**Quiet Breathing Analysis R Package: Methods**

This document describes the statistical methods and algorithms implemented in the Quiet Breathing Analysis R Package. The package is designed to analyze plethysmography respiratory data, categorize breathing behaviors, and quantify irregularities. It focuses on key techniques: data loading and validation, Quiet Breathing (QB) tagging and iterative refinement, breathing classification, QB session adjustment, and output generation.

**1. Data Loading and Validation**

**Overview**

The analysis begins by loading the input data from an Excel file and validating the presence of required columns. This step ensures the data is correctly formatted for subsequent analysis.

**Methodology**

The package uses the readxl package to read the user-selected Excel file. It checks for the following required columns:

* Te (msec): Expiratory time in milliseconds
* Ti (msec): Inspiratory time in milliseconds
* MV: Minute ventilation
* TV: Tidal volume
* PIF: Peak inspiratory flow
* PEF: Peak expiratory flow
* RT (msec): Relaxation time in milliseconds
* P (msec): Pause time in milliseconds
* f (bpm): Frequency in breaths per minute
* Penh: Enhanced pause
* Protocol Type: Indicates the protocol type (e.g., "Baseline" for analysis)

If any required columns are missing, the code halts execution with an error message.

**Algorithm**

1. Prompt the user to select an Excel file using file.choose().
2. Extract the file name without extension using tools::file\_path\_sans\_ext(basename(file\_path)).
3. Read the Excel file using read\_excel(file\_path).
4. Verify the presence of all required columns.
5. If any columns are missing, stop execution and display an error message.

**2. QB Tagging and Iterative Refinement**

**Overview**

This section details the identification and refinement of Quiet Breathing (QB) sessions, which are periods of stable breathing with low frequency and variability.

**Methodology**

The code initially tags potential QB breaths in the "Baseline" protocol where frequency ≤ 250 bpm. It groups consecutive QB breaths into sessions, considering variability in total breath time (Ttotal). Sessions with high variability or insufficient length are iteratively refined.

**Algorithm**

1. **Initial QB Tagging**:
   * Filter data for "Baseline" protocol.
   * Initialize a QB tag counter.
   * For each breath, if frequency ≤ 250 bpm and the previous breath was also QB (or it's the start of a session), assign the current QB tag.
   * If the variability in Ttotal from the previous breath exceeds 40%, or if there are consecutive non-QB breaths, end the current session.
2. **Iterative Refinement**:
   * Calculate QB Variability: [ \text{QB Variability} = \left| \frac{\text{Ttotal}*i - \text{Ttotal}*{i-1}}{\text{Ttotal}\_{i-1}} \right| \times 100% ]
   * Calculate QB\_Var\_Dev: [ \text{QB\_Var\_Dev} = \left| \text{QB Variability}*i - \text{QB Variability}*{i-1} \right| ]
   * Remove breaths from QB sessions if QB\_Var\_Dev > 40 or if Ttotal or TV is zero.
   * Recalculate variability and averages after each removal.
   * Repeat up to 25 iterations or until no changes are made.
3. **Session Validation**:
   * After refinement, remove QB sessions with fewer than 10 breaths.

This process ensures only stable QB sessions are retained for analysis.

**3. Breathing Classification**

**Overview**

Breathing classification categorizes each breath into types such as QB, Sigh, Sniff, Apnea, Post-sigh Apnea, or Hypopnea based on thresholds derived from QB averages.

**Methodology**

Using dataset-wide QB averages, the code applies the following criteria:

* **QB (0)**: Breaths within refined QB sessions.
* **Sigh (1)**: TV ≥ 2.5 × average QB TV.
* **Sniff (2)**: Frequency ≥ 2 × average QB frequency.
* **Apnea (3)**: Te ≥ 2 × average QB Te.
* **Post-sigh Apnea (3.1)**: Te ≥ 2 × average QB Te and TV ≥ 2.5 × average QB TV.
* **Hypopnea (4)**: TV ≤ 0.7 × average QB TV and Te ≥ 2 × average QB Te.

Breaths qualifying for multiple classifications are assigned the highest-priority class: Post-sigh Apnea > Hypopnea > Apnea > Sigh > Sniff > QB.

**Algorithm**

1. Calculate dataset-wide averages for QB breaths (e.g., average TV, Te, frequency).
2. For each breath, evaluate the classification criteria.
3. Assign the highest-priority classification if multiple criteria are met.
4. For breaths not in QB sessions, assign the appropriate classification or leave as NA if no criteria are met.

This classification identifies breathing irregularities and patterns.

**4. QB Session Adjustment**

**Overview**

After tagging and classification, QB sessions are adjusted to ensure continuity and sufficient length by splitting sessions with large gaps and removing short sessions.

**Methodology**

The code examines QB breath indices to identify gaps > 5 breaths. Sessions with such gaps are split, and sessions with < 10 breaths are removed.

**Algorithm**

1. Identify QB breaths and their original indices.
2. For each QB session, check for gaps > 5 breaths between consecutive QB breaths.
3. If a gap is found, assign a new QB tag to breaths after the gap.
4. After splitting, remove sessions with < 10 breaths.
5. Renumber remaining QB sessions sequentially.

This ensures QB sessions are cohesive and substantial for analysis.

**5. Output Generation**

**Overview**

The code generates outputs summarizing the analysis, including processed data, QB averages, and breathing classification summaries.

**Methodology**

Outputs include:

* **Processed Data Excel File**: Original data with added columns for QB Tag, variability metrics, averages, and breathing classification, color-coded by breathing class.
* **Average QB Values Table**: PNG image of dataset-wide QB averages.
* **Breathing Analysis Summary Excel File**: Multi-sheet workbook with counts and averages for each breathing classification.

**Algorithm**

1. Calculate averages for each breathing class.
2. Create a workbook with sheets for total counts, sighs, QB sessions, apneas, and hypopneas.
3. Generate a grob table for QB averages and save as PNG.
4. Save processed data with conditional formatting based on breathing class.

These outputs provide comprehensive insights into the respiratory data analysis.

**Conclusion**

The Quiet Breathing Analysis R Package integrates these methods to deliver a robust analysis of respiratory data:

* **Data Loading and Validation** ensures data integrity.
* **QB Tagging and Iterative Refinement** identifies stable breathing periods.
* **Breathing Classification** categorizes breathing behaviors.
* **QB Session Adjustment** refines session continuity.
* **Output Generation** provides detailed summaries and visualizations.

This structured approach offers flexibility and reliability for respiratory data analysis.