Whole protein sequencing and quantification without proteolysis, terminal residue cleavage, or purification: A computational model

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Abstract. Sequencing and quantification of whole proteins in a sample without separation, terminal residue cleavage, or proteolysis are modeled computationally. Similar to recent work on DNA sequencing (*PNAS* **113**, 5233–5238, 2016), a high-volume conjugate is attached to every instance of amino acid (AA) type AA_i, $1 \leq i \leq 20$, in an unfolded whole protein, which is then translocated through a nanopore. From the volume excluded by 2L residues in a pore of length L (a proxy for the blockade current), a partial sequence containing AA_i is obtained. Translocation is assumed to be unidirectional, with residues exiting the pore at a roughly constant rate of ~1/μs (*Nature Biotechnology* **41**, 1130–1139, 2023). The blockade signal is sampled at intervals of 1 μs and digitized with a step precision of 70 nm^3; the positions of the AA_is are obtained from the positions of well-defined quantum jumps in the signal. This procedure is applied to all 20 standard AA types, the resulting 20 partial sequences are merged to obtain the whole protein sequence. The complexity of subsequence computation is O(N) for a protein with N residues. The method is illustrated with a sample protein from the human proteome (Uniprot id UP000005640_9606). A mixture containing M unknown protein molecules (which may include multiple copies) is sequenced by mapping their partial sequences to a graph G_M with 20M vertexes; G_M contains M disjoint cliques of degree 20. Unlike in general clique identification (computationally an NP-hard problem) the M cliques can be obtained through a connected graph components algorithm in polynomial time. Quantification is done by sorting the M sequences on the sequence strings and counting duplicates down the sequence. The complexity of sequencing and quantification of a mixture of M proteins is O(MN). The possibility of translating this procedure into practice and related implementation issues are discussed.

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1. Protein sequencing in the bulk and at the single molecule level

The primary sequence of a protein, the sequence of amino acids (AAs) that make up its primary structure, is central to practice in laboratory procedures in analytical chemistry and medical diagnostics and to studies in structural biology and biological modeling. The earliest known method of protein sequencing is Edman degradation [1], which is limited in its scope but continues to be used in the laboratory on a small scale. A second well-known method that is somewhat more prevalent is gel electrophoresis [2]. The most widely used method is mass spectrometry (MS) [3,4], a *de facto* industry standard that is undergoing continual improvement. All three methods are premised on the availability of bulk-sized samples. Unlike with DNA sequencing, which has transitioned from Sanger sequencing in the bulk to high-throughput Next Generation Sequencing methods that can work with sparse samples, in part because of the ability of PCR-based methods to amplify low-volume samples, there is no efficient way to amplify a protein sample. Protein sequencing is further hampered by the varying levels of electrical charge carried by individual residues, which can be positively or negatively charged or neutral, which makes their transport properties hard to predict or model. Discrimination among them is more difficult, in part because there are 20 individual AA types to identify (compared with 4 bases in DNA), many of which are very similar in their physical and chemical properties.

In its current state of development MS requires tens of thousands to a million or more copies of a protein. In many situations, such as single cell level analysis, this level of copy number is not available [5,6]. Ideally a protein sequencing method must be able to sequence a protein from a single copy or perhaps a few tens of copies. Such single molecule methods of protein sequencing (SMPS), have been pursued over the last decade or two, they continue to be a focus of research laboratories [7]. One such method is based on electrophoretically translocating a single protein molecule through a nano-sized pore in an electrolytic cell (e-cell) under the influence of an electric field [8]. During its passage through the pore the normal electrolytic current that flows in the absence of an analyte (which may be a polymer like DNA, RNA, or protein) experiences a drop or blockade, the size of which may be related to the monomer in some well-defined manner. Unlike nanopore DNA sequencing nanopore protein sequencing is yet to make significant strides toward reliable sequencing for research or for use in the field.

For recent reviews of protein sequencing, including SMPS, see [9,10]. Methods on the horizon include ongoing NIH-funded projects [11]. For a recent review of nanopore-based methods, see [12]. Specific studies can be found in [13-20].

2. Sequencing of whole proteins without proteolysis and/or purification/separation

Most protein sequencing methods, whether at the bulk or at the SM level, are destructive of the sample. Thus a sample protein may be proteolyzed with an enzyme into its constituent peptides, which are then sequenced separately or together. Other methods may sequentially cleave the terminal residue and identify it. Sequencing may be done of a peptide in the protein rather than of the whole protein, or of a subsequence of the protein. Following this the protein may be identified by comparison with sequences stored in a database. Ideally it must be possible to sequence a protein *de novo* without any reference to a database or without prior knowledge of the protein. As a result MS and antibody-based methods are strictly not *de novo*.

While non-destructive methods are preferred the number of known *de novo* whole protein sequencing methods (in any stage of development) is small. From this perspective nanopore-based methods are more likely to be successful as the protein can be translocated through the pore without proteolysis. Such a sequencing method has some seemingly conflicting requirements:

1) It must be able to translocate a protein molecule through the nanopore unidirectionally, from say the *cis* chamber to *trans*, in an e-cell;

2) The translocation must be at a uniform rate so that transport properties can be modeled/computed/measured predictably;

3) Successive residues while inside the pore or when exiting the pore can be distinguished from one another; this usually requires high-bandwidth detectors, which in turn means very high signal-to-noise ratios.

Protein sequencing often assumes that the assay is pure, that is, the analyzed sample is made up of copies of a single protein. In practice a sample is more often than not a mixture of different proteins, as it is often hard to separate the component proteins in a mixture. This is especially true when the sample comes from single cells, where some proteins may occur with such low copy numbers that the purification levels required are generally out of reach with currently available methods. One can now add the following fourth desirable property for nanopore-based protein sequencing:

4) The method must be able to sequence proteins in a mixture without purification and/or separation.

One way to identify a monomer in a polymer is to attach a label of some kind, such as a fluorescent dye [21], and use a method like Total Internal Reflection Fluorescence to detect the dye and thence the monomer. Labeling and label detection tend to add labor-intensive stages to the workflow. One can now add a fifth desirable property (regardless of the method used):

5) The method is preferably label-free.

During the last several years a large number of nanopore-based protein sequencing methods have been reported; none of them appears to resolve all five problems. The study reported in [22] comes closest. While it succeeds with 1 and 2 it is yet to be applied to full-fledged sequencing. The report shows that by adding guanidium chloride to the solution and using some additional artifices a whole protein is unfolded, drawn to a 5 nm biological nanopore, and translocated unidirectionally from *cis* to *trans* at a roughly constant rate, with residues exiting the pore into *trans* at a rate of about one per μs.

The present study

The present report builds on [22] and uses a method similar to one used earlier in DNA sequencing with nanopores [23] to show that in theory the first four of the five requirements listed above can be satisfied. It is based on attaching conjugate molecules to all residues of a given AA_i, $1 \leq i \leq 20$, to selectively increase the blockade current level. (It requires an experimentally distinguishable extension to a target AA type to detect it, so it is intrinsically in violation of requirement 5.) If the whole protein is translocated through the pore as in [22], then with low-frequency low-precision volume measurements (where residue volume acts as a proxy for the blockade level) the partial sequence consisting of AA_i can be obtained. By repeating this with all 20 standard AAs, the full sequence can be constructed *de novo*, thus no prior knowledge of the protein or database comparisons are needed. Computational results are given for a sample protein from the human proteome (Uniprot id UP000005640_9606). The model is extended to sequencing of unknown whole proteins in a mixture containing M protein molecules without their separation or purification; copy counts are obtained as a byproduct. The complexity of the sequence extraction algorithm given here is O(N) for a single protein with N

residues and O(MN) for a mixture. The potential for translating the procedure into practice either in the lab or in the field is discussed; related implementation issues are addressed.

3. Whole protein sequencing with a nanopore from subsequence volumes: A computational model

While events corresponding to residues exiting from the pore in succession can be observed with a time resolution of 1 μs as described in [22], the residue itself cannot be identified exactly or even approximately (such as, for example, belonging to a subset of the 20 AAs [24]). This is because the exclusion volume resolution available is currently limited, the best known to date is ~70 nm^3 [24]. Table 1 shows the volumes (in nm^3) of the 20 AAs. Many of the values in the table are close to each other, requiring very high measurement precision to discriminate among the 20 AAs based on single residue volumes. For example the volumes of M (methionine) and I (isoleucine) differ by 0.9 nm^3; at present distinguishing these two AAs is impractical if not impossible.

Table 1 Volumes (nm^3) of the 20 standard AAs, data from [25]

AA	**G**	**A**	**S**	**C**	**D**	**T**	**N**	**P**	**V**	**E**
Mean vol	59.9	87.8	91.7	105.4	115.4	118.3	120.1	123.3	138.8	140.9
AA	**Q**	**H**	**M**	**I**	**L**	**K**	**R**	**F**	**Y**	**W**
Mean vol	145.1	156.3	165.2	166.1	168	172.7	188.2	189.7	191.2	227.9

To get around this problem residue identification can be based on measurement of subsequence volumes. (In [26] such an approach was suggested for protein identification; it was shown in theory that over 90% of the proteins in the proteome of *H. pylori* (UniProt id UP000000210) can be identified with subsequences of length 4 to 8.) In the present study a residue exiting from the pore is associated with the volume excluded by it and its K-1 successor residues during the exit interval of 1 μs. If now a conjugate is added to all instances of AA_i in the protein sequence, the \volume of the subsequence inside the pore will be biased near the positions of occurrence of AA_i in the sequence. From the biased volume sequence a partial sequence containing only AA_i can be obtained. By repeating this procedure with all 20 AAs and merging the 20 partial sequences the whole sequence can be computed.

Table 2 shows the modified volume table that would be used by the sequencing procedure if a conjugate of volume ΔV is attached to all instances of AA alanine (A). (The value of ΔV used below is 1400-2000 nm^3 This choice for the conjugate volume is discussed below.)

Table 2 Modified version of Table 1 with volume of A augmented by attached tag of volume ΔV nm^3

AA	**G**	**A**	**S**	**C**	**D**	**T**	**N**	**P**	**V**	**E**
Mean vol	59.9	87.8 + ΔV	91.7	105.4	115.4	118.3	120.1	123.3	138.8	140.9
AA	**Q**	**H**	**M**	**I**	**L**	**K**	**R**	**F**	**Y**	**W**
Mean vol	145.1	156.3	165.2	166.1	168	172.7	188.2	189.7	191.2	227.9

In the following paragraphs the above notions are used to formally develop a sequencing procedure for whole proteins.

Assumptions

1) With an e-cell in which analytes (that is, sample proteins) are loaded into the *cis* chamber and translocate to the *trans* chamber, translocation signals can be measured with a time resolution of 1 μs [22]

2) A protein is in a stretched state as it translocates through the pore unidirectionally from *cis* to *trans*. In [22] the pore used is the biological pore alpha Hemolysin (AHL), which has a length of L = 5 nm. With such a pore there are 10 residues inside the pore at any time. A profile dimension per residue (its length along the pore axis) of 0.5 nm is assumed for all residues. (The residue to residue distance along the backbone of a linear stretched protein is roughly the same for all residue pairs; AA volume differences are largely in the side chain.) With this assumption there are K = 2L = 10 residues inside the pore at any time.

3) Successive residues exit at a rate of 1/μs at the *trans* end of the pore into *trans* without regressing.

4) Analyte volume is used as a proxy for the blockade current level. Current blockades in a nanopore occur due to the analyte physically excluding current carriers (ions in an electrolyte, typically K^+ and Cl^- in a solution

containing KCl) in the volume occupied by the analyte while it translocates through the pore. This exclusion volume is assumed to be proportional to the drop in the current that would normally flow in the absence of an analyte.
5) The resolution with which blockade exclusion volumes are measured is ~70 nm^3. (This level of precision was used in [24] to distinguish among four subsets of the AAs labeled S(mall), M(edium), I(ntermediate), and L(arge) according to their volumes.)

Notation
k = index of residue at the *trans* end of the pore
Δt = time duration of exit of *trans* end residue into *trans*
K = number of residues in protein segment inside pore (= 10 = 2L for a pore of length L = 5 nm)
p_i = i-th residue in protein
Vol_i = volume of p_i (see Table 1)
$p_k\ p_{k+1} \ldots p_{k+K-1}$ = protein segment inside pore (p_k = residue at trans end of pore)
$psVol_{k,K}$ = total volume of $p_k\ p_{k+1} \ldots p_{k+K-1}$ (there are K residues in the pore at any time)
$cpsVol_{k,K}$ = total volume of $p_k\ p_{k+1} \ldots p_{k+K-1}$ with AA_i occurrences conjugated
$T_{k,m}$= translocation time of subsequence of length k starting at m
V_{step} = volume precision = 70 nm^3
dV_x = digitized volume of $V_x = \lfloor V_x/V_{step} \rfloor$

Consider a protein P with N residues given by

$$\mathbf{P} = \mathbf{P}_{0,N-1} = p_0\ p_1 \ldots p_{N-1} \quad (1)$$

A segment with K = 10 residues from the k-th to the (k+K-1)-th that are resident in the pore is given by

$$\mathbf{P}_{k,k+K-1} = p_k\ p_{k+1} \ldots p_{k+K-1}\ . \quad (2)$$

Now consider a whole protein translocating from *cis* to *trans* through the pore. The time taken for the segment inside the pore $\mathbf{P}_{k,k+M-1} = p_k\ p_{k+1} \ldots p_{k+M-1}$, k=0,1,...N-K+1 to translocate out can be considered in terms of the times taken by each residue as it exits the pore. Since the latter is the same for all residues [22] this time can be written as

$$T_{k,k+K-1} = \sum_{i=k\ldots i=k+K-1} T_i = K\,\Delta t \quad (3)$$

The volume excluded by this segment is the pore sequence volume

$$psVol_{k,K} = \sum_{i=k\ldots i=k+K-1} Vol_i \quad (4)$$

where Vol_i is the volume of residue i (Table 1).

Given the limited volume measurement precision of V_{step} (= 70 nm^3, see above), the measured volume is the digitized pore sequence volume

$$dpsVol_{k,K} = \lfloor psVol_{k,K}/KV_{step} \rfloor \quad (5)$$

The digitization in Equation 5 may lead to truncation errors, this is taken into account in the sequencing procedure given below.

To obtain the exact identity of a residue from these digitized volumes an artifice analogous to the use of base-specific tags for DNA sequencing with a nanopore [23] is used. In [23] the tag molecules are base-specific and are attached to the corresponding bases in a DNA sequence. The DNA strand is pulled with an enzyme motor attached to the membrane near the entrance to the pore. A tag is removed by a chemical reaction when the base comes near the pore entrance. The released tag falls through the pore causing a current blockade of a unique size. As the strand ratchets through the motor the tags of successive bases are detached and identified when they fall through the pore so that the sequence of blockade levels caused by them unambiguously yields the base sequence of the strand.
In the present case conjugates that add volume ΔV are attached to a given AA type, this pushes up the measured volume of the pore sequence near the conjugated AA, from which the position of occurrence of every residue of

the type in the whole sequence is extracted. By applying this step separately to each of the 20 standard AAs the full sequence can be obtained. The value chosen for ΔV is based on the following considerations:
1) With a volume measurement precision of 70 nm^3 the measured exclusion volume due to the 10 residues resident in the pore at any time is on the order of 700 nm^3. Digitization imposes a truncation (or roundoff) error of up to 700 nm on the pore sequence volume that is sampled every µs. With a conjugate volume ΔV = 1400 nm^3 or more there is a minimum change in the signal volume of 700 nm^3.
2) The unconjugated volume varies somewhat over the full length of the protein. This is further affected by truncation/roundoff errors in digitization.

With residues of a selected AA type conjugated Equations 4 and 5 can be rewritten as the conjugated pore sequence volumes before and after digitization:

$$cpsVol_{k,K} = \sum_{i=k...i=k+K-1} CVol_i \quad (6)$$
$$dcpsVol_{k,K} = \lfloor cpsVol_{k,K}/KV_{step} \rfloor \quad (7)$$

where $CVol_i$ is the volume of residue i from Table 2. Equation 8 gives the signal corresponding to the difference between the unconjugated sequence volume and conjugated sequence volume:

$$\Delta Vol_{k,K} = dcpsVol_{k,K} - dpsVol_{k,K} \quad (8)$$

Rewrite Equation 7 as

$$dcpsVol_{k,K} = \lfloor cpsVol_{k,K}/KV_{step} + k'\Delta V)/KV_{step} \rfloor \quad (8)$$

where k' is the number of occurrences of the conjugated AA_i in [k, k+K-1]. If ΔV is set to k" KV_{step}, where k" is a small positive integer (1 or 2), then

$$dcpsVol_{k,K} = \lfloor cpsVol_{k,K}/KVstep \rfloor + k'k'' \quad (9)$$

With k" = 2, the added volume is 1400 nm^3 and the digitized pore sequence volume increases by an integer value of 2 for every occurrence of the the conjugated AA_i in the pore sequence. Effectively a conjugated AA_i at position m adds a digital volume of 2 to the pore volume sequence at positions u in [m-(M-1)+1, m], this added volume is removed when the residue leaves the pore. This effectively adds a rectangle of height 2 to the digitized unconjugated sequence signal; the rectangles may overlap. Sequencing in effect reduces to finding the positions of each rectangle, overlapping or not. The algorithm to do this is given next. It is based on locating the start of the first rectangle, subtracting this rectangle from the difference between the conjugated and unconjugated sampled volume sequences, locating the start of the next rectangle, and repeating this process over the full signal sequence. Finding the start of the first of the remaining rectangles in this process consists of scanning the remaining sequence to locate the rising edge of that rectangle. This procedure returns 20 lists with the positions of occurrence of a conjugated AA, one list per AA. Following this the 20 lists are merged into a single list based on the positions of each AA. Merging can be done with a 20-way sorted merge. The pseudocode for is given below in the two procedures.

Procedure FindRectanglesforConjugatedResidues
Input: Array $\Delta V_{m,K}$, containing differences between conjugated and unconjugated pore volume sequences
K = pore length (= 5 nm); N= protein length (number of residues)
P = p_0 p_1 ... p_{N-1} = sample protein extended with header and trailer of 40 D or E residues
AAvol = vol_0 ...vol_{19} = table of 20 AA volumes [A R N D C Q E G H I L K M F P S T W Y V]
(see Tables 1 and 2)
Cvol = conjugate volume = k"*1400 nm^3, k" ∈ {1,2,3,...}, Vstep = digitized volume step =70 nm^3
Output: 20 lists of positions of conjugated residues in sequence,one for each AA type

```
1. for k = 0 to 19 do:                          // each of the 20 AAs
   1.1 Set number of conjugated AAs to 0
   1.2 Add Cvol to Aavol[k] ;                   // add conjugate to k-th AA
   1.3 Set m to 0;                              // initialize scan index
   1.4 while (m<N-K+1)                          //scan over sample volume difference sequence to identify
                                                // start of next rectangle
       1.4.1  if ΔV_{m+1,K} has a rising edge at N+1-m   // remove rectangle
```

1.4.1.1 **for** j=0 **to** K-1 subtract Cvol/k"*Vstep from $\Delta V_{m,K+2+j}$
end if
1.4.2 Add m+K to position list for AA_k
1.4.3 Add 1 to m
end while
1.5 Subtract Cvol from Aavol[k] ; // remove conjugate from k-th AA
end for

Procedure FindProteinSequence
Input: 20 lists of positions of conjugated AA, one per AA
Output: Sequence of AAs for protein
1. Call K-WayMergeSort algorithm with K = M = 20 to merge-sort 20 sequences of integers corresponding to positions of AA in conjugated sequence

The above method will give exact sequencing information for all 20 conjugated sequences. Less rigid values can be used for ΔV with somewhat more involved heuristics but the results may contain false positives and false negatives. Thus let ΔV be set to (k" + Δ) KV_{step}, + where Δ, 0 < Δ < 1. Then Equation 9 becomes

$$dcpsVol_{k,K} = \lfloor psVol_{k,K} / KVstep + \Delta \rfloor + k'k'' \quad (10)$$

The height of the rectangle resulting from a single conjugated AA is no longer fixed at k", it could be k" or k" +1, which could cause the algorithm given above to produce false positives or false negatives.
Better heuristics may be used to reduce the number of false positives and negatives to a negligible level.

Complexity of computing the sequence of a single protein
In FindRectanglesforConjugatedResidues the while loop moves the scanner m from to near the end of the sequence of length N, recording successively increasing values for the positions of the conjugated AA in the subsequence for A. This a one-way move, there is no backtracking. The resulting complexity is thus of order O(N).
In FindProteinSequence the 20 lists carrying position information for the 20 AAs are all sorted on the position of conjugated AAs. As a result the merge operation is once again a one-way move without any backtracking, the complexity is O(N).
The overall complexity of computing the sequence of a single protein from the 20 lists of conjugated AA positions is thus O(N).

The above development is illustrated in the next section with an example protein and ΔV values of 1400 and 1500.

4 Computational results: An example

The whole protein sequencing procedure described above is illustrated with protein 5 (Uniprot id A6NL46, 340 residues) in the human proteome (Uniprot id UP000005640_9606). The top half of Figure 1 shows the protein sequence. The bottom half shows the sequence with a header and trailer of 40 E (glutamic acid) residues each.

```
MRLCLIPWNTTPHRVLPPVVWSAPSRKKPVLSARNSMMFGHLSPVRNPRLRGKFNLQLPSLDEQVIPTRLPKMEVRAEEPKEA
TEVKDQVETQGQEDNKTGPCSNGKAASTSRPLETQGNLTSSWYNPRPLEGNVHLKSLTEKNQTDKAQVHAVSFYSKGHGVTSS
HSPAGGILPFGKPDPLPAVLPAPVPDCSLWPEKAALKVLGKDHLPSSPGLLMVGEDMQPKDPAALRSSRSSPPRAAGHRPRKR
KLSGPPLQLQQTPPLQLRWDRDEGPPPAKLPCLSPEALLVGKASQREGRLQQGNMRKNVRVLSRTSKFRRLRQLLRRRKKRWQ
GRRGGSRL

EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEMRLCLIPWNTTPHRVLPPVVWSAPSRKKPVLSARNSMMFGHLS
PVRNPRLRGKFNLQLPSLDEQVIPTRLPKMEVRAEEPKEATEVKDQVETQGQEDNKTGPCSNGKAASTSRPLETQGNLTSSWY
NPRPLEGNVHLKSLTEKNQTDKAQVHAVSFYSKGHGVTSSHSPAGGILPFGKPDPLPAVLPAPVPDCSLWPEKAALKVLGKDH
LPSSPGLLMVGEDMQPKDPAALRSSRSSPPRAAGHRPRKRKLSGPPLQLQQTPPLQLRWDRDEGPPPAKLPCLSPEALLVGKA
SQREGRLQQGNMRKNVRVLSRTSKFRRLRQLLRRRKKRWQGRRGGSRLEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
EEEEE
```

Figure 1 Protein 5, id A6NL46, in human proteome (Uniprot UP000005640_9606)

Figure 2 shows the sequence of residue volumes for the first 345 residues; for space reasons the x axis displays every other residue.

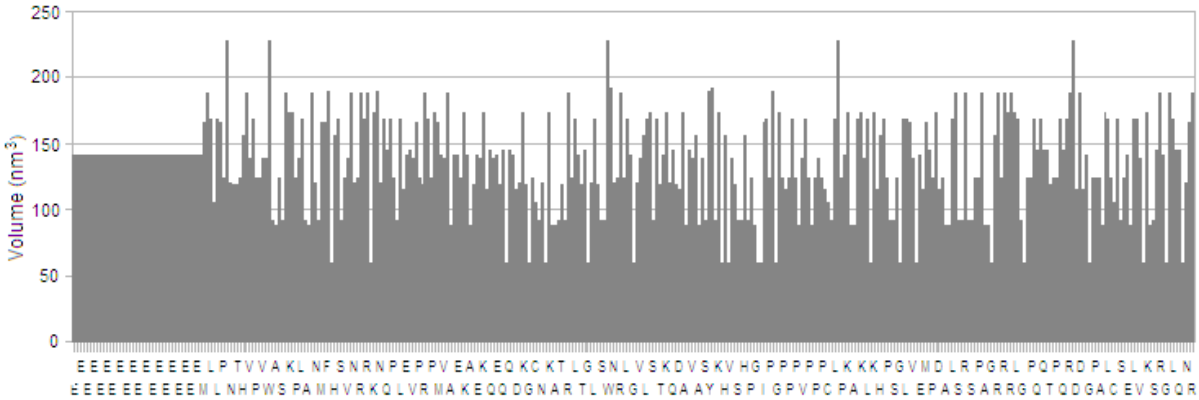

Figure 2 Residue volumes of the first 345 residues in Protein 5, id A6NL46, in human proteome

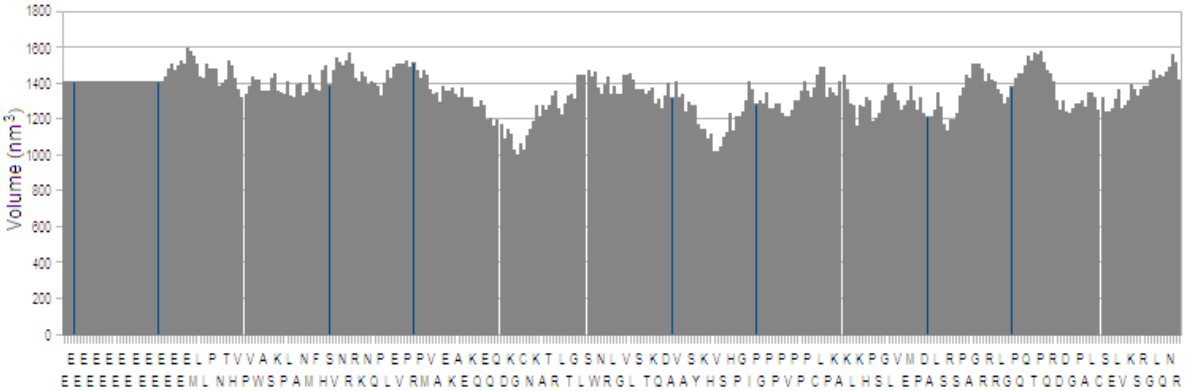

Figure 3 Graph of measured pore sequence volumes along protein sequence (first 345 residues shown)

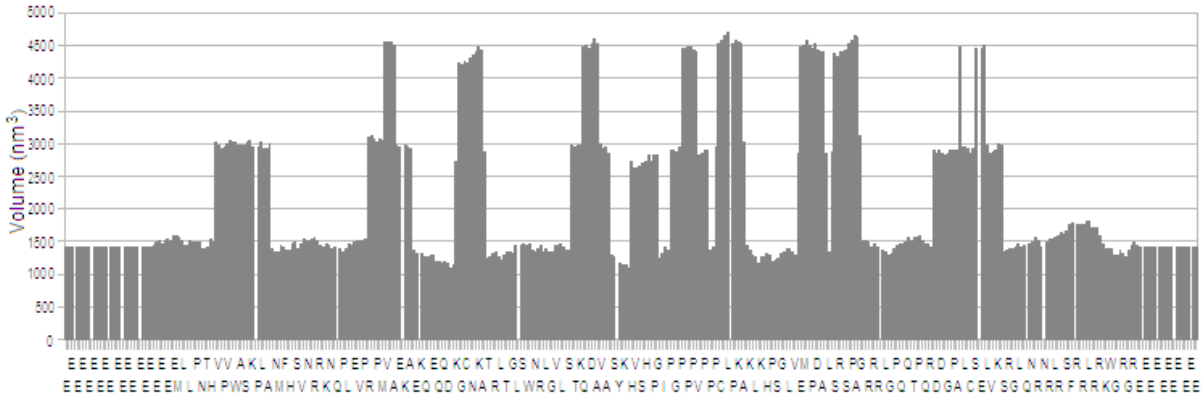

Figure 4 Graph of measured pore sequence volumes along protein sequence with alanines conjugated (first 345 residues in sequence are shown). There are 20 alanines in the full sequence, those to the right of position 345 are not shown.

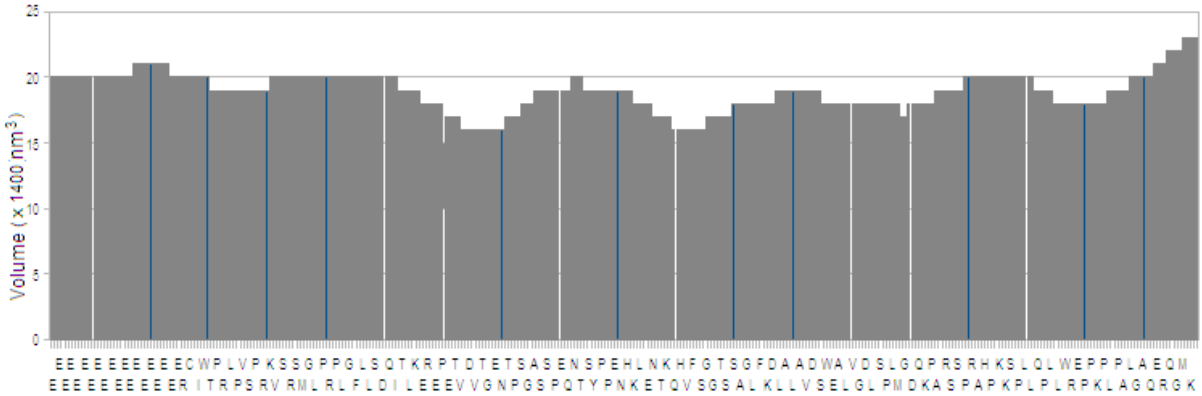

Figure 5 Graph of digitized version of pore sequence volumes in Figure 3 with 1400 nm^3

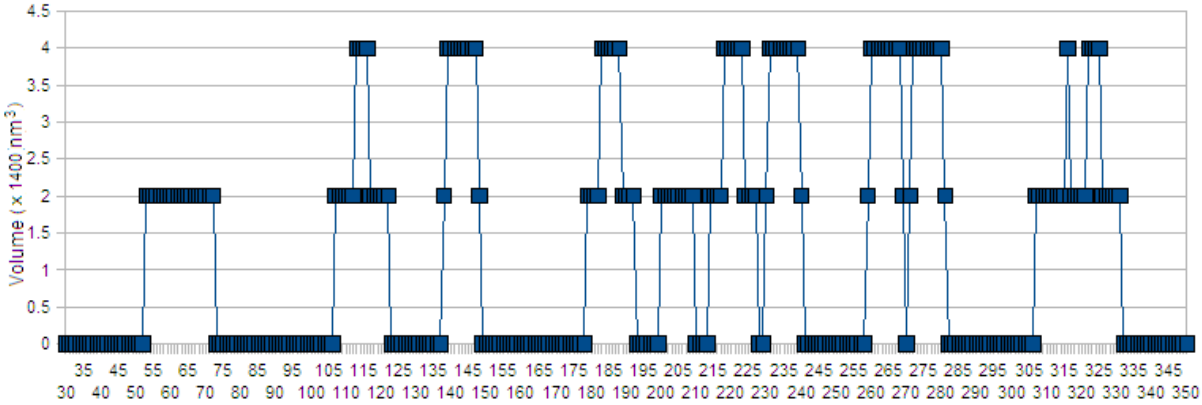

Figure 6 Graph of difference between digitized conjugated and unconjugated pore sequence volumes in Figures 3 and 4 with conjugate volume of 1400 nm^3

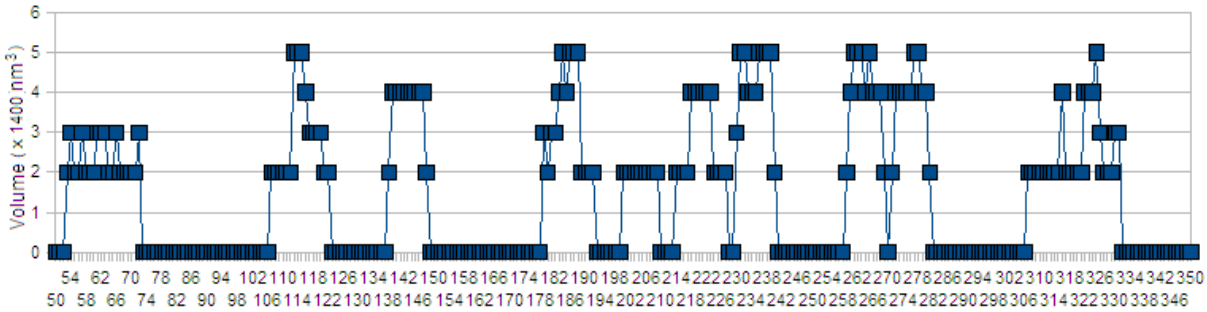

Figure 7 Graph of difference between digitized conjugated and unconjugated pore sequence volumes in Figures 3 and 4 with conjugate volume 1500 nm^3

Figure 8 shows the actual and computed sequences with ΔV = 1400 nm^3. The match is exact for reasons discussed above, see Section 3. Figure 9 shows the actual and computed sequences with ΔV = 1500 nm^3. There are a number of mismatches, resulting in false positives and false negatives. As noted earlier, these mismatches can be traced to to the truncation error that occurs in Equations 7-9.

Tables 3A and 3B show lists of actual and detected positions of all 20 AAs in the protein sequence when ΔV = 1500 nm^3. At the bottom of each table the number of false positives and of false negatives for each AA is given.Table 4 collects these numbers in a single place for convenience and also includes the total number for errors.

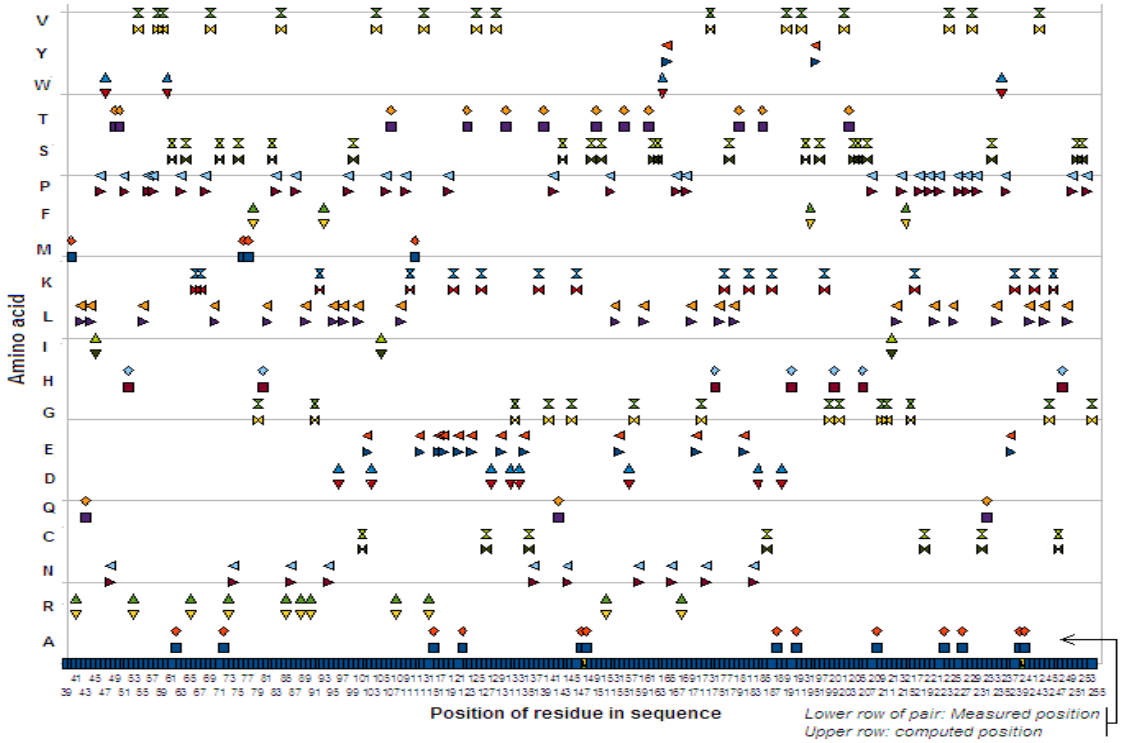

Figure 8 Computed sequence matches exactly with actual sequence when ΔV = 1400

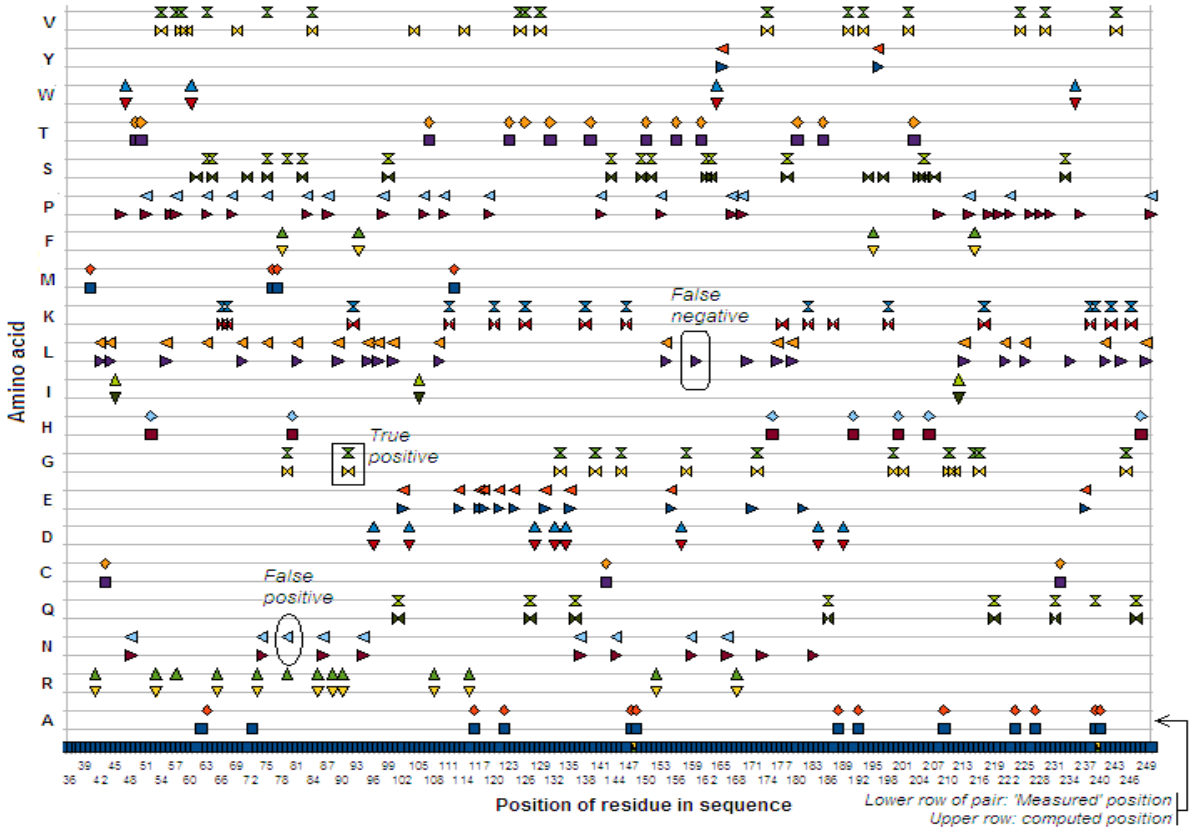

Figure 9 Computed sequence matches and actual sequence when ΔV = 1500. Examples of true match, false positive, and false negative are shown in enclosing boxes of different shapes.

Table 3A Positions of AAs (left column of AA) in actual sequence and in computed sequence (right column) with ΔV = 1500. Blue: false negative, Red: False positive

A	A	R	R	N	N	D	D	C	C	Q	Q	E	E	G	G	H	H	I	I
62	63	41	41	48	48	101	101	43	43	96	96	102	102	79	79	52	52	45	45
72	116	53	53	74	74	127	127	142	142	103	103	113	113	91	91	80	80	105	105
116	122	65	57	86	79	136	136	232	232	128	128	117	117	133	133	175	175	212	212
122	147	73	65	94	86	186	186	320	320	132	132	118	118	140	140	191	191		
147	148	85	73	137	94	219	219			134	134	121	121	145	145	200	200		
148	188	88	79	144	137	231	231			157	157	124	124	158	158	206	206		
188	192	90	85	159	144	247	239			184	184	130	130	172	172	248	248		
192	209	108	88	166	159	261	247			189	189	135	135	199	199	283	283		
209	223	115	90	173	166	266	261			263	263	155	155	201	210				
223	227	152	108	183	342	308	266			296	296	171	237	210	215				
227	239	168	115	342	346	310	308			298	298	181	260	211	216				
239	240	271	152	346			310			299	299	237	311	216	245				
240	268	274	168							304	304	260	324	245	254				
268	269	279	271							333	333	311	326	254	259				
269	280	284	279							339	339	324	335	259	312				
280	281	286	286							340	340	335		282	329				
281	316	288	288							361				292	336				
316	325	306	306							371				312	341				
325	331	309	309											329	372				
331		334	337											336	375				
		337	352											341	376				
		344	357											372					
		348	360											375					
		352	365											376					
		357	366																
		358	369																
		360	373																
		364	378																
		365																	
		366																	
		369																	
		373																	
		374																	
		378																	
Numbers below are number of false negatives (left column) and number of false positives (right column) for each AA																			
1	1	7	2	2	1	0	1	0	0	2	0	2	1	2	1	0	0	0	0

Table 3B Positions of AAs (left column of AA) in actual sequence and in computed sequence (right column) with ΔV = 1500. Blue: false negative, Red: False positive

L	L	K	K	M	M	F	F	P	P	S	S	T	T	W	W	Y	Y	V	V
42	42	66	66	40	40	78	78	**46**	51	**61**	63	49	49	47	47	165	165	54	54
44	44	67	67	76	76	93	93	51	57	64	64	50	50	60	60	196	196	58	57
55	55	92	92	77	77	195	195	**56**	63	71	75	107	107	164	164			**59**	58
70	**63**	111	111	112	112	215	215	57	68	75	**79**	123	123	235	235			**69**	**63**
81	70	120	120	257	257	356	356	63	**75**	82	82	131	**126**	307	307			84	**75**
89	75	126	126	262	262			68	83	99	99	139	131	370	370			**104**	84
95	81	138	138	343	343			83	87	143	143	150	139					**114**	125
97	89	146	146					87	98	149	149	156	150					125	126
100	95	**177**	182					98	106	151	151	161	156					129	129
109	97	182	198					106	110	162	162	180	161					174	174
154	100	**187**	217					110	119	163	163	185	180					190	190
160	109	198	238					119	141	178	178	203	185					193	193
170	154	217	**239**					141	153	**194**	205	300	203					202	202
176	176	238	242					153	167	**197**	233	353	300					224	224
179	179	242	246					167	169	**204**	251		353					229	229
213	213	246	265					169	214	205	252							243	243
221	221	265	287					**208**	222	**207**	272							258	258
225	225	287	289					214	250	233	273							328	328
234	241	289	317					**218**	253	251	275							347	347
241	249	317	**326**					**220**	264	252	276							349	349
244	255	330	330					222	278	272	291								
249	256	**345**	367					**226**	285	273	**326**								
255	270	**355**	368					**228**	293	275	351								
256	290	367						**230**	294	276	354								
270	297	368						**236**	301	291	377								
290	303							250	302	**322**									
295	318							253	314	**332**									
297	321							264	**315**	351									
303	326							**267**	**319**	354									
305	327							**277**		377									
318	338							278											
321	350							285											
326	359							293											
327	362							294											
338	363							301											
350	379							302											
359								**313**											
362								314											
363								315											
379								319											
								323											
Numbers below are number of false negatives (left column) and number of false positives (right column) for each AA																			
5	1	4	2	0	0	0	0	**11**	3	7	2	0	1	0	0	0	4	0	2

Table 4 False positives and false negatives in computed sequence for protein 5 with $\Delta V = 1500\ nm^3$

AA	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V	Total
No of false positives	1	7	2	0	0	2	2	2	0	0	5	4	0	0	11	7	0	0	0	4	47
No of false negatives	1	2	1	1	0	0	1	1	0	0	1	2	0	0	3	2	1	0	0	2	18

5. Sequencing and quantification of proteins in a mixture

Consider a mixture of M protein molecules $P_1, P_2, ..., P_M$. The output of the sequencing procedure described in the previous section when applied to the mixture consists of 20M partial sequences. For each of the M molecules there are 20 conjugated sequences of length N, one per AA_k, $1 \leq k \leq 20$. Sequencing consists of finding the set of conjugated sequences corresponding to the same parent molecule. To do this the lists are mapped to an undirected graph G_M with 20M vertexes, one per conjugated sequence. Two vertexes in the graph are adjacent if and only if the their lists have no common entries. Since there can be more than one list with the same entries either because they are from two copies of a protein or because two distinct proteins can have AA_k in the same positions, a vertex is set adjacent to another only if there is no other vertex already determined to be adjacent to the latter. All vertexes that are adjacent to each other correspond to conjugated sequences for a single molecule. It follows that G_M consists of M cliques (subgraphs in which every vertex is adjacent to every other) of degree 20. Sequencing of the M molecules then reduces to identifying these cliques. On the face of it this might look computationally difficult because the clique identification problem is known to be NP-hard [27]. However the problem is simplified considerably on recognizing that the M cliques are mutually disjoint. Thus G_M consists of M components each of which is a clique. It then suffices to identify these components, such identification can be done in polynomial time with a graph components algorithm, which is commonly based on depth-first search and runs in O(20M) time (or less) [27]. Since a component is defined by its vertexes, separating it isolates the 20 lists for the component. The full sequence can then by obtained from the corresponding 20 sequences containing the positions of AA_k, $1 \leq k \leq 20$, as described in Section 5. By adding M counters the mixture can also be quantified. Alternately the M sequences can be sorted on the sequence and copies extracted from the sorted list of sequences. This latter approach is used below. The mixture sequencing and quantification procedure is given in pseudocode next. There are two parts:
1) MakeGraphFromConjugatedSequences; 2) ConstructMixtureSequencesFromGraph.

Procedure MakeGraphFromConjugatedSequences
Input: 20M lists containing positions of occurrence of each AA in each of M sequences in the mixture given by ConjSeq[M][20] (array of lists of integers with values in the range 0 to N-1, where N is length of protein)
Output: Adjacency graph of 20M vertexes for the 20 lists input- G_M [M×20][M×20] with boolean elements
Initialize G_M [M×20][M×20] to all 0s

```
1. for k1 = 1 to M do:                                  // each of M molecules in sample
   1.1 for k2 = 1 to 20 do:                             // each of 20 AAs
       1.1.1 for m1 = 1 to M do:                        // each of M molecules in sample
       1.1.1.1 for m2 = 1 to 20 do:                     // each of 20 AAs
               1.1.1.1.1 if (ConjSeq[k1][k2] and ConjSeq[m1][m2] have no elements in common and
                             there is no other list ConjSeq[k1'][k2'] = list ConjSeq[k1][k2] such that GM[k1',k2']
                             [m1,m2] = 1 or GM[m1,m2][k1',k2'] = 1  )
                           set G_M [k1,k2][m1,m2] and G_M [m1,m2][k1,k2] to 1   // adjacency matrix is symmetric
                         end if
               end for
             end for
         end for
   end for
```

Procedure ConstructMixtureSequencesFromGraph
Input: Adjacency graph: G_M [M×20][M×20] = 20M × 20M boolean matrix; 20 M lists of conjugated AA positions
Output: M protein sequences

1. **Call** ConnectedComponentsAlgorithm with G_M, return with M sets of 20 vertexes each corresponding to a list of pairs of the form (position, AA)
2. **for** each of the M cliques corresponding to the set of 20 vertices in a component **do**
   2.1 Merge the 20 position lists of (position, AA) pairs into a single list ordered on the position field
   2.2 Read sequence of AA values in ordered list of pairs, output as sequence for clique

end for

3. Sort the M sequences on the sequence strings (constructed from the second field)
4. Scan sorted sequence, count number of occurrences of unique strings down the sequence, output as copy count for that sequence

Complexity of mixture sequencing and quantification

1) In MakeGraphFromConjugatedSequences, the embedded loops with loop variables (k1,k2) and (m1,m2) require computation on the order of $O(M^2)$.

2) In ConstructMixtureSequencesFromGraph, the call to ConnectedComponents algorithm requires work on the order of O(M). The Merge step has complexity O(N), there are M merges, so the total work is O(MN).The quantification step requires sorting M strings of length N. For constant N, this would require O(M log M) time. Counting duplicates is linear on the sorted set of M strings, so the effort required is O(M). The overall complexity appears at first glance to be $O(M^2)$. However this can be done more efficiently with appropriate data structures. Ultimately the determinant of complexity is the Merge step, so the overall complexity is O(MN).

6 Discussion

Assuming that conjugate molecules specific to each AA can be designed, it would appear that the technology needed to translate the proposed method into practice is available. A number of implementation and procedural issues are considered next.

1) The proposed procedure may be implemented in the bulk if samples of sufficient size are available.

2) If sufficient quantities of sample molecules are not available the procedure can be implemented serially in 20 cycles, one per AA. Each cycle would then consist of the following sequence of steps: 1. Attach conjugates for AA_i to every protein molecule in the sample; 2. Sequence the conjugated sample mixture; 3. Detach conjugates and wash away conjugates.

If a sufficient quantity of the sample is available then 20 channels, one per AA type, can be used to obtain conjugated sequences with that AA. Following this the assembly of sequences can be done as in Section 5.

3) With a parallel array of 10000 nanopores, a conservative time estimate of 1 hour for conjugation and 1 hour for detaching and washing, and negligible data processing time, 10000 samples with M molecules in each can be sequenced and quantified in ~2 hours.

4) In [22] a header and trailer of 20-30 charged D residues is used to draw the protein into the pore and encourage undirectional translocation. Incidentally this artifice can also be used to determine the entry orientation of the protein, namely C-terminal to N-terminal or the reverse. In the present case, additionally it is useful to circumvent edge effects due to filling of the pore at the front end and emptying at the back end.

5) Notice that almost all of the data processing can be done offline.

6) The procedure is non-destructive. By detaching conjugates after each cycle in the serial version or at the end in the parallel version the sample can be fully recovered. Thus the procedure has an archival character. (As usual it is assumed in either case that there are no losses due to adsorption, washing, and other factors.)

7) It is assumed that the presence of conjugates does not adversely affect the unidirectional and approximately constant translocation rate properties displayed in [22]. In particular conjugate molecules may be designed to be charge-neutral.

8) The proposed procedure can be used for protein identification by using only a small number (2 to 4) of AA types for detection, as is done, for example, in [21]. In general identification can be done in much less time than sequencing.

9) With suitable changes the procedure may be adapted for the detection of post-translational modifications (PTMs) in proteins. For example, a PTM behaves like a conjugate attached to an AA as it adds volume to the latter. An unconjugated sequence may contain clues to the position and identity of the PTM.

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