>Homo sapiens</i> (Human)	PIRSF002402	506-522;
P29974/CNGA1_MOUSE	cGMP-gated cation channel alpha-1; (Alternate: Full=cNG channel alpha-1; Short=cNG-1; Short=cNG1; Altname: Full=Cyclic nucleotide-gated channel alpha-1; Altname: Full=Cyclic nucleotide-gated channel, photoreceptor; Altname: Full=Cyclic nucleotide-gated channel alpha-1; Altname: Full=full-photonreceptor cGMP-gated channel subunit alpha)	694	<i>Mus musculus</i> (Mouse)	PIRSF002402	499-514;
P36600/CAKP_SCIOPO	cAMP-dependent protein kinase regulatory subunit; (Short=cPKA regulatory subunit)	412	<i>Schizosaccharomyces pombe</i>	PIRSF000548	171-187; 205-321;
P49605/KAPR_USTMA	cAMP-dependent protein kinase regulatory subunit; (Short=cPKA regulatory subunit)	525	<i>Ustilago maydis</i> (Smut fungus)	PIRSF000548	241-257; 375-391;

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And you will get the sequences which contain the particular pattern. So, if you click on this, any of this sequence if you click.

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The screenshot shows a protein sequence alignment interface. At the top, it says "Length = 210" and "POAC18". Below this is a sequence bar with three colored segments: red, brown, and pink. A blue line indicates a specific pattern. The sequence itself is a long string of amino acids from position 1 to 210. Below the sequence, a pattern is highlighted in red: "Pattern: LIHQGEKAETLYYIVKG [LIVM]-[VIC]-x(2)-G-[DENQTA]-x-[GAC]-x(2)-[LIVMFY](4)-x(2)-G". This pattern is overlaid on the sequence. Below this, a new beta-signal motif is defined: "New β-signal motif : P_oxGh_yxH_yxH_y". The motif is shown with residues: [K,R,H,Q,N,S,T] (underlined), G (circled in red), [I,V,L,F,M,Y,W] (underlined), [A,C] (circled in red), and [I,V,L,F,M,Y,W]. The entire motif is enclosed in a green box. At the bottom, the word "Algorithm" is centered, followed by the citation "K. Imai, M.M. Gromiha and P. Horton (2008) Cell" and the note "M. Michael Gromiha, NPTEL, Bioinformatics, Lecture 12".

So, will get this full sequence and you can see the pattern in this sequence, where does start from? Here right VKG, from here to here. So, if you check this is L, L is here and the I is here and 2 residues here and then G, this is a conserve G it is here, and E is here and then K and then A and then E and T and L Y, L is here Y is here and I right, then 2x, V and K and final G, that is fine, this works, right the program works.

So, you can get this type of patterns and then see whether each specific pattern is important for a particular set of proteins. I explain with one example. So, this is your specific motif for the beta signal; that means, for the insertion and assembly of beta barrel membrane proteins, this is a type membrane protein I discussed earlier right. So, this type of motif is essential. Experimentally they observe, computationally we can do this analysis using this search.

So, here P_o means polar. So, any polar residues, and here there is one x. So, here put x, here dot, and G. So, G is conserved and any hydrophobic residues is H_y and any x and hydrophobic here and x and hydrophobic. There is a difference between this small h_y and capital H_y ; small h_y includes these small residues, alanine, cysteine, but capital H_y , it does not include this A and C.

Now, the question is why experimentally they showed that this specific motif that is important, that is true or not, how to verify?

Student: If it is present in.

Right if it is present or not. So, first we take all proteins of beta barrel membrane proteins, and then easily we can write a pattern because if you go here and if we write this pattern then I will get the list of proteins, or other way you can do it, first download all the beta barrel membrane proteins and then see whether this pattern is available or not. The 2 options, one is the whole sequence, we can search or we can see where this is important, of the N-terminal or the C-terminal; mainly C-terminal for the insertion, you can see, take this C-terminal forty residues and see whether the pattern is available or not, fine.

So, if you find this pattern then you are happy. Then next question is how to verify, this is important for this particular type of proteins? You have to compare. So, this should be present in this type of proteins, and should not be present in other type of proteins. So, we can construct different datasets; where shall we get the sequences?

Student: UniProt.

UniProt database right. So, then you get the different sequences like normal globular proteins, we can see the inner membrane proteins, all beta proteins, different type of proteins you can construct and see whether is the pattern is available or not, if available?

Student: There is not.

That is not specific, if it is not available, very specific. When we do this, we can find this particular motif, only for the beta barrel proteins; that means, this signal is important for the insertion assembly, then we can find something. Likewise you can define several motifs and you can see some novel patterns and you can explain why this is important and what is the main use of these particular motifs in any sequences, you can do lot of analysis with different types of proteins.