Protein secondary structure prediction based on quintuplets

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Abstract

Simple hidden Markov models are proposed for predicting secondary structure of a protein from its amino acid sequence. Since the length of protein conformation segments varies in a narrow range, we ignore the duration effect of length distribution, and focus on inclusion of short range correlations of residues and of conformation states in the models. Conformation-independent and -dependent amino acid coarse-graining schemes are designed for the models by means of proper mutual information. We compare models of different level of complexity, and establish a practical model with a high prediction accuracy.

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1 Introduction

Methods for predicting the secondary structure of a protein from its amino acid sequence have been developed for 3 decades. Besides neural network models and nearest-neighbor methods, the Chou-Fasman/GOR statistical method is well-established and commonly used. In 1974, assuming an oversimplified independency to cope with the large size 20 of the amino acid alphabets at a small size of database, Chou and Fasman (1974) derived a table of propensity for a particular residue to be in a given secondary structure state. By combining with a set of rules, the protein secondary structure was predicted using this propensity. Later, in the first version of the GOR program (Garnier, Osguthorpe, and Robson, 1978), the state of a single residue $a_i$ was predicted according to a window from $i - 8$ to $i + 8$ surrounding the residue. Unlike Chou-Fasman which assumes that each amino acid individually influences its own secondary structure state, GOR takes into account the influence of the amino acids flanking the central residue on the central residue state by deriving an information score from the weight matrix describing 17 individual amino acid frequencies at sites $i + k$ with $-8 \leq k \leq +8$. By using a single weight matrix, the correlation among amino acids within the window was still ignored. In the later version GOR III (Gibrat, Garnier, and Robson, 1987), instead of single weight matrix for every structure state, 20 weight matrices, each of which corresponds to a specific type of the central residue, were used. These conditional weight matrices take the pair correlation between the central residue and a flanking one into account. In the most recent version of GOR (GOR IV, Garnier, Gibrat, and Robson, 1996), all pairwise combinations of amino acids in the flanking region were included.

Hidden Markov models (HMMs) (Rabiner, 1989) have been applied to molecular biology, in particular in gene-finding. There is a constant tendency in developing HMMs for protein structure prediction (Asai et
A probabilistic approach similar to the gene finder Genscan has been developed for protein secondary structure prediction without using sliding windows (Schmidler, Liu and Brutlag, 2000). In terms of Bayesian segmentation, the method integrated explicit models for secondary structure classes helices, sheets and loops with other observed structure aspects such as segment capping signals and length distributions, and reached an accuracy comparable to GOR.

Compared with DNA sequences, protein sequences are generally short, and their amino acid alphabet is of a large size 20. The range of lengths of secondary structure segments is rather small. The effect of duration might play a less important role. Here we develop a simple hidden Markov model with higher order correlations included for the secondary structure prediction. We propose several schemes for the amino acid alphabet reduction in order to incorporate residue correlation in the model. While the model is much simpler than the Bayesian segmentation model, its performance is still competitive.

2 Methods

A simplified version of the model can be constructed in the frame of the Chou-Fasman propensity scheme. We shall start with this model to explain several key points, and then discuss more realistic models.

In the Chou-Fasman approach, discriminant thresholds and post-prediction filtering rules are required. They can be avoided in a full probabilistic model.

As in the most methods, we consider 3 states \( \{h, e, c\} \) generated from the 8 states of Kabsch and Sander (1983) by the coarse-graining \( H, G, I \rightarrow h, E \rightarrow e \) and \( X, T, S, B \rightarrow c \). Let \( R = R_1 R_2 \ldots R_n \) be a sequence of \( n \) amino acid residues, and its corresponding secondary structure sequence be \( S = S_1 S_2 \ldots S_n \). The structure prediction is the mapping from \( R \) to \( S \). The main restriction to a structure sequence is that the shortest length of the consecutive state \( h \) must be 3, and that of \( e \) be 2. To cope with this restriction, we use triplet states instead of the 3 single states \( c, e \) and \( h \). In the total 27 triplets, only 19 are legitimate. The forbidden 8 are of the type \( \overline{ee} \) or \( \overline{hh} \), where \( \overline{e} \) indicates a non-\( e \), i.e. either \( c \) or \( h \), and the meaning of \( \overline{h} \) is analogous. The first order Markov model for the triplets is the third order Markov model for the original mono-states. Any of the 19 triplets can only transit either to 3 or to 1 state. That is, the transition matrix is rather sparse. The 19 triplets and their transited states are listed in Table 1.

Denoting by \( \sigma_i \) the triplet states, we may translate \( S_1 = S_2 = \ldots S_{n-1} = \sigma_2 \sigma_3 \ldots \sigma_{n-1} \) of length \( n-2 \). (Note that the subscripts \( i \) for \( \sigma_i \) are from 2 to \( n-1 \) for convenience.) The Markov process for \( \sigma \) is characterized by the set of probabilities for initial states

\[
\pi(l) = \text{Prob}(\sigma_2 = l),
\]

and the transition rates

\[
T_{kl} = \text{Prob}(\sigma_i = l|\sigma_{i-1} = k) = T(\sigma_{i-1}, \sigma_i).
\]

Sequence \( R \) is then related to \( \Sigma \) or \( S \) by the emission probabilities

\[
P(x|\delta) = \text{Prob}(R_i = x|\sigma_i = \delta),
\]

which generate \( S_2, \ldots S_{n-1} \). Extra probabilities

\[
Q(x|\delta) = \text{Prob}(R_j = x|\sigma_{j\pm 1} = \delta), j \in \{1, n\}
\]

are needed for generating \( R_1 \) and \( R_n \).
In this model the probability for the state sequence $S$ or $\Sigma$ is

$$
P(\Sigma) = \pi(\sigma_2) \prod_{i=2}^{n-2} T(\sigma_i, \sigma_{i+1}),
$$

and the likelihood for $R$ to be at $S$ is

$$
P(R|\Sigma) = Q(S_1|\sigma_2)Q(S_n|\sigma_{n-1}) \prod_{i=2}^{n-1} P(S_i|\sigma_i).
$$

The joint probability is then

$$
P(R, \Sigma) = P(R, S) = P(R|\Sigma)P(\Sigma).
$$

The predicted structure is inferred as

$$
\Sigma^* = \arg \max_{\Sigma} P(\Sigma|R) \propto \arg \max_{\Sigma} P(R, \Sigma).
$$

By means of the recursion relation

$$
\Gamma_2(\sigma) = Q(S_1|\sigma)\pi(\sigma)P(R_2|\sigma),
$$

$$
\Gamma_i(\sigma) = \max_{\delta} \Gamma_{i-1}(\delta)T(\delta, \sigma)P(R_i|\sigma), \quad 2 < i < n,
$$

$$
\Gamma \equiv \Gamma_n = \max_{\delta} \Gamma_{n-1}(\delta)Q(S_n|\delta),
$$

and by recording the pre-state leading to the maximal $\Gamma_i(\sigma)$, the ‘best’ path $\Sigma^*$ can be traced back from the last $\sigma_{n-1}^*$. This is the so-called Viterbi algorithm for dynamic programming.

According to the standard forward-backward algorithm for HMMs, the forward and backward variables $A_i$ and $B_i$ may be defined as follows.

$$
A_2(\sigma) = Q(S_1|\sigma)\pi(\sigma)P(R_2|\sigma),
$$

$$
A_i(\sigma) = \sum_{\delta} A_{i-1}(\delta)T(\delta, \sigma)P(R_i|\sigma), \quad 2 < i < n.
$$

Similarly,

$$
B_{n-1}(\sigma) = Q(S_n|\sigma),
$$

$$
B_i(\sigma) = \sum_{\delta} B_{i+1}(\delta)T(\sigma, \delta)P(R_{i+1}|\delta), \quad 2 < i < n-1.
$$

It can be seen that for non-ending $i$, $A_i(\sigma) = \text{Prob}(R_{1:i}, \sigma_i = \sigma)$, $B_i(\sigma) = \text{Prob}(R_{i+1:n}|\sigma_i = \sigma)$, and the partition function

$$
Z \equiv \sum_{\Sigma} P(R, \Sigma) = \sum_{\sigma} A_i(\sigma)B_i(\sigma)
$$

$$
= \sum_{\sigma} A_i(\sigma)B_i(\sigma), \quad 2 \leq i \leq n-1.
$$

Denoting $\sigma_i^{(0)}$ the center $S_i$ of the triplet $\sigma_i = S_{i-1}S_iS_{i+1}$, and introducing the characteristic function for $z \in \{c, e, h\}$

$$
\delta(\sigma_i, z) = \begin{cases} 
1, & \text{if } \sigma_i^{(0)} = z, \\
0, & \text{otherwise},
\end{cases}
$$
we may infer single residue state from the marginal posterior

$$\text{Prob}(S_i = z|R) \propto \sum_{\sigma} A_i(\sigma)B_i(\sigma)\delta(\sigma, z).$$

(20)

This is the Baum-Welch algorithm for single residue states.

So far, only the correlation of conformation states has been considered. Residue triple will involve $20^3 = 8000$ parameters for each state $\sigma$. To avoid large training sets and model overfitting, a reduced amino acid alphabet is desired. For example, the reduction of 20 amino acids to 3 classes leads to only 27 combinations. However, there are as many as

$$\frac{1}{3!} \sum_{j=0}^{3} C_j^3 (-1)^j (3-j)^{20} \approx 5.8 \times 10^8$$

ways of clustering 20 amino acids into 3 classes (Duran and Odell, 1974). For a given clustering $\{a_i\}_{i=0}^{19} \rightarrow \{b_j\}, b_j \in \{0, 1, 2\}$, denoting by $\rho_i = r_{i-1}r_i r_{i+1}$ the reduced residue triple corresponding to state $\sigma_i$, we may calculate the mutual information between the reduced residue triple $\rho$ and the triple state $\sigma$:

$$I(\rho, \sigma) = H[\rho] + H[\sigma] - H[\rho, \sigma],$$

(21)

where $H[x]$ is the Shannon entropy of $x$. (If the clustering independent $H[\sigma]$ is ignored, $I$ would become the conditional entropy $H[\sigma|\rho]$.) The best clustering may be determined by maximizing the objective function $I(\rho, \sigma)$. The replacement of the above $P(R_i|\sigma_i)$ with $P(\rho_i|\sigma_i)$ leads to a version which takes some residue correlation into account.

A more realistic model uses quintuplets. Among the total $3^5 = 243$ quintuplets of the conformation states, only 75 are legitimate. Exclusion of 7 rare ones (eceeh, hceeh, heece, heeeh, heeh, hceeh, and hhee) further reduces the total number of states into 68, which are listed in Table 2. We shall still use the same notation $\sigma_i$ for these 68 conformation states. To take residue quintuplet correlation into account, we substitute the central residue score $P(R_i|\sigma_i)$ with $P(R_i|\sigma_i, r_{i-2}r_{i-1}r_{i+1}r_{i+2})$, where $r_i$ stands for reduced residue classes. More words need to be said about the amino acid clustering. We have observed the fact that counts of ccccc, eeeee and hhhhh in databases are dominant over those of remaining 65. The various propensities of amino acid residues to different conformations imply that amino acid clustering should depend on conformations. We want to cluster amino acids separately for each conformation. For this purpose, for example, to find the best clustering at conformation $c$, we collect a subset of residue quintuplets whose conformation is ccccc. Denote by $R_0$ the central residue of a residue quintuplet, and by $r_{-2}r_{-1}r_1 r_2$ the reduced classes of the other 4 residues. Taking the mutual information $I(R_0, r_{-2}r_{-1}r_1 r_2)$ as the objective function, we determine the best clustering at $c$. To find at which position the residue depends most strongly on others, we calculate mutual information for nonreduced residue placed at different positions of a residue quintuplet. While the largest $I$ is found when the nonreduced residue is at the center for conformation $c$, the position of the nonreduced residue which gives the largest $I$ is the second position for conformation $c$, and is the fifth for $h$. However, for either $c$ or $h$, the largest $I$ is still very close to $I(R_0, r_{-2}r_{-1}r_1 r_2)$. The mutual information excesses with respect to $I(R_0, r_{-2}r_{-1}r_1 r_2)$ for different positions at conformations $c, e$ and $h$ are listed in Table 3. Thus, for simplicity, we always place the nonreduced residue at the center for all conformations. We then calculate refined residue scores from the conformation-dependent clustering. For example,

$$P(R_i|\sigma_i = ccchh, r_{i-2}r_{i-1}r_{i+1}r_{i+2}) \rightarrow P(R_i|\sigma_i, r_{i-2}c r_{i-1}^c r_{i+1}^h r_{i+2}^h),$$

(22)
where the superscript of $r_i$ indicates its conformation. The whole procedure for the dynamic programming remains almost the same, except for some care when dealing with two more end sites.

3 Result

We create a nonredundant set of 1612 non-membrane proteins for training parameters from PDB_SELECT (Hobohm and Sander, 1994) with amino acid identity less than 25% issued on 25 September of 2001. The secondary structure for these sequences are taken from DSSP database (Kabsch and Sander, 1983). As mentioned above, the eight states of DSSP are coarse-grained into 3 states: $h$, $e$ and $c$. This learning set contains 268031 residues with known conformations, among which 94415 are $h$, 56510 are $e$, and 117106 are $c$. The size of the learning set is reasonable for training our parameters. There are 296 unknown residues. We add an extra ‘unknown’ amino acid category called $X$ to the 20 known ones.

In order to assess the accuracy of our approach, we use the following 2 test sets: Sets 1 and 2. A set of 124 nonhomologous proteins is created from the representative database of Rost and Sander (1993) by removing subunits A and B of hemagglutinin 3hmg, which are designated as membrane protein by SCOP (Murzin et al, 1995). The 124 sequences and the learning set are not independent of each other according to HSSP database (Dodge, Schneider and Sander, 1998). That is, some proteins of the 124 sequences are homologous with certain proteins in the learning set. Removing the homologous proteins from the 124 sequences and 5 sequences with unknown amino acid segments longer than 6, we construct Set 1 of 76 proteins. Nonredundant 34 proteins with known structures of the CASP4 database issued in December of 2000 are taken as Set 2 (CASP4, 2000).

3.1 Amino acid clustering

The first method for clustering uses the mutual information $I(\rho, \sigma)$ between the reduced oligo-peptide $\rho$ and its corresponding conformation $\sigma$. Setting the number of reduced classes at 3, 4 and 5, and fixing $\sigma$ to be triplets, we find the conformation-independent clustering of amino acids as shown in Table 4. Roughly speaking, class 0 is the hydrophobic, and is the same for the all 3 clusterings (except for the ‘unknown’ $X$ in the clustering into 5). Increasing the number of classes from 3 to 4, 5 results in new classes forming by single special amino acids P(Pro) and G(Gly). The similar clustering may be conducted in terms of quintuplets, but the results do not coincide with those from triplets.

The second method for clustering is conformation-dependent. We collect residue quintuplets of conformations $cccc$, $eeee$ and $hhhh$ separately. The objective function for clustering now is the mutual information $I(R_0, r_{-2}r_{-1}r_1r_2|\sigma)$ with conformation $\sigma$ fixed. The results of clustering into 3 and 4 classes are listed in Table 5. Indeed, the cluster patterns for different conformations are quite dissimilar.

3.2 Secondary structure prediction

We shall index different models by $N_s-N_a$, where $N_s$ and $N_a$ are the numbers of conformation states and residue combinations, respectively. For example, the simplest model is model 19-21, which uses $P(R_i|S_{i-1}S_iS_{i+1})$ to score residues. We may also use the propensity scores $P(R_i|S_{i-1}S_iS_{i+1})/P(R_i)$, which result in an extra factor $\prod_{i=0} P(R_i)$. Since the factor is independent of conformation sequences, it brings no new effect. When the scores are replaced by $P(r_{i-1}r_ir_{i+1}|S_{i-1}S_iS_{i+1})$ with $r_i$ being the reduced 3-class residues, we have model $19-3 \times 3 \times 3$. The first and last sites of the predicted conformation of any sequences are always set at
For model 19-21 we determine the best conformation sequence as whole by the Viterbi algorithm and single residue conformation states by the Baum-Welch algorithm. To assess prediction methods, we calculate for each conformation the sensitivity $s_n$ and specificity $s_p$

$$s_n = \frac{TP}{TP + FN}, \quad s_p = \frac{TP}{TP + FP},$$

where $TP$, $FP$ and $FN$ are site counts of the ‘true positive’, ‘false positive’ and ‘true negative’ with respect to the observed real conformation. The results of model 19-21 are listed in Table 6, where the total sensitivity $Q_3$ for all conformations is also given. It is clearly seen that the inference from the Baum-Welch marginal posterior is significantly superior to that from the Viterbi algorithm in $Q_3$ value.

The next examined model uses reduced residue triplets. Reducing amino acids into 3 and 4 classes, we have models 19-27 and 19-64, respectively. The prediction accuracies of these two models are also listed in Table 6. We see that the inclusion of residue correlation dramatically improves the prediction accuracy.

The remaining part of Table 6 shows the prediction accuracies of quintuplet models. We examine the models on both test Sets 1 and 2. For all the models we take $P(R_i|r_{i-2}r_{i-1}r_{i+1}r_{i+2}, \sigma_i)$ as the residue scores. We first compare conformation-independent with conformation-dependent clustering of amino acids. We find that the conformation-dependent clustering gains about 1 percent in the prediction accuracy for model 68-81×21. The conformation-independent clustering is then not considered later on. Model 68-256×21 contains more information about correlated residues, and has a better performance. The accuracies obtained on Set 1 are generally higher than those on Set 2. Besides the popular predictor GOR IV, there is another secondary structure predictor SSP (Solovyev and Salamov, 1991, 1994) based on discriminant analysis using single sequence. To compare with them, their accuracies on the same test sets are also listed in the table.

4 Discussions

We have presented simple hidden Markov models to predict secondary structure using single protein sequence. The hidden sequence is generated by a Markov process of multi-site conformation states. Considering that structure segments of proteins are generally short, we have ignored the duration effect, and focused on short range correlations. We proposed several schemes for coarse-graining the amino acid alphabet in order to include multi-residue correlation. Such reduction has been used in the Bayesian segmentation of protein secondary structure (Schmidler, et. al., 2000). However, here we derived the coarse-graining schemes specially for scoring residues to fit conformations. We have discussed only the principle of taking proper mutual information as an objective function for clustering, but did not exhaust all possibilities for clustering. For example, to diminish parameters, one may consider residue triplets at conformation quintuplet states. Another possibility is to use quartuples for both residues and conformations. One can also cluster quintuplet conformation states to less states.

There are rooms for further improvement of our approach. Simple weights (3 values) may be introduced to adjust residue scores according to its single-site conformation. Moreover, we may divide a training set into several, say 2, subsets according to residue statistics. Again, for this purpose the coarse-graining schemes help. The two subsets are then used separately for training to get refined models. We first classify a query sequence into one of the two categories, and then apply to it the corresponding refined model. We have tested this on the simple triplet models. The primitive result of up to 2% in accuracy improvement is encouraging. This, and the protein family recognition using multiple reduced amino acid residues, are under study.
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Table 1. Triplet states and their transited states.

| State | Transited | State | Transited |
|-------|-----------|-------|-----------|
| 0 CCC | 0, 1, 2   | 10 EEH | 11        |
| 1 CCE | 3         | 11 EHH | 18        |
| 2 CCH | 4         | 12 HCC | 0, 1, 2   |
| 3 CEE | 8, 9,10   | 13 HCE | 3         |
| 4 CHH | 18        | 14 HCH | 4         |
| 5 ECC | 0, 1, 2   | 15 HEE | 8, 9,10   |
| 6 ECE | 3         | 16 HHC | 12,13,14  |
| 7 ECH | 4         | 17 HHE | 15        |
| 8 EEC | 5, 6, 7   | 18 HHH | 16,17,18  |
| 9 EEE | 8, 9,10   |       |           |

Table 2. 68 quintuplet states.

| Conformation | Position of the nonreduced |
|--------------|-----------------------------|
|              | 1   | 2   | 4   | 5   |
| c            | -19.5 | 2.7 | -3.0 | -7.4 |
| e            | -46.1 | -10.2 | -15.5 | -82.3 |
| h            | -49.6 | -33.8 | -0.5 | 1.8 |

Table 3. Mutual information excesses ($\times 10^{-3}$) for different positions of the nonreduced residue with respect to the mutual information for the nonreduced residue at the quintuplet center. The center is referred to as position 3.
Table 4. Conformation-independent clustering of amino acids into 3, 4 and 5 classes.

| Amino Acid | A | V | C | D | E | F | G | H | I | W | K | L | M | N | Y | P | Q | R | S | T | X |
|------------|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 3-class    | 1 | 0 | 0 | 2 | 1 | 0 | 2 | 1 | 0 | 0 | 1 | 0 | 0 | 2 | 0 | 2 | 1 | 1 | 1 | 1 | 1 |
| 4-class    | 1 | 0 | 0 | 2 | 1 | 0 | 2 | 2 | 0 | 0 | 1 | 0 | 0 | 2 | 0 | 3 | 1 | 1 | 2 | 2 | 1 |
| 5-class    | 1 | 0 | 0 | 2 | 1 | 0 | 4 | 2 | 0 | 0 | 1 | 0 | 0 | 2 | 0 | 3 | 1 | 1 | 2 | 2 | 0 |

Table 5. Conformation-dependent clustering of amino acids into 3 and 4 classes.

| Amino Acid | A | V | C | D | E | F | G | H | I | W | K | L | M | N | Y | P | Q | R | S | T | X |
|------------|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| c, 3-class | 1 | 2 | 0 | 0 | 1 | 2 | 0 | 0 | 2 | 2 | 1 | 2 | 2 | 0 | 2 | 0 | 1 | 1 | 1 | 1 | 2 |
| e, 3-class | 0 | 2 | 0 | 1 | 1 | 2 | 0 | 1 | 2 | 2 | 1 | 0 | 0 | 1 | 2 | 0 | 1 | 0 | 1 | 1 | 1 |
| h, 3-class | 0 | 2 | 0 | 1 | 1 | 2 | 1 | 1 | 2 | 2 | 1 | 2 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 |
| c, 4-class | 1 | 2 | 2 | 0 | 1 | 2 | 3 | 1 | 2 | 2 | 1 | 2 | 2 | 0 | 2 | 0 | 1 | 1 | 1 | 1 | 2 |
| e, 4-class | 0 | 1 | 2 | 3 | 3 | 1 | 2 | 0 | 1 | 0 | 3 | 2 | 2 | 3 | 1 | 2 | 3 | 0 | 0 | 3 | 2 |
| h, 4-class | 1 | 2 | 1 | 3 | 0 | 2 | 3 | 3 | 2 | 2 | 0 | 2 | 2 | 3 | 1 | 3 | 3 | 0 | 3 | 0 | 1 |

Table 6. Accuracy of secondary structure predictions for different models. Here, VI and BW stand for ‘Viterbi’ and ‘Baum-Welch’ algorithms, respectively. For all models 68-k, conformation-dependent reductions are used except for model 68-81\times21^* where the single conformation-independent reduction is used.

| Model      | Test set | $S^c_n$ | $S^c_p$ | $S^c_s$ | $S^h_n$ | $S^h_p$ | $Q_3$ |
|------------|----------|---------|---------|---------|---------|---------|------|
| 19-21, VI  | 2        | 48.69   | 62.92   | 7.94    | 64.09   | 84.17   | 48.07 | 53.24 |
| 19-21, BW  | 2        | 70.67   | 62.27   | 30.74   | 54.55   | 66.12   | 60.11 | 60.45 |
| 19-27, VI  | 2        | 62.50   | 63.87   | 56.02   | 46.58   | 55.82   | 61.48 | 58.63 |
| 19-64, VI  | 2        | 64.10   | 65.31   | 50.11   | 47.59   | 62.45   | 63.06 | 60.50 |
| 68-81\times21^*, VI | 2 | 60.12   | 69.16   | 44.54   | 54.89   | 75.48   | 60.26 | 62.53 |
| 68-81\times21, VI | 2 | 62.01   | 68.21   | 44.26   | 57.79   | 76.51   | 61.98 | 63.64 |
| 68-81\times21, BW | 2 | 74.51   | 61.71   | 47.18   | 59.99   | 61.52   | 68.93 | 63.83 |
| 68-81\times21, VI | 1 | 70.92   | 66.51   | 54.27   | 53.45   | 62.00   | 69.07 | 64.46 |
| 68-81\times21, BW | 1 | 71.01   | 68.98   | 52.97   | 57.58   | 67.37   | 66.69 | 66.00 |
| 68-256\times21, VI | 2 | 65.35   | 68.41   | 54.73   | 58.41   | 70.11   | 64.58 | 64.86 |
| 68-256\times21, BW | 2 | 70.90   | 68.15   | 57.60   | 60.86   | 68.85   | 69.84 | 67.30 |
| 68-256\times21, VI | 1 | 68.34   | 69.97   | 55.34   | 57.68   | 70.12   | 66.23 | 66.18 |
| 68-256\times21, BW | 1 | 73.22   | 69.77   | 57.40   | 59.61   | 67.20   | 70.38 | 67.90 |
| GOR4       | 1        | 79.3    | 66.1    | 54.7    | 55.3    | 63.3    | 68.5  | 66.2  |
| SSP        | 1        | 59.2    | 52.8    | 69.0    | 55.3    | 67.0    | 68.1  | 60.0  |
| GOR4       | 2        | 81.9    | 62.0    | 43.0    | 54.6    | 67.1    | 64.3  | 63.4  |
| SSP        | 2        | 74.7    | 58.8    | 45.7    | 55.6    | 66.3    | 63.3  | 61.4  |