

Sleep Breathing Impairment Index (SBII) V1.0

User Guide

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1. Introduction

Currently, the diagnosis and severity classification of Obstructive Sleep Apnea (OSA) heavily rely on traditional frequency indices such as the Apnea-Hypopnea Index (AHI) and Oxygen Desaturation Index (ODI), observed during sleep. However, these indices fall short in comprehensively considering the duration of ventilatory disturbances and the subsequent severity and duration of oxygen desaturation events. Consequently, they inadequately capture the pathophysiological abnormalities in OSA patients, limiting their efficacy in predicting the risk of associated adverse complications.

Polysomnography (PSG), the gold standard for OSA diagnosis, offers a wealth of physiological information and broad clinical feasibility, creating an avenue for new index development. In recent years, both domestic and international research teams have introduced a range of new PSG-derived indices to quantify OSA severity. Examples include mean respiratory event duration and hypoxic burden. However, consensus on the association between these new indices and OSA complications remains elusive, with varying outcomes in different studies.

The Sleep Breathing Impairment Index (SBII) calculation software addresses these issues by integrating the frequency and duration of respiratory events with associated oxygen saturation decline. This approach allows for a more nuanced quantification of OSA severity. The software facilitates automated batch processing of European Data Format (EDF) files and their annotation files (in XML format), making it suitable for large-scale OSA assessments. Simultaneously, it aids in exploring and managing target organ damage associated with the condition.

2. Program Principles

The SBII program can automatically extract oxygen saturation (SpO₂) information related to abnormal respiratory events from PSG-EDF files and their corresponding annotation files (.xml). These sources provided original SpO₂ signal data sampled at 1Hz, along with manually calibrated annotations for respiratory events like apneas and hypopneas.

The SBII was calculated by multiplying the duration of each respiratory event by the associated desaturation area. In this study, we made further improvements to enhance calculation precision and address the correction of desaturation artifacts. The specific principles of the program are outlined below:

We identified all manually calibrated apnea or hypopnea events, along with their respective desaturation search windows occurring within 100 seconds after the start of each event. The desaturation area associated with each respiratory event is calculated by integrating the cumulative desaturation areas within the designated search window (Figure 1, top and middle). Artifacts related to oxygen desaturation events (default threshold: SpO₂ < 20%) are detected and subsequently corrected by aligning them with proximate normal values (Figure 1, bottom). The individual-specific SBII is then calculated by dividing the sum of the products of all respiratory events and their corresponding desaturation areas by the total sleep duration. Consequently, the improved SBII is formulated as follows:

$$SBII = \sum_{f \in F} (T_{(f,duration)} * \int_{t_{(h,start)}}^{t_{(h,stop)}} (S_{t_{(h,start)}} - S_t) dt) / T_{totalSleepTime} \quad (1)$$

In the provided equations, the symbol "*F*" denotes all airflow events, "*H_f*" represents the hypoxia events identified within the 100-second search windows that follow the initiation of each airflow event. The notation "*T_(f,duration)*" indicates the duration of each airflow event. "*t_(h,start)*" and "*t_(h,stop)*" correspond to the initiation and conclusion moments of the desaturation area's duration. "*S_t*" denotes the SpO₂ value at the moment "*t*", while "*S_{t_(h,start)}*" signifies the start point of the duration of the desaturation area. Specifically, "*(S_{t_(h,start)} - S_t)*" captures the depth of oxygen desaturation at the precise time point "*t*". The overall desaturation areas are computed

through integration. Only respiratory events associated with a maximum oxygen desaturation depth of $\geq 3\%$ are considered, and their respective event-specific impairment values are calculated.

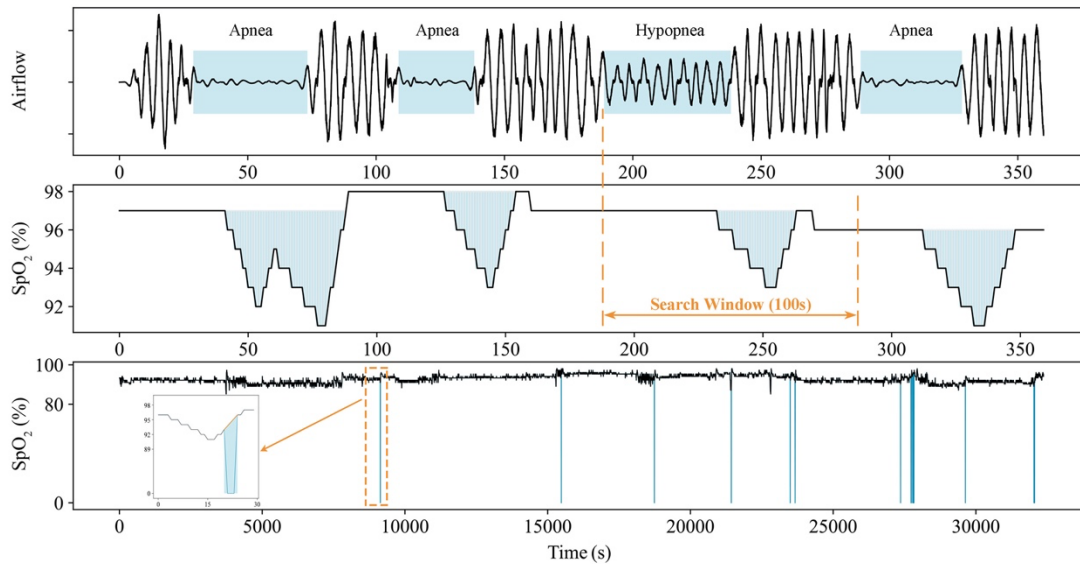


Figure 1. Enhanced algorithm representation for SBII. The top and middle graphs in the figure depict a specific time segment of an individual's sleep process, illustrating nasal cannula airflow and annotated respiratory events (top), along with relevant desaturation events exceeding 3% (middle). Within a 100-second search window after the onset of an individual respiratory event, we accumulate all relevant desaturation areas. These are then multiplied by the duration of the corresponding respiratory event, resulting in an individual event-specific impairment value. The summation of these event-specific impairment values throughout the night is then divided by the total sleep duration, ultimately generating the SBII. The bottom graph displays the oxygen saturation signals (SpO_2) for the entire nocturnal period. Within the orange dashed box, the blue solid line denotes artifacts occurring during a desaturation event, defined as a sudden drop in SpO_2 to below 20%. Normal SpO_2 values before and after the artifact are utilized for smoothing the desaturation curve, thereby ensuring the precise integration of desaturation areas (bottom).

3. Installation Instructions

The software primarily supports online usage, accessible at the following URL: <http://61.160.194.165:3080/SBII/>. Detailed instructions on how to use the software are outlined in section 4, “**User Guide**”. To optimize operational efficiency, especially considering the potential time consumption of batch uploads due to the typically large size of EDF files, the software also supports local database generation. Instructions for local environment configuration and script download are provided below:

3.1 Environment Configuration

- (1) Operating System: Windows/Linux/Mac OS.
- (2) Runtime Environment: Python (version 3.9.6 or later).
- (3) Installation of specific versions of Python dependencies:
 - Access the download link <http://61.160.194.165:3080/SBII/download.html>, download ‘[requirements.txt](#)’, and navigate to the folder containing the file.
 - Run the following command in the command line or terminal:

```
pip install -r requirements.txt
```

3.2 Script Download and Database Generation

- (1) Place all EDF files and their corresponding paired XML files into the same folder (e.g., `test/`). Ensure that the paired EDF and XML files have exactly the same file names, such as `test1.edf` and `test1.xml`.
- (2) Access the download link <http://61.160.194.165:3080/SBII/download.html>, download the Python script ‘[mainCreateDB.py](#)’, and place it in the parent folder of the `test/` folder, for example: `SBII/`.
- (3) Navigate to the `SBII/` folder and execute the command to generate the database:


```
cd SBII/
python3 mainCreateDB.py test/
```
- (4) After running the above command, all channels in the EDF files will be displayed. Please enter the oxygen saturation channel (e.g., `SaO2` or `SpO2`). Once entered, the script will generate the database files (`out.db`) in batches.

```
(venv) MacBook-Pro-4:SBII huixinjie$ python3 mainCreateDB.py test/
Available signal channels: ['SaO2', 'H.R.', 'EEG(sec)', 'ECG', 'EMG', 'EOG(L)', 'EOG(R)', 'EEG', 'SOUND', 'AIRFLOW',
'THOR RES', 'ABDO RES', 'POSITION', 'LIGHT', 'AUX']
Please select the Oxygen Saturation Channel to use: SaO2

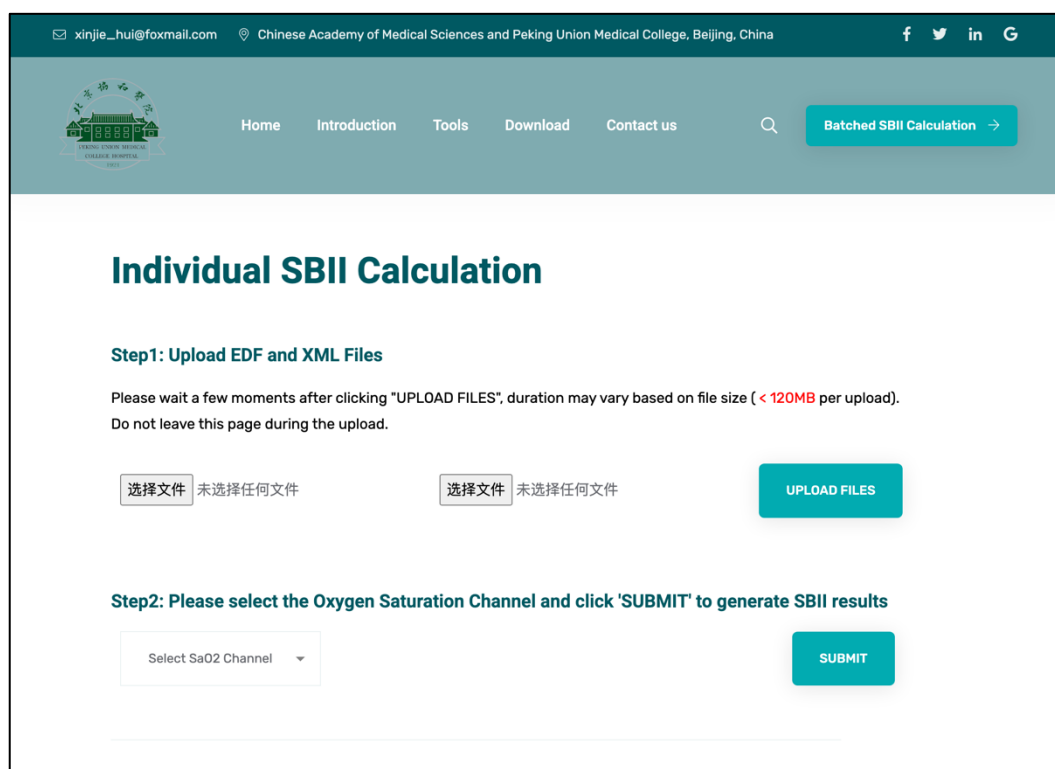
XML data processing is successfully finished, and it has been written to the database.
Starting the processing of EDF data:
67%|███████████████████████████████████████████████████████████████████████████████████████████████████████| 2/3 [00:00<00:00, 12.09it/s]
EDF data processing is successfully finished, and it has been written to the database.
67%|███████████████████████████████████████████████████████████████████████████████████████████████████████| 2/3 [00:00<00:00, 6.78it/s]
```

- (5) The generated database file (`out.db`) can be further utilized for SBII calculation via the following link: <http://61.160.194.165:3080/SBII/batchSBII.html>.
- (6) For local SBII calculations, please contact us via the website or email.

4. User Guide

The SBII calculation software webpage provides two links: one for single-instance calculation, where **EDF and XML files are uploaded separately** (<http://61.160.194.165:3080/SBII>), and another for batch calculation, where **database files (.db)** can be uploaded (<http://61.160.194.165:3080/SBII/batchSBII.html>).

4.1 Manual of Individual SBII Calculation Website



The screenshot shows the 'Individual SBII Calculation' webpage. The header includes the email 'xinjie_hui@foxmail.com', the location 'Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, China', and social media icons for Facebook, Twitter, LinkedIn, and Google+. The navigation menu contains 'Home', 'Introduction', 'Tools', 'Download', and 'Contact us'. A search bar and a 'Batched SBII Calculation' button are also present. The main content area is titled 'Individual SBII Calculation' and is divided into two steps:

Step1: Upload EDF and XML Files

Please wait a few moments after clicking "UPLOAD FILES", duration may vary based on file size (< 120MB per upload). Do not leave this page during the upload.

Two file selection buttons labeled '选择文件' (Select File) with the text '未选择任何文件' (No file selected) are shown. To their right is a teal 'UPLOAD FILES' button.

Step2: Please select the Oxygen Saturation Channel and click 'SUBMIT' to generate SBII results

A dropdown menu labeled 'Select SaO2 Channel' is shown, and to its right is a teal 'SUBMIT' button.

- (1) Please follow steps 1 and 2 sequentially.
- (2) In step 1, use the two separate upload buttons to upload the EDF and XML files.
 - Make sure both files have identical names except for the extension, such as 'test.edf' and 'test.xml'.
 - After selecting the correct files, click "UPLOAD FILES".
- (3) After successful file upload, you will receive a **Job ID** for this session. All channel names contained within the EDF file will be listed and available for selection in the dropdown menu in step 2.

Step1: Upload EDF and XML Files

Please wait a few moments after clicking "UPLOAD FILES", duration may vary based on file size (< 120MB per upload).
Do not leave this page during the upload.

选择文件

 test.edf

选择文件

 test.xml

UPLOAD FILES

Job ID: 8951703804741

Files have been uploaded successfully.

Available signal channels: ['SaO2', 'H.R.', 'EEG(sec)', 'ECG', 'EMG', 'EOG(L)', 'EOG(R)', 'EEG', 'AIRFLOW', 'THOR RES', 'ABDO RES', 'POSITION', 'LIGHT', 'NEW AIR', 'OX stat']

- (4) In step 2, choose the **oxygen saturation channel** from the dropdown menu and click "**SUBMIT**." The program will automatically calculate SBII and display it on the current page:

Step2: Please select the Oxygen Saturation Channel and click 'SUBMIT' to generate SBII results

SaO2 ▾

SUBMIT

Job ID: 8951703804741

Database has been generated.

SBII result has been generated.

The final **SBII** and **pRED_3p** indices both need to be divided by Total Sleep Time (TST, hours), which can be readily obtained from the PSG report.

id	pRED_3p * TST	SBII * TST
test	0.742	72.316

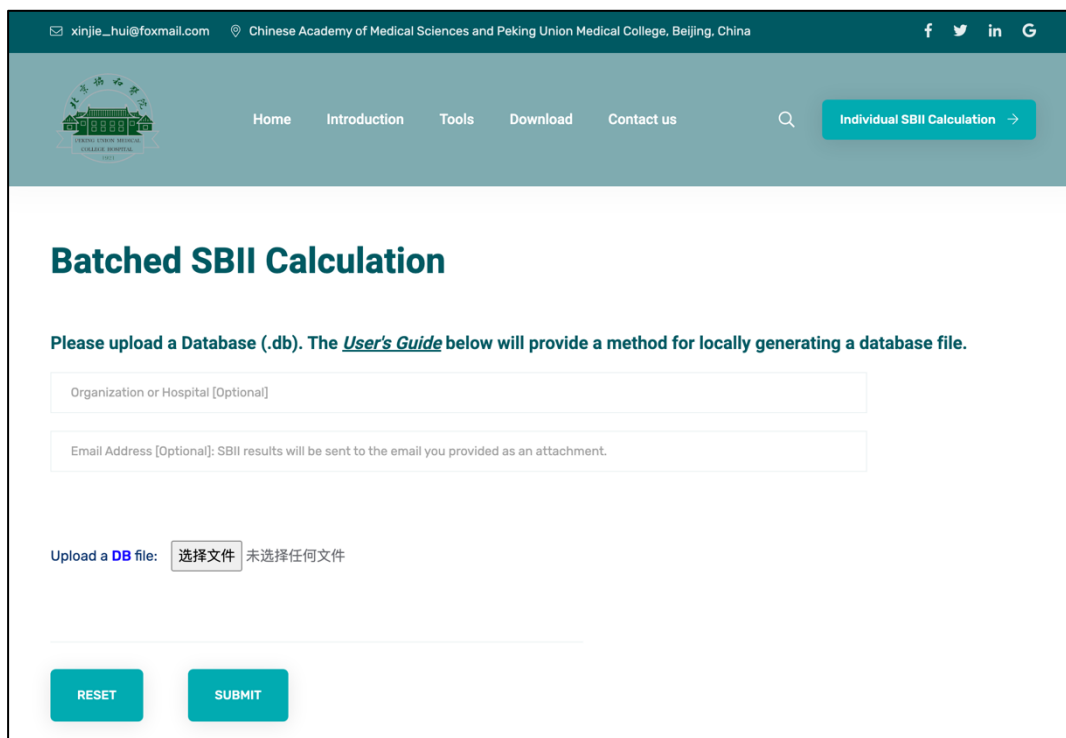
- (5) If you forget to select a channel in step 2 and submit, an error message will appear. In this case, there's no need to re-upload files from step 1. Simply select the correct channel and resubmit.

Please note that once SBII results are displayed on the page (i.e., when the calculation is successful), the original uploaded files will be immediately deleted. If you wish to recalculate, you will need to re-upload the files in step 1.

- (6) **Ensure that the Job ID in step 1 precisely matches the one in step 2 to guarantee precise calculation results.**
- (7) The final SBII and pRED_3p indices **both need to be divided by Total Sleep Time (TST, hours)**, which can be readily obtained from the PSG report.

4.2 Manual of Batched SBII Calculation Website

Considering the substantial size of EDF files and the extended upload and processing times, we suggest users utilize the Python script provided by us locally to generate the database. The setup and execution steps are straightforward. Please refer to “**3. Installation Instructions**” for detailed guidance on local database generation.



Batched SBII Calculation

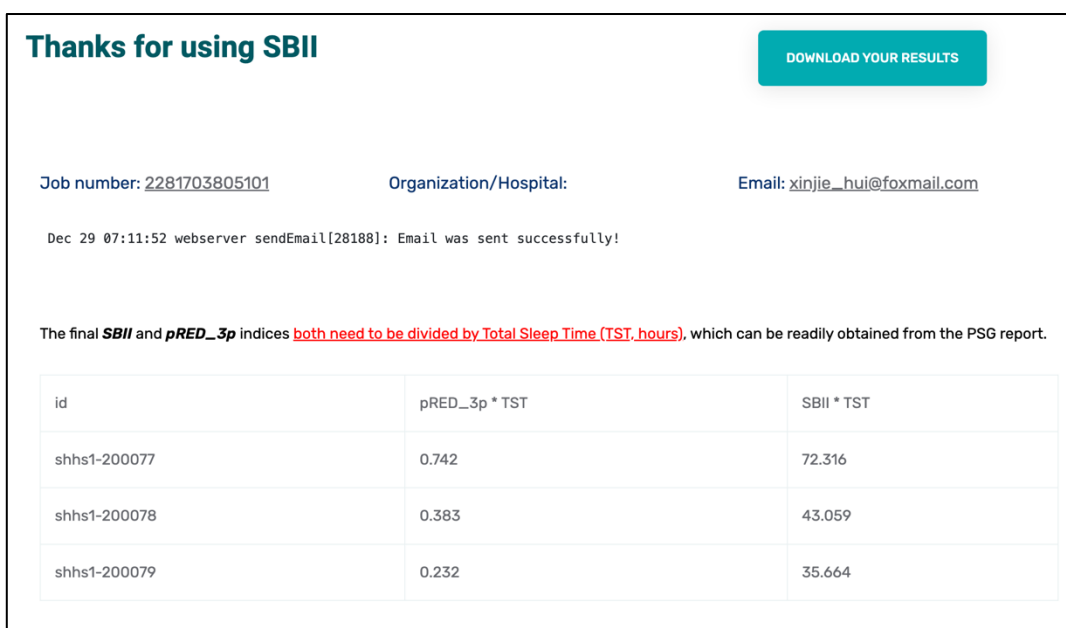
Please upload a Database (.db). The [User's Guide](#) below will provide a method for locally generating a database file.

Organization or Hospital [Optional]

Email Address [Optional]: SBII results will be sent to the email you provided as an attachment.

Upload a DB file: 未选择任何文件

- (1) After running the local script, you can **upload the generated database file (out.db)** on this page and click “**SUBMIT**” to start the batch SBII calculation.



Thanks for using SBII

Job number: 2281703805101 Organization/Hospital: Email: xinjje_hui@foxmail.com

Dec 29 07:11:52 webserve sendEmail[28188]: Email was sent successfully!

The final **SBII** and **pRED_3p** indices **both need to be divided by Total Sleep Time (TST, hours)**, which can be readily obtained from the PSG report.

id	pRED_3p * TST	SBII * TST
shhs1-200077	0.742	72.316
shhs1-200078	0.383	43.059
shhs1-200079	0.232	35.664

- (2) If you prefer to receive the SBII calculation results via email, simply enter your email address in the [\[Email Address\]](#) field before submitting the database. Once the SBII calculation is finished, the result files will be sent directly to your email inbox, allowing you to proceed without waiting on this page.


Please upload a Database (.db). The [User's Guide](#) below will provide a method for locally generating a database file.


Organization or Hospital [Optional]

Email Address [Optional]: SBII results will be sent to the email you provided as an attachment.

Upload a DB file: 未选择任何文件


SBII_Results ☆

 hcdlab 发给 我

 邮件可翻译为中文 [立即翻译](#)

Thanks for using SBII. Your job [2281703805101](#) is finished! Please check the email attachment.

附件 1

 out.txt
166.00B