Computational Modeling of Sleep Stage Dynamics using Weibull Semi-Markov Chains

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Abstract: In this paper, a semi-Markov chain of sleep stages is considered as a model of human sleep dynamics. Both sleep stage transitions and the durations of continuous bouts in each stage are taken into account. The semi-Markov chain comprises an underlying Markov chain that models the temporal sequence of sleep stages but not the timing details, together with a separate statistical model of the bout durations in each stage. The stage bout durations are modeled explicitly, by the Weibull parametric family of probability distributions. This family is found to provide good fits for the durations of waking bouts and of bouts in the NREM and REM sleep stages. A collection of 244 all-night hypnograms is used for parameter optimization of the Weibull bout duration distributions for specific stages. The Weibull semi-Markov chain model proposed in this paper improves considerably on standard Markov chain models, which force geometrically distributed (discrete exponential) stage bout durations for all stages, contradicting known experimental observations. Our results provide more realistic dynamical modeling of sleep stage dynamics that can be expected to facilitate the discovery of interesting and useful dynamical patterns in human sleep data in future work.

1 INTRODUCTION

Sleep is an active process of the body associated with biophysical changes that can be detected using polysomnography (PSG). PSG includes amongst other things an electroencephalogram (EEG) that records electrical changes in the brain, an electrooculogram (EOG) that measures eye movement, and an electromyogram (EMG) that detects muscle activity. In 1968, A. Rechtschaffen and A. Kales proposed a scoring technique to map each 30 second interval of a human subject's night sleep into one of three main phases: wake stage, non-rapid eye movement (NREM) stage, and rapid eye movement (REM) stage (Rechtschaffen and Kales, 1968). The NREM stage is further divided into stage 1, stage 2, and stage 3. Human sleep dynamics can be described in terms of the alternation among these five stages (Susmakova, 2004).

A sample diagram of the distribution and time evolution of sleep stages, also known as a hypnogram, is shown in Fig. 1. This hypnogram is one of the 244 polysomnographic recordings used in the present paper. It consists of 1,020 30-second epochs, which amounts to 8.5 hours of sleep. Sleep progression generally starts with the wake stage and then there are cycles in which REM and NREM alternate, particularly between REM stage and stage 2. During the whole night sleep recording, stage 2 exhibits long uninterrupted bouts as the night goes on. REM episodes tend to get longer in the second half part of the night sleep, while stage 3 occurs earlier in the first half of the night. Finally, there are several times of short wakefulness throughout the night, after the initial onset of sleep. Regardless of these typical patterns of human sleep, hypnogram details vary across individuals and are affected by age, circadian rhythms (Dijk and Lockley, 2002), and other factors.

Sleep stage composition is a basic description of sleep structure that comprises total sleep time, sleep efficiency, and percentage of sleep period time in each of the stages within a night of sleep (Khasawneh et al., 2011). However, these features provide an incomplete description of human sleep that does not capture the dynamical information in hypnograms. Sleep stage duration is widely used in applications to sleep-wake architecture, where exponential and power-law functions have been proposed as parametric models for

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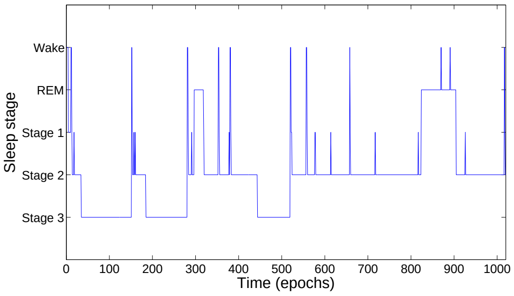


Figure 1: Sample hypnogram in the present study.

the distributions of the wake and sleep bout durations (Chu-Shore et al., 2010). Sleep stage transitions are additional indicators of the dynamics of human sleep. For example, (Kishi et al., 2008) argues that dynamic transition analysis of sleep stages is a useful tool for elucidating human sleep regulation mechanisms.

Markov chains (Rabiner, 1989) have been used to model the dynamics of sleep stage transitions. A simple time-homogeneous Markov chain was the first applied in the sleep domain (Zung et al., 1965). However, Markov chains (and more generally, hidden Markov models) do not model sleep stage transitions accurately, because these models force geometrically distributed stage bout durations for all sleep stages, contradicting known experimental observations (e.g., (Chu-Shore et al., 2010) and the present paper). Semi-Markov chains, a variant of Markov chains (Rabiner, 1989), are more suitable for describing sleep stage sequences as they do not assume an exponential distribution of stage durations (Yang and Hursch, 1973) and (Kim et al., 2009).

In the present paper, a semi-Markov chain of sleep stages is considered as a model of human sleep dynamics. The hypnograms of 244 human patients are used to construct a semi-Markov chain on three sleep stages: wake stage, NREM stage (stage1, stage2, and stage 3 combined), and REM stage (see section 2.1). Both sleep stage transitions and the durations of continuous bouts in each stage are taken into account. To compensate for the scarcity of bout durations in the dataset, kernel density estimation is used to smooth the data (see section 2.2.2). Exponential, power law, and Weibull density functions are fit to the smoothed stage bout duration data (see section 2.3). A new metric for evaluating the goodness of fit is introduced and used to select the best fit (see section 2.3.4). Thorough experimentation identified the Weibull family of density functions as the best fit for bout durations in wake, NREM, and REM stages (see section 3.2). This contrasts with previous reports that bout durations in these sleep stages follow a simple exponential or a power law distribution (Kishi et al., 2008).

The resulting semi-Markov chain is presented in section 3.2. A comparison of this semi-Markov chain's equilibrium distribution and bout duration probability density functions against those of a classical Markov chain shows the superiority of the semi-Markov chain model in capturing the statistics of sleep dynamics (see section 3.3). Furthermore, hypnograms generated by this semi-Markov model are more similar to a typical hypnogram in our patients' dataset, than are the hypnograms generated by a Markov chain model (see section 3.4).

2 METHODS

2.1 Human Sleep Data

The dataset used in this paper consists of a total of 244 fully anonymized human polysomnographic recordings. They were extracted from polysomnographic overnight sleep studies performed in the Sleep Clinic at Day Kimball Hospital in Putnam, Connecticut, USA. This population consists of 122 males and 122 females, all suffering from sleep problems. The subjects' ages range from 20 to 85 and their mean value is 47.9.

Each polysomnographic recording is split into 30-second epochs and staged by lab technicians at the Sleep Clinic. Staging of each 30-second epoch into one of the sleep stages (wake, stage 1, stage 2, stage 3, and REM) is done by analyzing EEG, EOG and EMG recordings during the epoch. In this paper stages 1, 2, and 3 are grouped into a non-REM stage, abbreviated as NREM. This condenses the representation of the sleep stages to three: Wake, NREM, and REM, collectively denoted WNR throughout the paper.

2.2 Descriptive Data Features

In contrast with prior work based on sleep composition features alone (Khasawneh et al., 2011), this paper directly uses human hypnogram recordings to capture dynamical features of sleep. The durations of continuous uninterrupted bouts in individual stages are natural candidates for the representation of the hypnogram recordings. In order to overcome the sparsity of stage duration data, kernel density estimation is applied to smooth these data.

2.2.1 Sleep Stage Bouts and Bout Durations

Sleep stage bouts and bout durations form the basis of the data representation in this paper. A stage bout is defined as a maximal uninterrupted segment of the given stage within a given hypnogram. For example, the hypnogram in Fig. 1 contains four different REM stage bouts (note that the REM plateau between epochs 800 and 900 is interrupted by two brief wake bouts, thus giving rise to three distinct REM bouts); also visible are three stage 3 bouts, and many bouts of other stages. The duration of a sleep stage bout is defined as the number of epochs which the bout spans. The frequency of a stage bout duration is the number of stage bouts of this same duration present in the hypnogram. The distribution of a stage's bout durations (that is, the frequencies of different bout durations for that stage) can be depicted by the distribution function (probability mass function). A sample distribution of REM stage bout durations over the population in the present paper is shown as the data points on the plots in Fig. 2. As in that figure, stage bout duration distributions in this paper are calculated over the entire dataset population, by aggregating bout durations of a given sleep stage (wake, NREM, or REM) over the 244 individual hypnograms.

2.2.2 Kernel Density Estimation

Kernel density estimation (KDE) is used for nonparametric probability density estimation. It is a useful statistical smoothing technique used when inferences about the population are to be made based on a finite data sample. The stage duration distributions calculated over our dataset of 244 patients contains many missing values for specific bout durations in each sleep stage. KDE is used to smooth these data distributions, thus providing meaningful values for durations of wake, NREM, and REM stages. A normal distribution with a kernel-smoothing window width of 1 was determined to produced the best results. All experiments were performed in MATLAB® (*The MathWorks*, 2012). The resulting kernel density estimation for the REM stage is depicted by the circular data points on the plots in Fig. 2.

2.3 Curve Fitting

Once the stage duration distributions have been smoothed using non-parametric kernel density estimation as described in section 2.2.2, parametric functions that closely approximate the shape of these duration distributions can be found. (Chu-Shore et al., 2010) and (Kishi et al., 2008) have shown that good approximations to stage bout duration distributions can be obtained by using single exponential functions and power law functions. In this paper, in addition to single exponential and power law functions, Weibull functions are considered as candidate fitting functions. The approach described in section 2.3.5 is followed for finding optimal parameter values and selecting the best fitting function for each sleep stage probability density distribution. A newly defined goodness of fit criterion described in section 2.3.4 is used to guide this selection. All curve fitting experiments were performed in MATLAB.

2.3.1 Exponential Density Function

The general form of a single exponential distribution is given in equation 1, where μ is the expected value.

$$f(x;\mu) = \frac{1}{\mu}\exp\frac{-x}{\mu}\ (x \geq 0) \tag{1}$$

Range of Initial Values for Parameter Estimation. The expected value of the exponential distribution for a given sleep stage in MLE corresponds to the expected value of durations over the sleep stage data. In this paper, the maximum length of stage bout duration for all sleep stages is 230 epochs. Therefore, the initial values for μ can be taken to be between 1 and 230.

2.3.2 Power Law Density Function

The general form of a power law distribution is given in equation 2.

$$f(x;\alpha,x_{min}) = \frac{\alpha-1}{x_{min}}\left(\frac{x}{x_{min}}\right)^{-\alpha}\ (x \geq x_{min}) \tag{2}$$

The estimation of α in the power law distribution using maximum likelihood estimation is shown in equation 3.

$$\alpha = 1 + n\left[\sum_{i=1}^{n}\ln\frac{x_i}{x_{min}}\right]\ (x_i \geq x_{min}\ \alpha > 1) \tag{3}$$

Range of Initial Values for Parameter Estimation. According to the estimation in equation 3, and based on the hypnogram dataset, x_{min} should be 1, and a large enough range for initial values for α is the range from 1 to 10 times the MLE estimate of α. A delta increment value of 0.01 is used to select sufficient α values in this range. Note that *n* is the number of observed empirical data, namely 244 patients.

2.3.3 Weibull Density Function

The general form of the Weibull distribution is given in equation 4.

$$f(x;\lambda,\mu) = \frac{k}{\lambda}\left(\frac{x}{\lambda}\right)^{k-1}\exp\left(-\left(\frac{x}{\lambda}\right)^{k}\right)\ (x \geq 0) \tag{4}$$

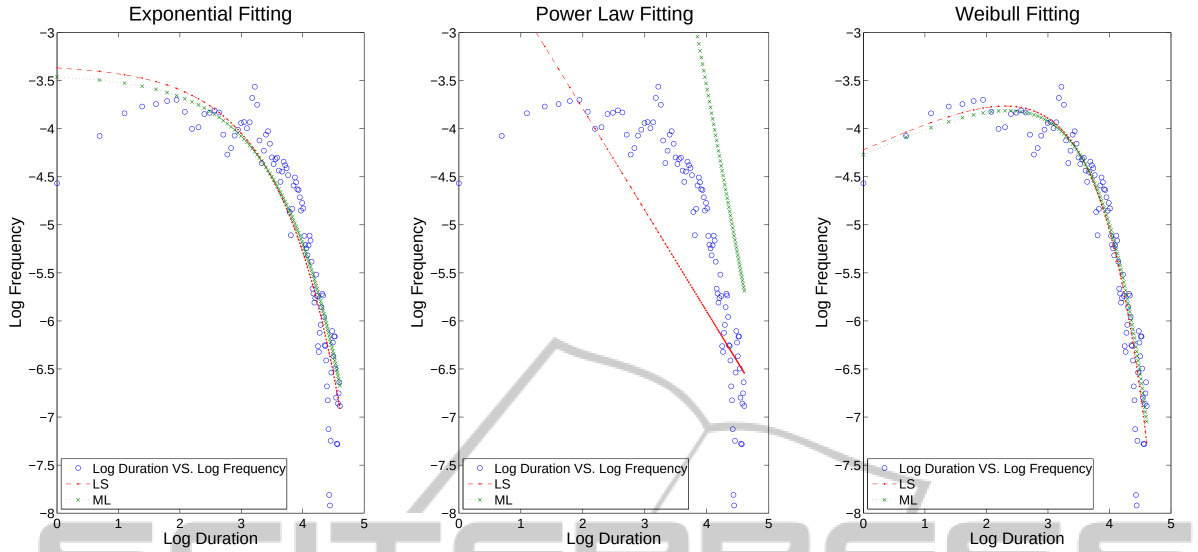


Figure 2: Curve fitting of the REM stage duration distribution. The three plots depict the fits obtained by using exponential functions (left), power law functions (center), and Weibull functions (right). In each plot, the results of the ML and LS approaches described in section 2.3.5 to find best fits are presented. Among all these candidate fits, the Weibull function achieves the best goodness of fit, as discussed in section 3.2.3.

where λ is scale parameter and k is shape parameter in the Weibull distribution. When $k = 1$, the Weibull distribution coincides with an exponential distribution. The expected value of the Weibull distribution is given by equation 5.

$$E(x) = \lambda\Gamma\left(1 + \frac{k}{\lambda}\right) \qquad (5)$$

where Γ is the gamma function, which extends the factorial function. When $k = 1$, $E(x) = \lambda$.

Range of Initial Values for Parameter Estimation. To be consistent with the kernel estimated data distribution, k is limited to a range between 0 and 2. λ can range from 1 to 230 (the maximum duration of any sleep stage).

2.3.4 Goodness of Fit

A goodness of fit metric is needed to quantify the discrepancy between data estimated by KDE in section 2.2.2 and fitting curves obtained by the above three fitting functions. This metric can also be used to select the best among several candidate fitting curves. A new such metric is introduced below in equation 6, which is similar to the Mean Square Error (MSE) metric applied to the logarithmically transformed frequency data, except that the parameter x appears in the denominator of the new metric. This new metric proved superior to other metrics (including MSE) in capturing the quality of the approximation as gauged by visual inspection during systematic experimentation.

$$GOF(x) = \sum_{k=1}^{n}\left(\frac{(\log s(x_k) - \log f(x_k))^2}{x_k}\right) \qquad (6)$$

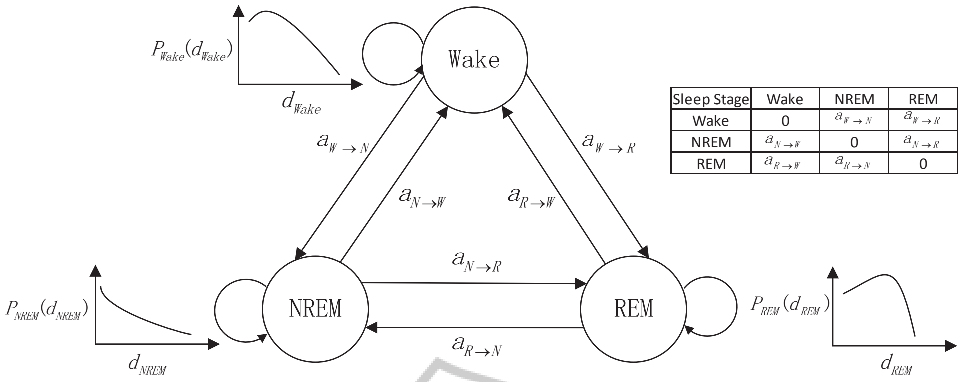
In equation 6, $s(x_k)$ refers to the nonparametric probability density estimation at duration x_k, and $f(x_k)$ refers to the fitting data on $s(x_k)$. Logarithms are taken on the estimated data $s(x_k)$ and fit data $f(x_k)$ to match the visual aspect of these values in a log-log scale plot such as the one in Fig. 2.

2.3.5 Searching for Best Curve Fits

The following approach was employed to search for the best possible curve fits for each sleep stage duration distribution (Wake, NREM, and REM).

1. Calculate the stage duration distribution from the 244 hypnograms as described in section 2.2.1.
2. Smooth this stage duration distribution using KDE as described in section 2.2.2.
3. Fit exponential, power law, and Weibull functions to the smoothed stage duration distribution using each of the following two approaches to estimate parameters:

   ML: Use Maximum Likelihood (ML) to estimate the parameters of each of the fitting function families. As an illustration, the plots in Fig. 2 depict the best ML approximation obtained for



Sleep Stage	Wake	NREM	REM
Wake	0	$a_{W\to N}$	$a_{W\to R}$
NREM	$a_{N\to W}$	0	$a_{N\to R}$
REM	$a_{R\to W}$	$a_{R\to N}$	0

Figure 3: Example of a semi-Markov chain model (SMCM). Similar to a Markov chain model (MCM), a SMCM consists of a state diagram (which in this case includes three stages: Wake NREM, and REM) together with a transition probability matrix that provides the probability of transition between each pair of states. The difference between a SMCM and a MCM is that the probability of a self-transition is made equal to 0 in the SMCM's transition matrix, and the duration of “staying” in that state is explicitly represented instead by the probability density function that approximates that stage duration distribution.

the REM stage duration distribution for each of the three fitting function families.

LS: Use Least Squares (LS) to estimate the parameters. In this case, the initial parameter values for the estimation were taken from the ranges described for each function family (exponential, power law, and Weibull) in sections 2.3.1-2.3.3. Repeat this for each possible initial point in the given range. Then use the GOF metric to select the best estimation obtained for each function family among all those obtained from the set of initial parameter values. The plots in Fig. 2 depict the best LS fits obtained (together with the best ML fits).

4. Use the GOF metric to select the best estimation obtained by the ML and LS approaches above across all function families. Output this estimation as the best approximation for the sleep stage duration distribution.

2.4 Markov Models

Markov models have been extensively used to model dynamic data. For an excellent survey of Markov models, see (Rabiner, 1989).

2.4.1 Markov Chain Models (MCM)

A Markov chain model is a particular kind of Markov model, in which all states are observable (that is, there are no hidden states). A Markov chain consists of a collection of states together with a state transition matrix that provides the probability of transition between each pair of states. The Markov assumption establishes that this transition probability depends only on the current state. Markov chains have been used to model sleep (Zung et al., 1965). However, Markov chains force exponential state duration distributions, which is not consistent with known experimental observations of sleep stage durations (see for instance Fig. 2). To overcome this limitation, semi-Markov chain models are investigated in this paper. Markov chains are used only as a baseline for comparison purposes. Training a Markov chain model over the sleep data requires only the calculation of the probability transition matrix over all 244 hypnograms.

2.4.2 Equilibrium Distribution

The equilibrium distribution represents the large-time asymptotic probability of occupation of the various states in a Markov chain. Therefore, the equilibrium distribution characterizes the long-term dynamics of human sleep in a Markov chain model. The equilibrium distribution of a Markov chain (but not of a general semi-Markov chain) may be computed as the normalized eigenvector of the transition matrix with eigenvalue 1.

2.4.3 Semi-Markov Chain Models (SMCM)

Different from the Markov chain in section 2.4.1, the semi-Markov chains as sleep dynamics models have two components: the stage transition matrix and stage duration distributions for all stages. The stage transition matrix is similar to that in the Markov chain except that the probability of a transition from any stage to itself is 0. The best fitting function selected by section 2.3 should be used as the description of the stage duration distribution for each stage. The operation of the semi-Markov chain model is as follows (see Fig. 3): it starts with a specific stage, usually the wake stage. The model stays in the current stage for a duration randomly sampled from the duration distribution for that stage (given by the fitting function of the stage), expressed as $P_{Wake}(d_{Wake})$, after which time it transitions from the current stage to another stage selected randomly according to the vector of stage transition probabilities $\{a_{W\to N}\ a_{W\to R}\}$. This cycle is repeated indefinitely.

2.4.4 Equilibrium Distribution Difference

To approximate the equilibrium distribution in a semi-Markov chain model, one can use simulation of the semi-Markov chain. Sufficiently long stage sequences are generated so that asymptotic probabilities of states can be estimated. These limiting values represent the equilibrium distribution of the semi-Markov chain model.

2.4.5 Fitting Function Difference

In addition to the equilibrium distribution in the semi-Markov chain model, fitting functions that represent distributions of stage durations can be compared through the parameter values if they are from the same family of functions, for example the Weibull density function family. Interpreting a sleep bout duration as a ”time-to-failure” as in statistical reliability theory, the Weibull distribution indicates a distribution where the failure rate is proportional to a power of time. The shape parameter k determines one of several cases: if $k < 1$, then failure rate decreases over time; if $k = 1$, then it does not change over time; otherwise failure rate increases with time.

3 RESULTS

3.1 Markov Chain Model

A Markov chain (section 2.4.1) provides a simple dynamical model of the transitions between sleep stages. We discuss the results of constructing a Markov model over the set of all 244 hypnograms.

3.1.1 Markov Transition Matrix

The resulting transition probability matrix is given in Table 1. Noticeably, the self–transition probabilities are much higher than the inter–state transition probabilities.

3.1.2 Markov Equilibrium Distribution

As in section 2.4.2, the equilibrium distribution of the Markov chain model is obtained by normalizing the eigenvalue 1 eigenvector of the Markov transition matrix. The equilibrium distribution is given in Table 2. It characterizes the long-term dynamics of human sleep as captured by this Markov chain model.

Table 1: Stage transition matrix for Markov chain model.

Sleep Stage	**Wake**	**NREM**	**REM**
Wake	0.9207	0.0764	0.0029
NREM	0.0239	0.9705	0.0056
REM	0.0216	0.0108	0.9676

Table 2: Equilibrium distribution for Markov chain model.

Equilibrium	**Wake**	**NREM**	**REM**
Value	0.23	0.64	0.13

3.2 Semi-Markov Chain Model

Semi-Markov models have similar inter-stage transition behavior to Markov models. But in contrast with the Markov chain model, the semi-Markov chain model allows an explicit representation of the stage duration distributions. We discuss the semi-Markov model constructed over the set of 244 hypnograms below.

In contrast with reports by other researchers (Kishi et al., 2008) that the durations of wake stage, NREM sleep stage, and REM sleep stage follow power laws or single exponential distributions, the work in the present paper suggests that individual sleep stages are better modeled by Weibull distributions as shown in Fig. 2 and Fig. 4.

3.2.1 Semi-Markov Transition Matrix

The stage transition matrix obtained for the semi-Markov chain model is given in Table 3. As discussed in section 2.4.3, the self-transition probabilities are 0. This matrix can be calculated from the Markov chain model transition probability matrix by normalizing the inter-state probabilities in each row. This very simple operation produces values that more directly reveal the relative likelihoods of various inter-stage transitions.

3.2.2 Semi-Markov Equilibrium Distribution

The model's empirically observed equilibrium distribution is given in Table 4. It provides the asymptotic probabilities of stages over a collection of simulation runs where the length of simulations ranged from 1,000 to 1,000,000. The semi-Markov chain equilibrium distribution in Table 4 is observed to be very close to that of the Markov chain model shown in Table 2.

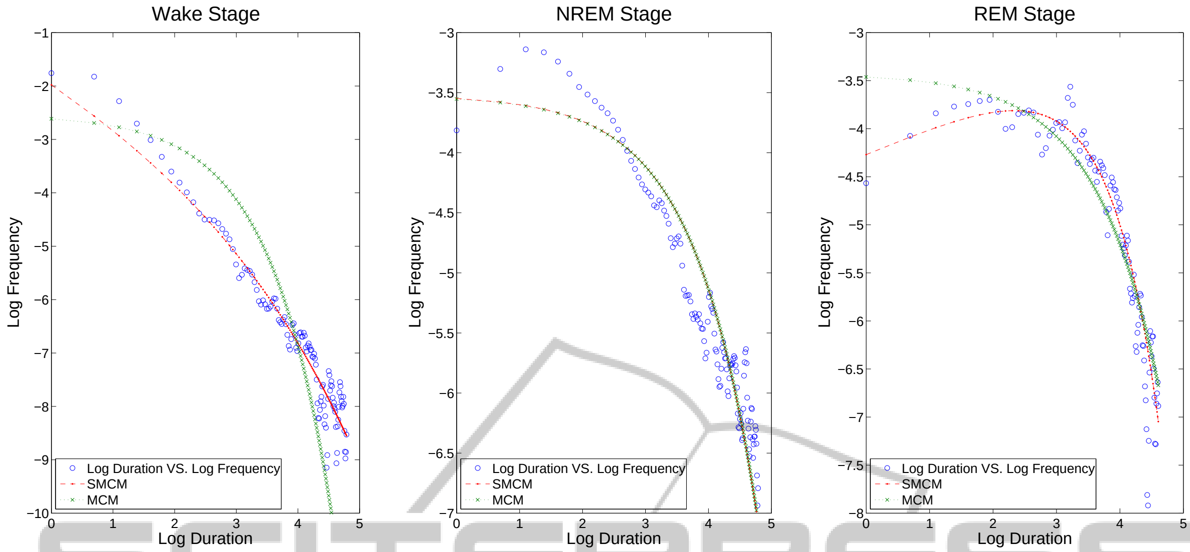


Figure 4: Comparison of fits for the stage duration distribution function used by the Markov chain model (MCM), exponential, and by the semi-Markov chain model (SMCM), Weibull.

Table 3: Stage transition matrix for semi-Markov chain model.

Sleep Stage	**Wake**	**NREM**	**REM**
Wake	0	0.9632	0.0368
NREM	0.8093	0	0.1907
REM	0.6655	0.3345	0

Table 4: Equilibrium distribution for semi-Markov chain model.

Equilibrium	**Wake**	**NREM**	**REM**
Limit	0.25	0.61	0.14

3.2.3 Semi-Markov Stage Duration Model

As a result of the search procedure described in section 2.3, the Weibull family of distributions was selected to model the stage durations in the semi-Markov model. The best fitting parameters were determined as described in section 2.3.5. The results are summarized in Table 5. It can be seen that for wake stage, the best fitting function is determined by least squares error estimation. For NREM and REM, the best fitting functions are determined by maximum likelihood estimation. Table 6 provides the parameter values for the best Weibull function fits found. The fact that the Weibull shape parameters for wake, NREM, REM are, respectively, smaller than, approximately equal to, and larger than 1, show that stage bout durations for these three stages have characteristic and distinct behaviors. Specifically, the “failure rate” for wake, NREM, and REM decreases, does not change, and increases over time, respectively. These very different behaviors, which are modeled precisely in the semi-Markov model, cannot be captured at all by the Markov model, for which all stage bout durations are exponentially distributed (constant failure rate, in the reliability metaphor).

Table 5: Goodness of fit (GOF) values, as defined in section 2.3.4. The lower this value, the better the fit. The best fit(s) for each stage is(are) underlined. EDF, PDF, and WDF denote exponential, power law, and Weibull density functions, respectively. ML and LS denote the search approaches described in section 2.3.5.

ML	**Wake**	**NREM**	**REM**
EDF	6.2963	0.5543	1.7284
PDF	2.0704	7.6185	6.0023
WDF	1.0418	0.5684	0.3046
LS	**Wake**	**NREM**	**REM**
EDF	5.0303	0.6352	2.0428
PDF	2.0704	5.8969	11.8552
WDF	0.7788	0.8949	0.3198

Table 6: Parameter values for the Weibull function fits.

Parameters	**Wake**	**NREM**	**REM**
λ (scale)	4.024	33.74	33.35
***k* (shape)**	0.4378	1.000	1.286

3.3 Comparison of Stage Duration Fits in MCM and SMCM

Fig. 4 depicts for each sleep stage a comparison between the exponential fit of the sleep stage duration distribution used by the Markov chain model, and the Weibull fit used in the semi-Markov chain model. It

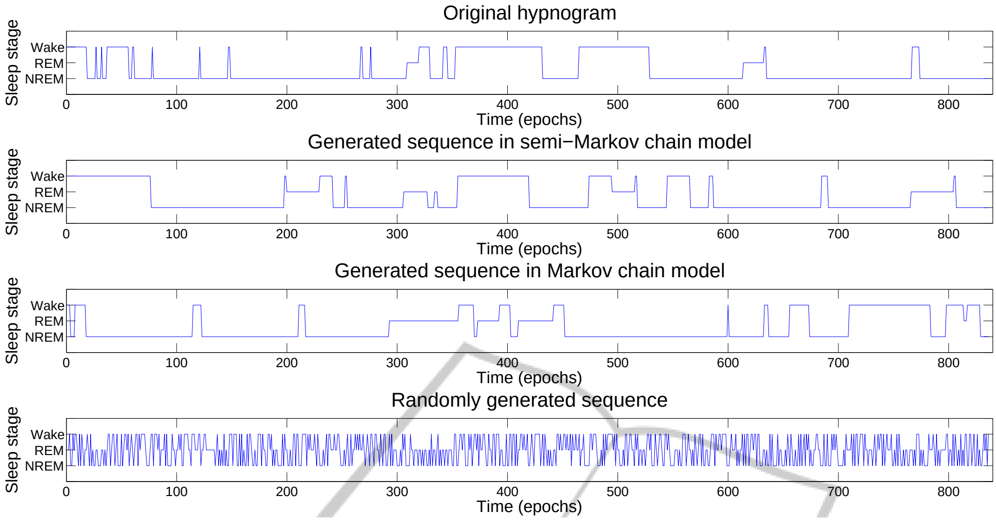


Figure 5: Comparison of an original dataset hypnogram, hypnograms generated by Markov chain and by semi-Markov chain models, and a randomly generated hypnogram.

can be seen in Fig. 4 that the Weibull funtions used in the semi-Markov chain model provide a much better fit for the wake and REM stages than the exponential functions used by the Markov chain model do. As examples, the exponential Markov fit underestimates the probability of longer wake bouts, and overestimates the probability of shorter REM bouts. The Weibull semi-Markov fit captures both of these behaviors well, by adjusting the shape parameter appropriately. The Markov and semi-Markov fits coincide in the case of NREM, as NREM durations are relatively well modeled by an exponential distribution.

3.4 Comparison of State Sequences Generated by MCM and SMCM

A comparison between sequences generated by each the Markov and semi-Markov models, and between these and the original dataset hypnograms, shed additional light on the stage transition dynamics captured by each of the models.

Fig. 5 shows an original dataset hypnogram, simulated stage sequences generated by the trained models, and a randomly generated sequence. The randomly generated sequence was obtained by assigning a randomly chosen sleep stage to each epoch using a uniform distribution over the sleep stages. The typical hypnogram shown, h, was selected from the dataset, such that its generative log likelihoods in the Markov chain model and the semi-Markov chain model, $P(h|\text{MCM})$ and $P(h|\text{SMCM})$, are close to the corresponding average log likelihood values over the entire dataset, which are approximately -148 and -152, respectively.

Fig. 5 shows, especially near the middle of the night, that the SMCM better captures the frequency of both short and long wake durations observed in the original hypnogram, as compared with the MCM. This is consistent with the discussion in section 3.3, in particular Fig. 4. At the onset of the night, the long uninterrupted duration of wake stage in SMCM simulates the original hypnogram for the same time period better than the short durations of wake stage in the MCM sequence do. Although MCM is comparatively worse than SMCM, its overall distribution of stages matches the all-night stage composition of the original hypnogram more accurately than the random sequence does. This single example is of course intended only as an illustration. The more general analysis of section 3.3 makes clear the superiority of the SMCM over the MCM as a model of stage bout durations, in a robust statistical sense.

4 CONCLUSIONS AND FUTURE WORK

Widely used Markov chain models of sleep stage dynamics do not succeed in capturing empirically observed statistical properties, in particular non-exponential distribution of certain sleep stage durations. This paper focuses on the semi-Markov model in characterizing the dynamics of human sleep stage bouts and transitions. Unlike a standard Markov chain model, the semi-Markov model allows describing the distribution of sleep bout durations independently from the sequence of stage transitions. This paper has described the process of constructing semi-Markov chain models of sleep dynamics, using three states that represent wake, NREM, and REM stages. The Weibull family of distributions are empirically found to faithfully describe the bout durations in these three stages, providing improved modeling as compared with a standard Markov chain. There are several possible directions for future work. Clustering of hypnograms based on semi-Markov sleep dynamical models can be considered. The semi-Markov models with hidden states, analogous to hidden Markov models, can also be explored. Finally, it is important to address whether differences in sleep behavior over the course of one night are adequately described by the transient (non-equilibrium) behavior of semi-Markov chains, or if it will instead be necessary to explicitly incorporate non-stationarity into the dynamical models.

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