Protein identification with a binary code, a nanopore, and no proteolysis

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Abstract. If protein sequences are recoded with a binary alphabet derived from a division of the 20 amino acids into two subsets, a protein can be identified from its subsequences by searching through a recoded sequence database. A binary-coded primary sequence can be obtained for an unbroken protein molecule from current blockades in a nanopore. Only two (instead of 20) blockade levels need to be recognized to identify a residue's subset; a hard or soft detector can do this with two current thresholds. Computations were done on the complete proteome of *Helicobacter pylori* (http://www.uniprot.org; database id UP000000210, 1553 sequences) using a binary alphabet based on published data for residue volumes in the range ~0.06 nm^3 to ~0.225 nm^3. With volumes normally distributed, more than 93% of binary subsequences of length 20 from the primary sequences of *H. pylori* are correct with a confidence level of 90-95%; they can uniquely identify over 98% of the proteins. Most of them have a large number of identifying subsequences so the false detection rate is low. Recently published work shows that a 0.5 nm diameter nanopore can measure residue volume with a resolution of ~0.07 nm^3, so the procedure described here is both feasible and practical. This is a non-destructive single-molecule method without the vagaries of proteolysis.

1. Overview

It is shown that proteins in a proteome can be uniquely identified from subsequences of primary sequences based on a binary code. The code is derived from a division of the standard set of 20 amino acids into two subsets based on their volumes [1]. Using a sample proteome (*Helicobacter pylori*) calculations show that the codes of subsequences 20 residues long are correct at a 90-95% confidence level, and that over 98% of the proteins in the proteome can be identified by exhaustively searching for the recoded subsequences in the recoded proteome database. The scheme described here can be translated into practice with a nanopore.

The proposed method is first analyzed computationally before looking at implementation issues. There are three steps: 1) Divide the set of amino acids into two ordered subsets S_1 and S_2; 2) Recode the primary sequences in a proteome with a binary code based on this two-way partition; 3) For every protein in the proteome find one or more subsequences in its binary coded primary sequence that identify the protein uniquely.

2. An amino acid partition

Table 1 shows the standard set of 20 amino acids **AA** = {G,A,S,C,D,T,N,P,V,E,Q,H,M,I,L,K,R,F,Y,W} grouped into two subsets S_1 and S_2 by volume, where

$$S_1 = \{G,A,S,C,D,T,N,P: 59.9 \leq \text{volume} \leq 123.3\} \quad (1a)$$
$$S_2 = \{V,E,Q,H,M,I,L,K,R,F,Y,W: \text{volume} \geq 138.8\} \quad (1b)$$

Table 1. The 20 amino acids in increasing order of volume. AA = Amino acid; Mean (μ) = Mean volume in nm^3; SD (σ) = Standard deviation of volume in nm^3. Shading shows division into ordered subsets S_1 and S_2; dividing line is between P and V. Data adapted from [1].

AA	Mean	SD	AA	Mean	SD	AA	Mean	SD	AA	Mean	SD
G	59.9	2.2	T	118.3	2.3	Q	145.1	5.1	K	172.7	5.9
A	87.8	2.3	N	120.1	4.1	H	156.3	6.1	R	188.2	9.6
S	91.7	1.8	P	123.3	1.8	M	165.2	1.8	F	189.7	7.4
C	105.4	5	V	138.8	3.6	I	166.1	3.4	Y	191.2	8
D	115.4	2.2	E	140.9	5.3	L	168	4.3	W	227.9	3.8

The dividing line is chosen between P and V so that the two sets have roughly similar sizes (8 and 12) and the difference between the volumes of P and V is relatively large. (There are higher differences between Y and W and

between G and A, but the resulting subset sizes are lopsided.) An amino acid X ϵ **AA** has a binary code C(X) given by

$$C(X) = i, \qquad X \in S_i;\ i = 1, 2 \tag{2}$$

The binary code for a protein sequence **X** = X_1 X_2 ... X_n, where X_i is one of the 20 amino acids, is then $C(X_1)$ $C(X_2)$ ... $C(X_n)$.

3. Binary subsequences of primary sequences as protein identifiers

Assume that amino acid volumes are normally distributed. Figure 1 shows the distributions for the 20 amino acids based on μ and σ values in Table 1.

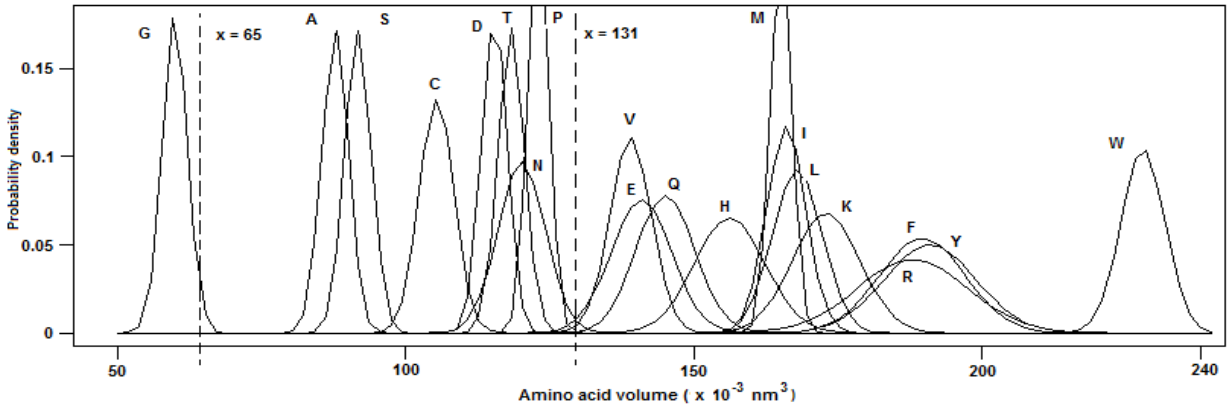

Figure 1. Normal distributions of amino acid volume with mean and standard deviation from Table 1.

Let F(x; μ, σ) be the cumulative normal distribution function with mean μ and standard deviation σ:

$$F(x; \mu, \sigma) = (1/\sqrt{2\pi}\sigma) \int_0^x . \exp(-(x- \mu)^2 /2\sigma^2) \tag{3}$$

The complement of F(x; μ, σ) is

$$G(x; \mu, \sigma) = 1 - F(x; \mu, \sigma) \tag{4}$$

Let the mean volume and standard deviation for amino acid aa be μ_{aa} and σ_{aa} (see Table 1). A residue is in S_1 if its measured volume is between T_1 and T_2 and in S_2 if > T_2. Then $e_{aa}(T_1,T_2)$, the error for amino acid aa, is given by

$$aa \in S_1: \quad e_{aa}(T_1,T_2) = F(T_1;\ \mu_{aa}, \sigma_{aa}) + G(T_2;\ \mu_{aa}, \sigma_{aa}) \tag{5a}$$
$$aa \in S_2: \quad e_{aa}(T_1,T_2) = F(T_2;\ \mu_{aa}, \sigma_{aa}) \tag{5b}$$

Assuming that successive residues in a sequence are independent (see later for more on this) the confidence level or probability that the binary code for a protein sequence **X** = X_1 X_2 ... X_n is correct is given by

$$c_X(T_1,T_2) = \Pi_{i=1\ ..\ n}\ (1 - e_{Xi}(T_1,T_2)) \tag{6}$$

The confidence level for a subsequence code can be computed from Equation 6 for subsequences of the primary sequences in a proteome coded as in Equation 2. The proteome of the gut bacterium *Helicobacter pylori* (Uniprot id UP000000210, 1553 sequences, http://www.uniprot.org) is used as an example. Referring to Figure 1 the widest separation near the middle (leading to subset sizes 8 and 12) occurs between the curves for P and V (this is also the line of division in Table 1). This value of 0.131 nm^3 is used for T_2. T_1 is set at 0.05 nm^3, which is below the mean for the lowest volume amino acid G. (In implementation with a nanopore, this is required, see later.) Figure 2 shows the

confidence level of binary codes for all subsequences in *H. pylori* that are of length 15, 20, or 25 (data point symbol ♦) for $T_1 = 0.05$ and $T_2 = 0.131$. As expected the level drops off as subsequence length increases because of the continued multiplication of fractions in Equation 6. (This also means that the full protein sequence cannot be used as an identifier, the confidence level falls to 0 rapidly.)

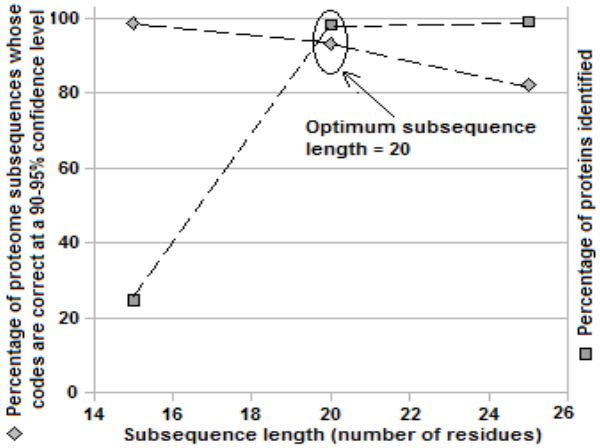

Figure 2. Percentage of protein subsequences in *H. pylori* whose volume-based binary codes have a confidence level of 90-95% vs subsequence length (♦). Percentage of proteins identified uniquely from their subsequences vs subsequence length (■). (Lines connecting data points added as visual aid.)

Using routine search methods subsequences of given lengths from every protein in the recoded proteome may be exhaustively compared with subsequences in every other protein to determine if they uniquely identify their container proteins. To reduce computation time search subsequences from a protein sequence of length S are spaced $\Delta = 5$ residues apart instead of at every position along the primary sequence. Thus subsequences of length L starting at positions 0, 5, 10, ..., S-5 are used. The percentages of proteins so identified are given for L = 15, 20, and 25 in Figure 2 (data point symbol ■). As expected, with larger L more proteins are identified. The number of proteins identified goes from ~25% with L = 15 to ~98% with L = 20 and ~99% with L = 25. The increase from L = 20 to L = 25 is less than 1%; thus subsequences longer than 20 yield diminishing returns. The use of $\Delta = 5$ is justified because the number of identifiers is close to 100% with L = 20 and 25, so the gains from reducing Δ are minimal. This is reinforced by calculations with L = 15: even with $\Delta = 1$ coverage is low as the number of proteins identified rises to just 24.66% (from 8.69% with $\Delta = 5$).

From Figure 2 one is led to conclude that L = 20 is a near-optimal length for identifier subsequences as it simultaneously optimizes the number of proteins identified and the confidence level of their subsequence codes.

The above computational procedure can be translated into practice by using a nanopore to measure residue volume.

4. Using a nanopore to identify proteins from binary subsequences

Nanopore sequencing of proteins [2] uses an electrolytic cell in which two chambers *cis* and *trans* containing an electrolyte like KCl or NaCl are separated by a membrane with a nano-sized pore. A potential difference across the membrane results in an ionic current through the pore. When a protein molecule is introduced into *cis* it translocates through the pore and causes a blockade of the ionic current. By measuring the level of the blockade, a residue can be identified. With proteins no enzymatic digests are required; the analyte is a denatured (unfolded) protein molecule. Normally identifying a residue in this molecule would require a blockade current resolution that can discriminate among 20 residue types (the standard set of amino acids is assumed here). Such resolution is virtually unattainable in practice, especially with noise present.

The method proposed here resolves this problem by reducing protein identification to measuring two (rather than 20) levels in the blockade current signal generated by an intact translocating protein. Following this subsequences in the resulting binary sequence are found such that they can uniquely identify the protein in a binary-coded proteome database. The blockade level is directly related to the volume of one or more residues translocating through the pore, so residue volume is used here as a proxy for the blockade current.

It was recently shown experimentally that a sub-nanometer-diameter (0.5 nm) nanopore can measure residue volume with a resolution of 0.07 nm^3 [3]. The threshold values T_1 and T_2 chosen earlier can be understood in light of this. If T_2 is considered in isolation, residues with mean volume > T_2 will be identified as belonging to the residue subset S_2, and those < T_2 as belonging to S_1. However blockades due to residues in the lower volume group have to be detected/differentiated from the open pore current (there is no protein occupying the pore either fully or partially). This is why a second and lower threshold T_1 corresponding to a volume of ~0.05 nm^3 was set in the computational analysis in Section 3.

5. Discussion

Some potential implementation-related issues are now considered.

1) The method described here works on single unbroken protein molecules without any proteolysis. It is thus free from the vagaries of the latter. Since there is no degradation the sample can be reused.

2) In practice, matching a measured subsequence with a subsequence in the (recoded) proteome will require a forward match as well as a reverse match because the protein may enter the pore C- terminal or N-terminal first.

3) Equation 6 assumes that successive residues in a protein are independent. This is not true in practice as there are inherent correlations. The latter can be extracted from the pore current signal and used in error correction, this leads to increased reliability. Software used in nanopore-based DNA sequencing routinely uses this kind of information to improve sequencing accuracy; see [4] for an example.

4) Almost every protein in the H. *pylori* proteome has a large number of identifying subsequences, which reduces the false detection rate (FDR) considerably. Figure 3 shows the distribution of the number of proteins vs the number of subsequences of length 20 that are identifiers. (Incidentally, mass spectrometry is most efficient with tryptic peptides that are up to ~20 residues long [5].)

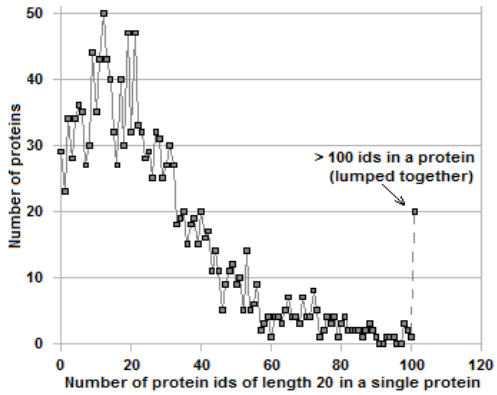

Figure 3. Distribution of number of proteins vs number of protein id subsequences of length 20 in a protein in *H. pylori* (1553 sequences). There are 29 proteins with no id, 23 with one id, and 1501 with more than one id. There are 20 proteins with more than 100 ids, these are lumped into a single point.

5) Depending on the primary sequence a protein may carry only a weak charge so that entry into and translocation through the pore may be a problem. One solution [6] is to attach a strongly charged carrier molecule like DNA (which has a uniform negative charge along its backbone) to the protein molecule.

6) Charged residues on the pore wall tend to interfere with the passage of an analyte when the latter has charged residues. (Seven amino acids, namely D, E, K, R, H, C, and Y, carry a negative or positive charge whose value depends on the pH of the electrolyte.) One possible solution is to neutralize the wall charge in some way. With DNA as the analyte a lipid coat has been shown to have this effect [7].

7) A persistent problem in nanopore-based sequencing is homopolymer recognition, which in the present case means successive residues from the same subset generating the same (binary) output value. With a thick (8-10 nm) biological or synthetic pore, multiple (typically 4 to 8) residues are resident in the pore at any time during translocation so that the boundary between two successive such values may be difficult to identify, although correlations in the measured signal can often provide useful information. Thus in [8] the blockade current was found to correlate well with four contiguous residues. The severity of the problem can be reduced by using a single atom

layer of graphene [9] or molybdenum sulphide (MoS_2) [10] for the membrane, or a biological pore with a narrow constriction as in MspA [11] or in CsgG [12], or an adapter such as β-cyclodextrin in αHL [13]. In this case roughly one residue will be resident in the pore or its constriction (or in the adapter) any time during translocation. Software based on hidden Markov models [4] or the Viterbi algorithm [14] can also be used to computationally separate successive residues with near identical blockade levels.

8) The high speed with which a peptide translocates through the pore makes it difficult for a detector with insufficient bandwidth to detect changes in the blockade current level [15]. Some potential solutions include use of: a) a room-temperature ionic liquid (RTIL), a high viscosity electrolyte that can slow down an analyte by a factor of ~200 [10]; b) an opposing hydraulic pressure field [16]; and c) an enzyme ('unfoldase') to unfold the protein before it enters the pore [17].

Alternatively the bandwidth may be reduced by averaging the raw pore signal and extracting protein-identifying information from it. If the time resolution is τ then the required bandwith is $B = 1/2\tau$. (This is a standard signal processing technique and is often the first step in basecalling algorithms used in nanopore-based DNA sequencing [4].) With binary coded subsequences (Equations 1 and 2) averaging can be approximated by counting the number of 2's in alternating subsequences of length L. This reduces the bandwidth by a factor of 2L. The output is a series of numbers in the range [0,L], which can be thought of as an (L+1)-ary sequence whose length is 1/2L of the original length). As an example consider protein sequence 0 in *H. pylori* (Protein id P56464, length 78). The full-alphabet and binary-coded sequences are:

MALFEDIQAVIAEQLNVDAVQVTPEAEFVKDLGADSLDVVELIMALEEKFGVEIPDEQAEKIINVGDVVKYI
EDNKLA
212221221221222121122211212222121111212222221222221222112212222212112222221122 1

With L = 6 there are 6 'periods': 212221221221, 222121122211, 212222121111, 212222221222, 221222112212, and 222121122222, and a half-'period' 211221. 'Averaging' is done by counting the number of 2's in the first half of each period (L = 6) while ignoring the second half (if any), leading to the base-7 sequence 4_4_5_5_5_4_3 where the _ stands for the second half in each period. A second such sequence can be obtained by counting the 2's in the second half of each period: _4_3_1_5_5_3 (where _ stands for the first half of the period). From one of these (L+1)-ary sequences subsequences of length K can be extracted and used as identifiers if they uniquely identify their container protein. Each of the two sequences yields a set of identifiers for that protein. The total number of proteins identified is the cardinality of the union of the two sets of all such identified proteins. Table 3 shows the results for different values of L and K; it shows a tradeoff between the bandwidth and the number of proteins identified. With L = 5 and K = 8 the bandwidth is reduced by a factor of 10 while the number of proteins identified in *H. pylori* falls from 1524 (98.13%) to 1372 (88.35%).

Table 3. Bandwidth reduction with averaging. Average over alternating windows of width L (= length of subsequence) is given by number of 2's in subsequence binary code. Resulting sequence of averages is an (L+1)-ary sequence; an id is an (L+1)-ary subsequence thereof of length K. Data for *H. pylori* (1553 sequences).

L	5	5	5	6	6	6	6	8	8	8
K	6	8	10	6	8	10	12	6	8	10
No of proteins id'd	849	1372	1346	1054	1337	1271	1185	1197	1227	1118

9) Consider a mixture of proteins $\{N_i: i = 1, 2, ...\}$ where N_i is the number of molecules of the i-th protein in the mixture. If the molecules enter the pore in some random order, then after a sufficiently long run N_i can be estimated as $\tilde{N}_i$, the number of molecules from protein i that are identified as described above. The corresponding fraction of the mixture is $\hat{G}_i = \tilde{N}_i/N_{total}$, where N_{total} is the total number of protein molecules going through the pore. The estimated number of protein molecules not identified is then $\tilde{N}_{not\text{-}identified} = N_{total} - \sum \tilde{N}_i$, where the summation is over all the identified proteins. Impurities in the sample are not considered.

The method described in this report is aimed at identification of any protein belonging to an arbitrarily large set such as a proteome, rather than particular ones as in [6, 18-20]. *de novo* identification is outside its scope, at least in its present form.

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