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On the Use of Neural Network Techniques to Analyze Sleep EEG Data

**Third Communication: Robustification of the Classifier by Applying
an Algorithm Obtained from 9 Different Networks**

Key Words

Neural networks
Sleep EEG
Automated sleep-stage scoring

Abstract

This is the third communication on the use of neural network techniques to classify sleep stages. In our first communication we presented the algorithms and the selection of the feature space and its reduction by using evolutionary and genetic procedures. In our second communication we trained the evolutionary optimized networks on the basis of multiple subject data in context with some smoothing algorithms in analogy of Rechtschaffen and Kales (RK). In this third communication we could demonstrate that the robustness concerning individual specific features of automatically generated sleep profiles could be reasonably improved by an additional modification of the procedure used by SASCIA (Sleep Analysis System to Challenge Innovative Artificial Networks). The outputs of nine different networks that were created by the data of 9 different subjects were used simultaneously for classification. The medians of the values obtained in each output measure were selected for the allocation to a sleep stage. The fitness criteria of 16 automatically generated sleep profiles showed reasonable concordance with the expert profile. Even though in single cases the concordance between conventional RK classifications and automatically generated profiles were a few percentages lower, the average correct classification of the 12 classified subjects improved substantially, thus proving that the classifier is more robust against individual-specific variability. Despite the fact that the expert generally employs three channels (EEG, EMG and EOG), at least to build up sleep profiles, the SASCIA system was able to produce profiles on the basis of only one EEG channel with 80% concordance and a correlation coefficient of 0.86. The feature selections were performed by genetic algorithms and the topologies of the networks were optimized by evolutionary algorithms. This algorithm will now be used for larger sample forward classification.

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Introduction

This paper is based on the neural network approaches communicated by Baumgart-Schmitt et al. [1–3]. The automatic analysis of sleep EEG is a nonlinear classification that is solved by neuronal networks. The sleep staging is represented by seven classes (stages wake, 1, 2, 3, 4, REM and movement). It is well known that neural networks can be trained and that they have the ability to generalize, comparable to real brain networks. Networks store their knowledge in a distributed mode and it is impossible to determine whether or not their knowledge is sufficient to make the right decision for all unknown cases. Networks can be optimized by evolutionary algorithms but the probability for a wrongly represented subspace and for a typical set of classification errors remains unequal to zero. One way to cope with it consists in using a population of networks instead of one network adapted with much effort. The members of that population will form more or less different conclusions. Because a decision is necessary, the knowledge of all networks has to be aggregated. Several operators were tested. As the most important result we proposed to use the median of the output values of all 9 networks. This averaging operation resulted in a robust classifier that, in connection with context rules, generated sleep profiles that were in reasonable agreement with the expert profiles. The developed system SASCIA (Sleep Analysis System to Challenge Innovative Artificial Networks) so far used only one EEG channel to extract features. Evolutionary and genetic approaches were applied to optimize the topology and learning parameters of the networks and to select the features from a high-dimensional feature space.

We decided to take only one single EEG channel for the analysis believing that both the rapid eye movements (REM) and the muscle activity as received by EMG are only epiphenomena of brain processes and that the EEG itself should carry all necessary information for the classification.

In two prior publications [2, 3], the feature extraction and the classification procedure were published in detail, including some smoothing rules in analogy to Rechtschaffen und Kales (RK) [4]. The main purpose of this third communication is to test the system for robustness using more than one classification rule simultaneously.

Methods

Subjects

The data were collected in a comprehensive investigation at the sleep laboratory of the Free University of Berlin. The sleep polysomnographics of 16 nights, derived from 9 healthy subjects, were analyzed. Four nights of 2 subjects and 3 nights for 1 subject were included. That means the results of 16 nights can be compared.

Recordings

The recording was done with Nihon Kohden EEG equipment. The analog signal was converted into digital signals with a 12-bit A-D converter. The recording using a time constant of 0.3 s and a low-pass filter of the EEG machine with about 6 dB/octave at 30 Hz. The sampling rate was 256 values per second of which every second point was taken for further analysis. From the 32 channels the central channel C4-A2 was selected. The conventionally classified profiles according to RK based on polysomnographic recordings were available for all nights. There was no artifact detection and no rejection of any segment.

Components of SASCIA [11]

The system SASCIA was used to teach and optimize neural networks and to test the abilities of the networks to generalize. The system consists of four main parts: (1) the feature extraction and selection; (2) the neural network component; (3) the evolutionary component, and (4) the genetic component.

The interaction of the main parts can be described in terms of hierarchical optimization procedure. According to the information flow chart shown in figure 1, the basic procedure is connected with the estimation of the weights of the networks. The evolution takes place at the next level. The topology and learning parameters of the networks are adapted to the task. The genetic algorithms are responsible for the optimal feature selection at the top level of the hierarchical optimization. The core of the system consists of neural networks that should separate the different sleep stages on the basis of features extracted from only one EEG channel. The features are taken by the input units of the supervised feed-forward networks and the excitations of the output units indicate the membership of the epochs to the sleep stages.

Genetic Algorithms and the Feature Space

The features based on the frequency range were extracted for each epoch with the length of 10 s. Segments with the length of 1 s were multiplied by the Hanning window. The transformation of the time series in the frequency range was performed by the fast Fourier transformation.

The windowing technique was used to make the results more insensitive to shifts of the boundaries of the epochs. The segments were overlapped and averaged to reduce the variance of the power spectrum. Originally 119 features were extracted [2]. To reduce the features space, a subset out of 31 pre-selected features was chosen by genetic algorithms [3]. This means that the number of input units was variable, while the number of output units was fixed (7 classes).

The following genetic procedures were applied [2, 3]: (1) recombination; (2) crossing-over; (3) mutation, and, (4) inversion.

Neural Networks and Evolutionary Strategies

The number of output units is connected with the number of sleep stages and the number of input units should fit the number of features that were selected by the genetic algorithms (in our case 31).

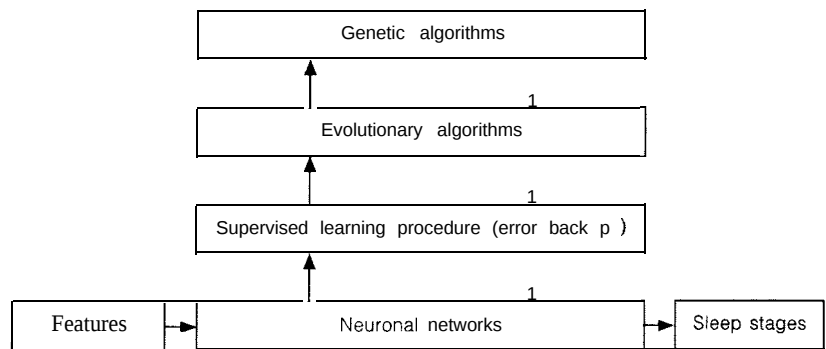


Fig. 1. Main components of SASCIA and information flow between them.

The optional number of hidden units that support the adaptation of the networks to the learning set in an optimal way is unknown. The learning is additionally influenced by different parameters: the learning rate, the momentum and the limits in the number of iterations. The evolutionary strategies are used to generate populations of networks with a variable number of hidden units in the first and second hidden layers and different values of the three learning parameters. The networks with the best reclassification results are regarded as members of the population with the greatest fitness. All members with a suitable fitness survive and give the opportunity to the next generation of networks to inherit their genes (parameters).

Context Rules

The knowledge to automatically generate sleep profiles is based on two sources: the manual scoring by an expert using the RK [4] rules and the RK rules themselves. Since RK apply context rules, we also developed context rules for our final (secondary) staging. That means the time horizon is restricted to one epoch in the numerical classification by neural networks. The following application of the rules uses a flexible time horizon. One example of the used context rules can be noted by

$$(\text{rem}, \text{rem}, \text{rem}) \Leftarrow (\text{rem}, \text{stage 2}, \text{rem})$$

with rem – sleep stage REM and stage 2 as sleep stage 2 transform triple of epochs. The sleep stage 2 epoch should be transformed to rem if the frame is formed by rem. The time horizon is restricted to length of three epochs. The next example

$$[\text{stage 2}, (\text{stage 2})\dots, \text{stage 2}] \Leftarrow [\text{stage 2}, (\text{stage 1})\dots, \text{stage 2}]$$

with ()... as repetition operator and stage 1 as sleep stage 1 is called ‘far range rule’ because the time horizon is widened and context-sensitive.

The complete set of rules is described by Haumgart-Schmitt et al. [3].

Results

The results of 16 automatically analyzed nights with the relevant sleep profiles were compared. The data of the 16 nights are based on 9 subjects. Four nights of 2 subjects, 2 nights of 1 subject and 1 night of 6 subjects were included in this study. The codes of the investigated nights are contained in the following set C with

$C = (k10810, k10821, k10832, k10843, k40410, k40421, k40433, k40442, k40310, k40322, k11510, k31132, k31510, k31231, k20923, k20831).$

The first three digits represent the codes of the subject, the following digits correspond to the number of the nights and the last digit has been joined with an experimental variation. That means for example that the code k108 10 is connected with the first night of subject 108 and by the code k40433 the 3rd night of subject 404 is indicated.

The used nets were trained by means of the data of the 9 nights:

(10810 31510 40410 40310 31132 31231 20831 11510 20923).

The best fitting net of each night was selected. The resulting 9 nets were simultaneously used to classify 1 night. The maximum output of each net indicated the individual decision. The final decision for one class was supported by the median overall maximum outputs of the networks. The median was preferred because no normal distribution could be assumed and the median is not sensitive to outlier values. As a precondition to the statistical operation of median the sleep stages had to be ordered according to the code MOVEMENT = 0, WAKE = 1,

Table 1. Mean percentages of q1 and q2 for all correctly classified epochs of the corresponding nights

Night	q1s	q1	q2s	q2
k10810	83.7	79.0	14.4	68.9
k10821	72.4	65.8	64.0	62.1
k10832	79.6	73.3	71.4	67.1
k10843	66.9	63.0	58.3	60.4
k31510	68.1	65.6	63.3	63.1
k40410	75.2	72.2	62.0	66.0
k4042 1	19.6	13.5	66.9	63.3
k40433	75.6	71.1	69.6	64.1
k40442	16.2	70.9	71.6	66.7
k40310	71.2	71.2	62.7	51.9
k40322	77.0	73.1	64.7	59.9
k31132	74.1	68.1	57.6	57.0
k31231	80.9	17.3	60.4	59.0
k20831	58.9	44.2	53.4	46.4
k11510	80.2	77.1	69.1	70.7
Mean	75.6	70.2	65.5	62.9
Standard dev.	6.3	8.1	6.4	6.2
Median	76.6	71.7	64.3	63.5
Semiquartile dist.	2.4	3.5	4.5	3.5

The values are averaged on all epochs. To classify the epochs the median of the net outputs of 9 networks were used. The results q1s and q2s were gathered with the application of context rules (EMG only used for checking BEM onset) and the results q1 and q2 were received without context rules. The means, standard deviations, medians and the semiquartile distances of all criteria are shown at the bottom of the table.

Table 2. Mean percentages of q1 and q2 for all correctly classified epochs of the corresponding nights

Night	q1s	q1b	q2s	q2b
k10810	83.7	79.3	74.4	71.4
k10821	12.4	75.0	64.0	66.3
k10832	79.6	76.5	71.4	70.0
k10843	66.9	10.6	58.3	61.6
k31510	68.1	66.9	63.3	62.0
k40410	75.2	72.5	62.0	66.0
k4042 1	19.6	76.4	66.9	64.0
k40433	15.6	78.4	69.6	69.3
k40442	16.2	75.5	71.6	69.4
k40310	11.2	75.4	62.1	64.3
k40322	77.0	76.2	64.1	66.4
k31132	74.1	83.0	57.6	69.6
k31231	80.9	77.7	60.4	51.9
k20831	58.9	77.0	53.4	60.4
k11510	80.2	77.4	69.1	71.6
k20923	84.4	83.8	18.7	75.1
Mean	75.6	76.3	65.5	66.5
Standard dev.	6.3	2.25	6.4	1.85
Median	76.6	76.4	64.3	66.3
Semiquartile dist.	2.8	1.2	4.5	3.1

The values are averaged on all epochs. The results were gathered with the application of context rules. The values of q1s and q2s are connected with median of the net outputs of 9 networks. The results q1b and q2b were received by means of the best nets of another subject compared to the nights. The means, standard deviations, medians and the semiquartile distances of all criteria are shown at the bottom of the table.

BEM = 2, S1 = 3, S2 = 4, S3 = 5, S4 = 6. That proposal should be justified by the similarities between the different sleep stages. Cluster analysis in the feature space supported this ordering. Whether or not the assumed mechanisms behind the sleep stages are in agreement with this ordering is an open question.

The values of the applied criteria are being shown in tables and graphs. With $r(i)$ number of epochs correctly assigned to the i -th class, $s(i)$ number of the epochs of the i -th class, and k number of classes (sleep stages), two criteria

$$q1 = 100\% \cdot \frac{\sum_{i=1}^k r(i)}{\sum_{i=1}^k s(i)} \text{ and} \tag{1}$$

$$q2 = 100\% \cdot \frac{1}{k} \sum_{i=1}^k \frac{r(i)}{s(i)}, \tag{2}$$

were used to evaluate the results. The values of $q1$ and $q2$ are identical if the epochs are equally distributed to the k different sleep stages. The distribution of the objects

(epochs) is extremely different in the classification of the sleep stages on the basis of the EEG. Therefore both criteria lead to a different evaluation of the fitness. The aim $q1$ prefers the strongly represented classes and $q2$ delivers a value that is equally influenced by the weakly represented classes.

Mean percentages of $q1$ and $q2$ for all correctly classified epochs of the corresponding nights are summarized in table 2. The values are averaged on all epochs. The results measured by $q1s$ and $q2s$ were gathered with the application of context rules (EMG only used for checking BEM onset before the stage 2 epoch). The results measured by $q1$ and $q2$ were received without context rules. The means, standard deviations, medians and the semiquartile distances of all criteria are shown at the bottom of tables 1 and 2. The improvements by the application of context rules are reflected by the differences between $q1s$ to $q1$ and $q2s$ to $q2$.

Both differences, $q1s-q1$ and $q2s-q2$, are significant according to the Wilcoxon nonparametric test for 2 de-

Table 3. Matrix of the results received by SASCIA in context with the expert opinions

Expert	SASCIA						
	S1	s2	s3	S4	REM	AWAKE	MOV
S1	10	3	0	0	7	1	0
s2	6	160	21	2	9	0	0
s3	0	5	21	17	0	0	0
S4	0	1	7	32	0	0	0
REM	2	2	0	0	91	0	0
AWAKE	12	1	0	1	3	8	1
MOV	1	1	0	0	1	1	8

The time ranges measured in minutes that conform with the expert are shown in the diagonal position. The deviant classifications are distributed in the other cells of the matrix. The automatic classifications averaged on 16 nights are the result of the combined working of networks and rules. As an example the epochs connected with expert decision for REM are automatically recognized as REM in 91 min, in 2 min as stage 1 and in 2 min as stage 2.

pendent samples at the level of 5 % with $n = 16$. The proof value is equal to 30 according to table 8 in Clauss and Ebner [5]. Figure 2 underlines the trend that the context rules seem to improve especially the strongly represented sleep stages.

Mean percentages of q1 and q2 for all correctly classified epochs of the corresponding nights are shown in table 3. The values are averaged on all epochs. The results were gathered with the application of context rules. The values of q1s and q2s are connected with median of the net outputs of 9 networks. The results with the values q1b and q2b were received by means of the best nets of another subject compared to the nights.

The means, standard deviations, medians and the semiquartile distances of all criteria are shown at the bottom of table 1. Both differences between q1s and q1b and between q2s and q2b are not significant according to the Wilcoxon nonparametric two-sided test for 2 dependent samples at the error level of 5% with $n = 16$. The proof value is equal to 30 according to table 7 in Clauss and Ebner [5].

Therefore it can be concluded that the median of the network outputs has the same classification performance as the best net.

The confounding matrix calculated in minutes is shown in table 3. Table 4 summarizes the same values in percentages. The expert opinions are connected with the rows of both matrices and the columns are referenced to the results of SASCIA.

Table 5 summarizes the values of the confounding matrix in percentages, but in opposition to table 4 the estimation of the mean on 16 nights was done by the median.

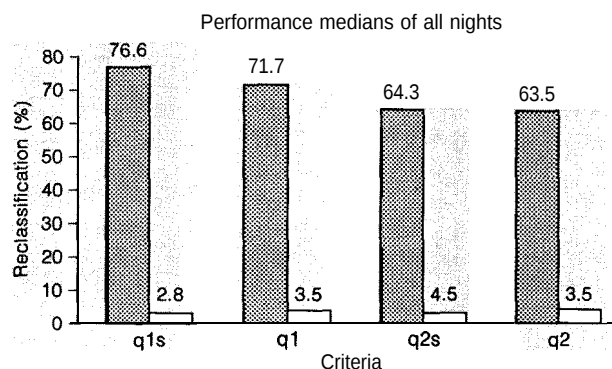


Fig. 2. Median of confounding matrix of 16 nights (see table 5).

The expert opinions are connected with the rows of both matrices and the columns are referenced to the results of SASCIA. The values of the semiquartile distances are shown in brackets. The chart of that matrix is shown in figure 3.

The sleep profile of subject k0010832 is shown by figure 4. The epochs were scored by the sleep scorer. The profile is used to compare it with the automatically generated profile of the same subject in the next figure.

The sleep profile of the night k10832 in figure 5 was automatically generated on the basis of the median of the outputs of 9 nets, which were adapted to the data of 9 subjects. The reclassification performance (q1) is 79.6%, the correlation coefficient between the two profiles (see fig. 4, 5) is $r = 0.860$.

Fig. 3. Medians (large columns) and semiquartile distances (small columns) for q1 and q2: The increased values for q1 and q2 result from the additional application of context rules.

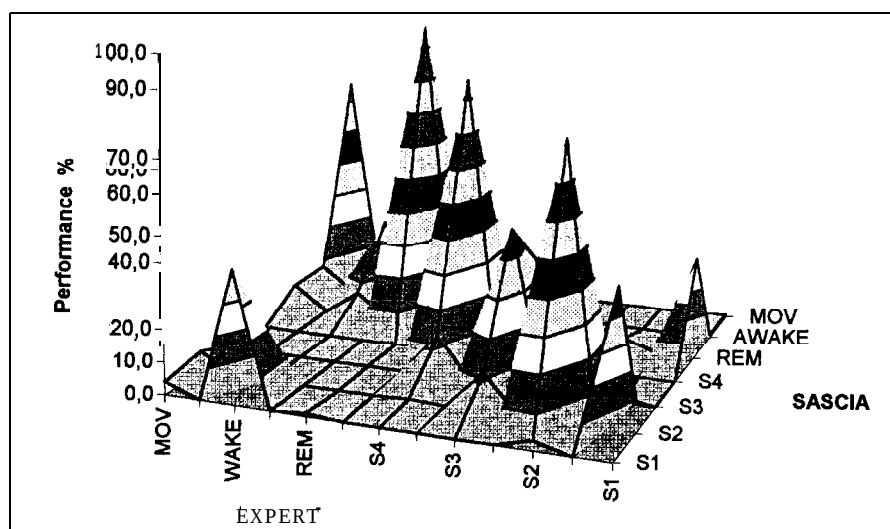


Table 4. Matrix of the results received by SASCIA in context with the expert opinions

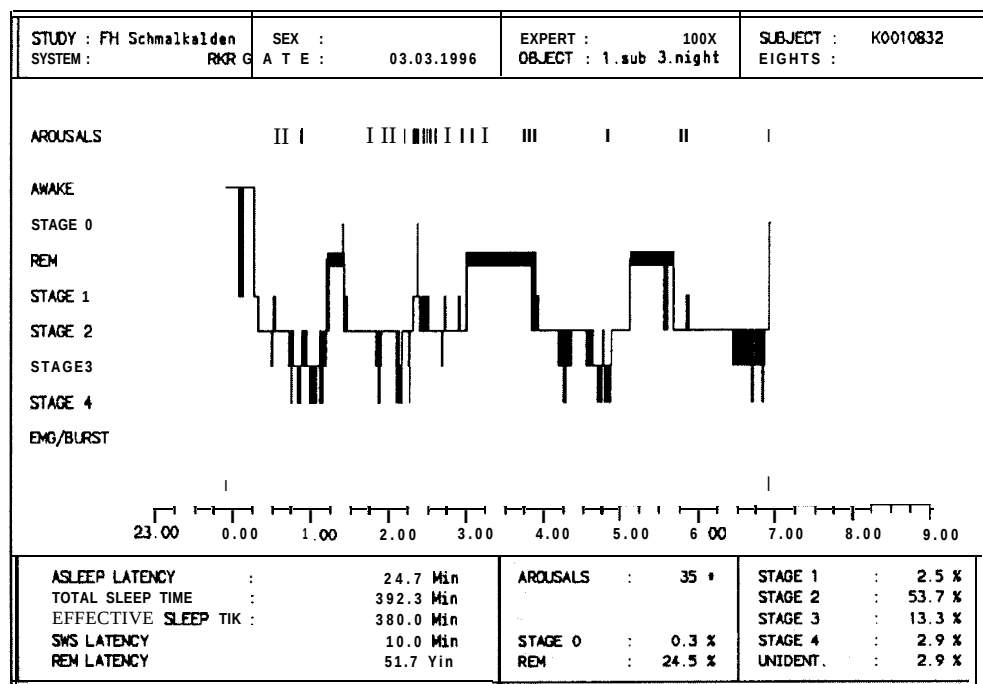
Expert	SASCIA						
	S1	s2	s3	s4	REM	AWAKE	MOV
S1	48.4 (± 17.2)	12.1 (± 11.2)	1.3 (± 1.7)	0.2 (± 0.2)	34.2 (± 14.6)	2.5 (± 2.9)	1.4 (± 1.4)
s2	3.2 (± 2.0)	80.4 (± 10.4)	10.5 (± 9.8)	1.2 (± 1.7)	4.4 (± 2.5)	0.1 (± 0)	0.2 (± 0)
s3	0.3 (± 1.0)	10.9 (± 14.6)	49.1 (± 15.8)	39.3 (± 22.4)	0.1 (± 0)	0.2 (± 0.5)	0.2 (± 0.5)
s4	0.1 (± 0.0)	1.3 (± 1.3)	17.4 (± 14.8)	81.0 (± 16.2)	0.0 (± 0.0)	0.1 (± 0)	0.2 (± 0.5)
REM	2.3 (± 3.5)	2.0 (± 4.7)	0.0 (± 0.0)	0.0 (± 0.0)	95.2 (± 8.0)	0.2 (± 0.2)	0.3 (± 0.2)
AWAKE	44.7 (± 25.9)	3.7 (± 7.9)	0.0 (± 0.0)	2.5 (± 3.5)	11.8 (± 10.1)	32.5 (± 27.0)	4.7 (± 4.1)
MOV	6.0 (± 4.2)	10.2 (± 7.1)	2.0 (± 2.2)	0.8 (± 1.2)	8.5 (± 4.5)	9.3 (± 5.0)	63.2 (± 15.8)

The percentage of the time ranges which conform with the expert are shown in the diagonal position. The deviant classifications are distributed in the other cells of the matrix. The automatic classifications averaged on 16 nights are the result of the combined working of networks and rules. As an example the epochs connected with expert decision for REM are automatically recognized as REM in 95%, in 2% as stage 1 and in 1% as stage 2. The values of the standard deviations are shown in parentheses.

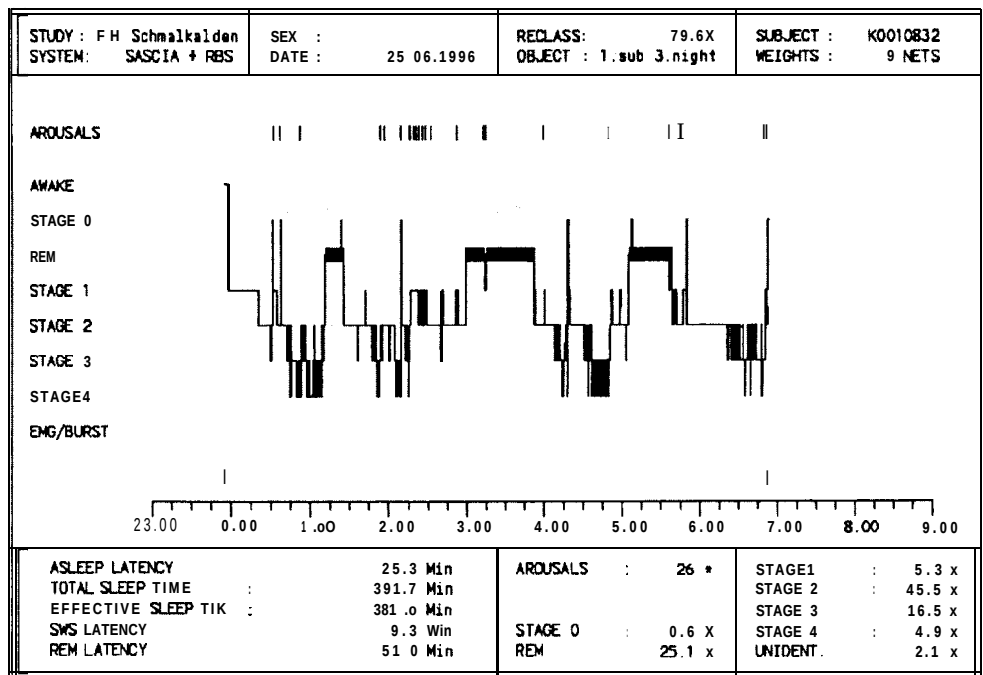
Table 5. Matrix of the results received by SASCIA in context with the expert opinions

Expert	SASCIA						
	S1	s2	s3	s4	REM	AWAKE	MOV
S1	49.5 (± 10)	9.5 (± 4.5)	0.0 (± 0.0)	0.0 (± 0.0)	32.0 (± 8.5)	1.0 (± 1.5)	1.0 (± 1.0)
s2	3.0 (± 1.5)	82.0 (± 4.0)	7.0 (± 3.5)	0.0 (± 0.5)	4.0 (± 1.5)	0.0 (± 0.0)	0.0 (± 0.0)
s3	0.0 (± 0.0)	11.5 (± 5.0)	48 (± 10.5)	33.5 (± 12)	0.0 (± 0.0)	0.0 (± 0.0)	0.0 (± 0.0)
s4	0.0 (± 0.0)	0.5 (± 0.5)	12.5 (± 4.5)	85.5 (± 5.0)	0.0 (± 0.0)	0.0 (± 0.0)	0.0 (± 0.0)
REM	1.0 (± 1.0)	0.0 (± 0.5)	0.0 (± 0.0)	0.0 (± 0.0)	96 (± 2.0)	0.0 (± 0.0)	0.0 (± 0.0)
AWAKE	40.5 (± 15)	0.0 (± 3.5)	0.0 (± 0.0)	0.0 (± 0.0)	7.5 (± 8)	25.5 (± 20)	4.0 (± 2.5)
MOV	4.0 (± 2.0)	6.0 (± 3.0)	1.0 (± 1.0)	0.0 (± 0.0)	7.5 (± 3.5)	7.5 (± 3.0)	65.5 (± 4.5)

The medians on 16 nights of percentages of epochs which conform with the expert are shown in the diagonal position. The deviant classifications are distributed in the other cells of the matrix. The automatic classifications averaged on 16 nights are the result of the combined working of networks and rules. As an example the epochs connected with expert decision for REM are automatically recognized as REM in 96% and with 1% as stage 1. The values of the semiquartile distances are shown in parentheses.



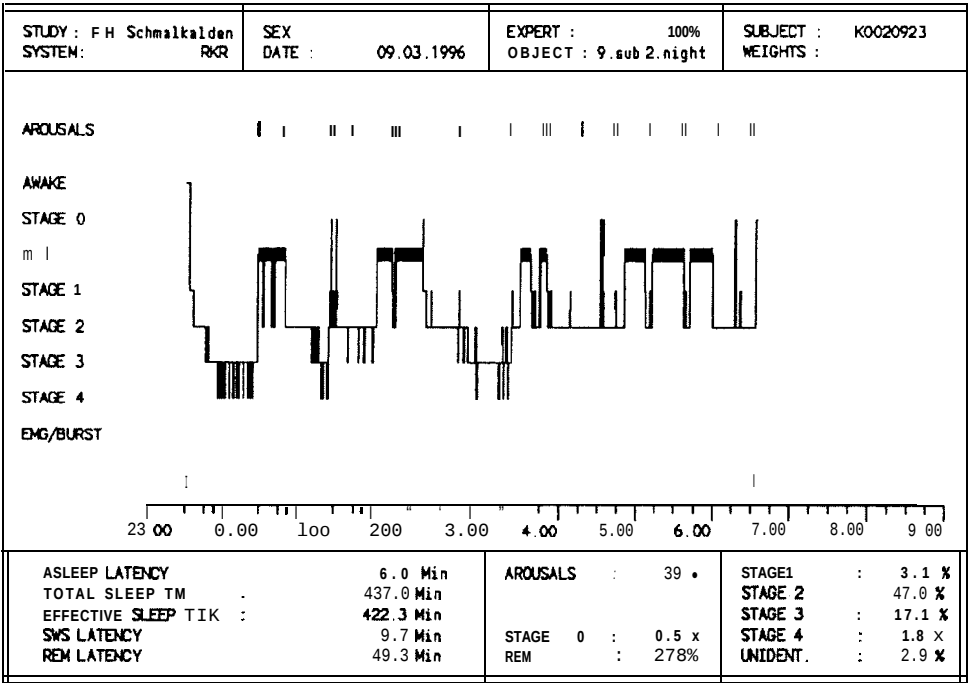
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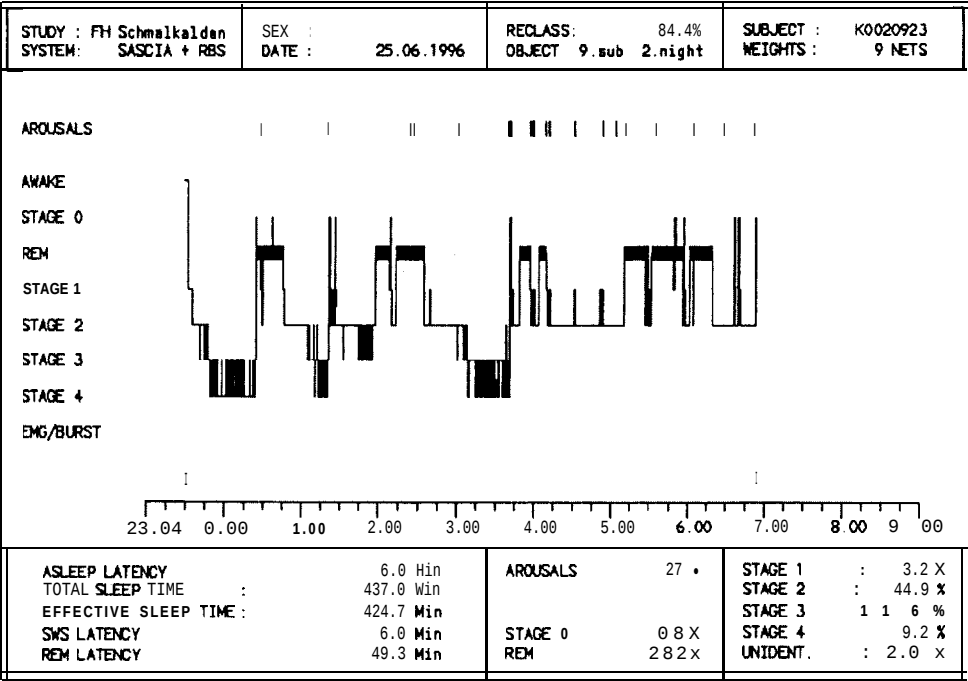
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Fig. 4. Sleep profile of subject k00 10832. The epochs were scored by the expert. The profile is compared with the automatically generated profile of the same subject in the next figure.

Fig. 5. Automatically generated sleep profile of the night k10832 on the basis of the median of the outputs of 9 nets, which were adapted to the data of 9 subjects. The reclassification performance (ql) is 79.6%. The correlation coefficient between this profile and the expert profile of figure 4 is $r = 0.860$.



6



7

Fig. 6. Sleep profile of subject k0020923. The epochs were scored by the expert. The profile is compared with the automatically generated profile of the same subject in figure 7.

Fig. 7. Automatically generated sleep profile of the night k0020923 on the basis of the median of the outputs of 9 nets, which were adapted to the data of 9 subjects. The reclassification performance (ql) is 84.4%. The correlation coefficient between this profile and the expert profile of figure 6 is $r = 0.930$.

The epochs of the sleep profile in figure 6 of subject k0020923 were scored by the expert. The profile is used to compare it with the automatically generated profile of the same subject in the next figure. The sleep profile of the night k0020923 in figure 7 was automatically generated on the basis of the median of the outputs of 9 nets, which were adapted to the data of 9 subjects. The reclassification performance (q 1) is 84.4% and the correlation coefficient between the two profiles (see fig. 6, 7) is $r = 0.930$. If figure 7 is compared with figure 7 of the first communication [2], the total sleep time, SWS and REM latency, stage 1 and especially REM fit better to the expert generated profile based on RK rules. Only SWS was marginally overestimated.

The arithmetic mean over the 16 correlation coefficients between the expert profiles and the automatically generated profiles by means of the median of the 9 network outputs is 0.864.

In using only one network to classify the epochs, the arithmetic mean of the 16 x 16 correlation coefficients is lowered to 0.819. Each night was classified by the weights of all other nights and by its own weights.

Discussion

The application of the median of multiple nets is guided by the main idea that a whole population of neural networks can solve the task of nonlinear classifying in a much better way than one single network. We got relatively robust classification results. The average agreement between SASCIA and the RK scorer may be as low as 76-84%. However, there are no complete failures so far. Even if the agreement between SASCIA and the scorer is only in the high 70ies, there is virtually no major difference in the sleep profiles as can be seen from figures 4-7. Comparing these profiles there should be no misinterpretation of the physiology of the sleep and the features of the sleep profile by the SASCIA-generated profiles.

Another possibility to adapt to individual subjects' profiles would be to perform a prescreening with the first sleep epochs, and then decide which of the networks should be applied.

We believe that REM identification should be possible without analyzing the REM, based on the current theories about the importance of the REM stage [6]. In the past, REM staging always has been a problem for the automatic methods [7]. Using neural networks seems to make it possible to classify REM more safely without using the eye movements and the EMG. The fact that we could identify

91 min out of the total REM time of 95 (see table 3) is considered as a breakthrough in automated REM detection without eye movements and supports our hypothesis that the EEG alone carries REM-specific information.

The fact that REM still has been substantially overestimated by SASCIA (see table 3) by 20 min (111 min instead of 91) has to be further investigated. It is probable that wake phases at the end of the night, while people are still in bed but not any more in REM sleep according to the RK classification, is detected by the SASCIA system falsely as REM.

In our feature matrix [3] (table I), we have not taken any coherence measure as suggested earlier by Waterman et al. [8]. Our own research suggests that coherence should be a factor to further improve REM staging, and we are in the process of systematically analyzing REM for coherence and resonance frequencies.

If indeed our system can be further improved using only one single EEG lead, then automatic sleep analysis could be applied with very simple equipment. To store and analyze the record of only one EEG lead would be very economical and could include more ambulatory sleep profiling into sleep research, especially more reliable prescreening before a patient is admitted to a sleep clinic. The most important for ambulatory equipment seems to be to deliver valid data for *normal* sleep profile versus *disturbed* sleep profile, which requires further investigation in a sleep laboratory.

The average agreement of 75-80% between SASCIA and a scorer according to RK may be regarded as low. However, we again have to ask the question raised many times earlier whether RK rules should be the only standard against which we should validate our SASCIA system [11]. It may well be that automated systems such as SASCIA better represent sleep physiology than RK rules do. This may be especially true for the 75- μ V amplitude criteria to recognize Z-waves as valid for SWS. SASCIA seems to represent sleep physiology in many cases better than RK do. This question will be clarified in further investigations comparing a new one-channel device called QUISI [9] and within a large EC funded program (SIESTA) [10] involving more than a dozen European sleep labs, starting in September 1997, called: 'A new standard for integrating polygraphic sleep recordings into a comprehensive model of human sleep and its validation in sleep disorders' [10].

We could demonstrate that the application of neuronal networks applied to parameters of the quantified EEG delivers remarkable results taking into account that this is our first approach and that we used only the information of one single lead and no eye movements. Our suggestions