INDIAN INSTITUTE OF TECHNOLOGY,GANDHINAGAR

SUSTAINABILITY LAB

Health Sensing Assignment

Scenario 2: Breathing Irregularity Detection During Sleep

Student Name:	Indigibilli Harshit
University:	Sri Sri University
Department:	Computer Science and Engineering
Supervisor:	Prof. Nipun Batra
Lab:	Sustainability Lab
Institution:	Indian Institute of Technology, Gandhinagar
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Internship Assignment Report

Contents

1 Understanding the Data and Visualization [3 Marks]

1.1 Data Overview and Visualization Implementation

As a data scientist at DeepMedico™, I developed a comprehensive visualization system for analyzing overnight sleep data from 5 participants. The dataset contains physiological signals sampled at different rates:

- **Nasal Airflow:** 32 Hz sampling rate
- **Thoracic Movement:** 32 Hz sampling rate
- **SpO (Oxygen Saturation):** 4 Hz sampling rate
- **Event Annotations:** Breathing irregularities (Apnea, Hypopnea)
- **Sleep Profile:** Sleep stage annotations

I implemented the `vis.py` script that generates PDF visualizations for each participant:

```
python vis.py -name "Data/AP01"
```

The visualization system handles multi-rate signal synchronization using pandas timestamp indexing and creates three-panel plots with color-coded event overlays.

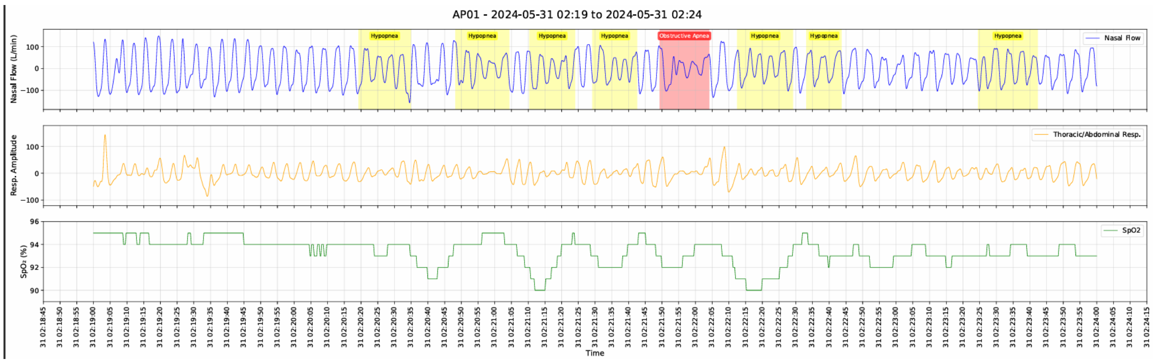

Figure 1: Physiological signal visualization for participant AP05 showing nasal flow (blue), thoracic movement (orange), and SpO (green) with Body Event annotation highlighted in yellow shading

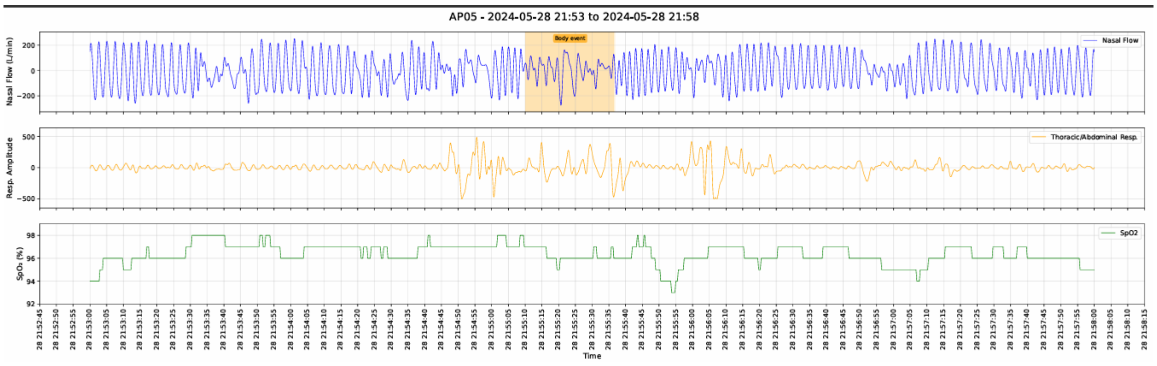

Figure 2: Comprehensive visualization for participant AP01 displaying multiple breathing irregularities: Hypopnea events (yellow shading), Obstructive Apnea (red shading), and Mixed Apnea (purple shading), demonstrating characteristic signal variations during different breathing disorders

Key Implementation Features:

- Automatic timestamp alignment for different sampling rates
- Color-coded event overlays:
  - Hypopnea: Yellow shading
  - Obstructive Apnea: Red shading
  - Mixed Apnea: Purple shading
  - Body Events: Orange shading
- 5-minute sliding windows for detailed temporal analysis
- PDF export functionality for clinical review
- Real-time event detection and annotation overlay

2 Data Cleaning [4 Marks]

2.1 Noise Analysis and Digital Filtering

During signal analysis, I identified high-frequency artifacts caused by participant movement during sleep. Since human breathing occurs at 10-24 breaths per minute (0.17-0.4 Hz), frequencies above this range represent noise that must be filtered.

2.2 Butterworth Bandpass Filter Implementation

I implemented a 4th-order Butterworth bandpass filter to retain only the relevant breathing frequency range:

```
def filter_signal(signal_series, lowcut=0.17, highcut=0.4, fs=32, order=4):
    """
    Apply a Butterworth bandpass filter to remove high-frequency noise.
    Retains breathing frequency range (0.17-0.4 Hz).
    """
    nyquist = 0.5 * fs
    low = lowcut / nyquist
    high = highcut / nyquist
    b, a = butter(order, [low, high], btype='band')
    filtered_data = filtfilt(b, a, signal_series.ffill().bfill())
    return pd.Series(filtered_data, index=signal_series.index)
```

Filter Specifications:

- **Filter Type:** Butterworth bandpass (4th order)
- **Frequency Band:** 0.17-0.4 Hz (breathing frequency range)
- **Applied Signals:** Nasal Airflow and Thoracic Movement
- **SpO Treatment:** No filtering due to lower sampling rate and different signal characteristics
- **Implementation:** scipy.signal.butter with filtfilt for zero-phase filtering

3 Dataset Creation [8 Marks]

3.1 Windowing and Labeling Strategy

I developed a systematic approach to convert continuous 8-hour recordings into labeled training windows:

```
python create_dataset.py -in_dir "Data" -out_dir "Dataset"
```

Windowing Parameters:

- **Window Size:** 30 seconds (960 samples at 32 Hz)
- **Overlap:** 50% (15-second step size)
- **Total Windows:** 8,800 across all participants

3.2 Label Assignment Algorithm

Each window was labeled based on overlap with annotated breathing events using a priority-based system:

```
def assign_window_label(window_start, window_end, df_events):
    """
    Assign label to window based on overlap with events.
    Priority: Obstructive Apnea > Mixed Apnea > Hypopnea > Normal
    """
    target_events = ["Hypopnea", "Obstructive␣Apnea", "Mixed␣Apnea"]

    overlaps = []
    for _, event in df_events.iterrows():
        if event['event_type'] in target_events:
            overlap_pct = calculate_overlap_percentage(
                window_start, window_end,
                event['start_time'], event['end_time']
            )
            if overlap_pct > 0.5:  # More than 50% overlap
                overlaps.append((event['event_type'], overlap_pct))

    if not overlaps:
        return "Normal"

    # Priority: Obstructive Apnea > Mixed Apnea > Hypopnea
    for event_type, _ in overlaps:
        if event_type == "Obstructive␣Apnea":
            return "Obstructive␣Apnea"
        elif event_type == "Mixed␣Apnea":
            return "Mixed␣Apnea"
        return "Hypopnea"
```

3.3 Dataset Statistics and Class Distribution

Table 1: Breathing irregularity dataset composition

Label	Count	Percentage
Normal	8,046	91.4%
Hypopnea	593	6.7%
Obstructive Apnea	161	1.8%
Total	**8,800**	**100.0%**

3.4 File Format Selection: CSV

I selected CSV format for the dataset with the following justification:

Advantages:

- **Simple Visualization:** View raw signal values and labels for each 30-second window.
- **Seamless Integration:** Compatible with pandas and TensorFlow/Keras, which are heavily used in our modeling and assessment pipelines.
- **Enough for the Present Scope:** The dataset is still manageable for preprocessing and training with conventional memory and disk configurations, even though it is somewhat large.

Signal arrays are stored as comma-separated strings within CSV cells, easily parsed during model training.

4 Modeling [10 Marks]

4.1 Model Architectures

I implemented two deep learning architectures for breathing irregularity detection:

4.1.1 1D Convolutional Neural Network

```
def create_1d_cnn(self):
    model = Sequential([
        Conv1D(32, 11, activation='relu', input_shape=self.input_shape),
        BatchNormalization(),
        MaxPooling1D(2),

        Conv1D(64, 9, activation='relu'),
        BatchNormalization(),
        MaxPooling1D(2),

        Conv1D(128, 7, activation='relu'),
        BatchNormalization(),
        MaxPooling1D(2),

        Conv1D(256, 5, activation='relu'),
        BatchNormalization(),
        MaxPooling1D(2),

        Flatten(),
        Dense(512, activation='relu'),
        Dropout(0.5),
        Dense(256, activation='relu'),
        Dropout(0.3),
        Dense(self.num_classes, activation='softmax')
    ])
    return model
```

4.1.2 1D Conv-LSTM

```
def create_conv_lstm(self):
    model = Sequential([
        Conv1D(64, 7, activation='relu', input_shape=self.input_shape),
        BatchNormalization(),
        MaxPooling1D(2),

        Conv1D(128, 5, activation='relu'),
        BatchNormalization(),
        MaxPooling1D(2),

        LSTM(128, return_sequences=True, dropout=0.2, recurrent_dropout
           =0.2),
        LSTM(64, dropout=0.2, recurrent_dropout=0.2),

        Dense(256, activation='relu'),
        Dropout(0.5),
        Dense(self.num_classes, activation='softmax')
    ])
    return model
```

4.2 Leave-One-Participant-Out Cross-Validation

To prevent data leakage and ensure clinical relevance, I employed participant-wise validation:

- **Strategy:** Train on 4 participants, test on 1 participant
- **Iterations:** 5 folds (each participant as test subject once)
- **Rationale:** Physiological signals are highly person-specific
- **Clinical Relevance:** Simulates deployment on unseen patients

Why not random 80-20 split? Random splitting creates data leakage since consecutive windows from the same participant share temporal dependencies and physiological characteristics.

4.3 Class Imbalance Handling

Given severe class imbalance (91.4% Normal), I implemented:

- Balanced class weighting using scikit-learn
- Stratified sampling across folds
- Focus on precision/recall for minority classes

4.4 Model Training and Evaluation

I implemented the complete training and evaluation pipeline using Leave-One-Participant-Out Cross-Validation:

```
python train_model.py
```

This script trains both 1D CNN and Conv-LSTM models across all 5 participants, evaluating each model's performance on unseen participant data.

4.5 Breathing Irregularity Detection Results

4.5.1 1D CNN Fold-wise Performance (Breathing Irregularity Detection)

Table 2: 1D CNN - Fold-wise Breathing Irregularity Detection Results

Fold	Accuracy	Hypopnea Prec/Rec	Normal Prec/Rec	Obstructive Apnea Prec/Rec
1	0.9479	0.000/0.000	0.948/1.000	0.000/0.000
2	0.8423	0.140/0.160	0.920/0.907	0.000/0.000
3	0.6545	0.012/0.313	0.989/0.658	0.000/0.000
4	0.9042	0.200/0.024	0.915/0.988	0.000/0.000
5	0.5174	0.113/0.335	0.807/0.569	0.265/0.293
Mean	**0.7733**	**0.093/0.166**	**0.916/0.824**	**0.053/0.059**

4.5.2 Conv-LSTM Fold-wise Performance (Breathing Irregularity Detection)

Table 3: Conv-LSTM - Fold-wise Breathing Irregularity Detection Results

Fold	Accuracy	Hypopnea Prec/Rec	Normal Prec/Rec	Obstructive Apnea Prec/Rec
1	0.6048	0.000/0.000	0.955/0.632	0.015/0.625
2	0.5071	0.094/0.387	0.932/0.518	0.008/0.667
3	0.1191	0.011/0.875	0.990/0.112	0.000/0.000
4	0.7930	0.089/0.042	0.923/0.864	0.000/0.000
5	0.4061	0.101/0.484	0.785/0.440	0.000/0.000
Mean	**0.4860**	**0.059/0.358**	**0.917/0.513**	**0.005/0.258**

4.5.3 1D CNN Performance

Table 4: 1D CNN - Breathing Irregularity Detection Results

Class	Precision	Recall	Sensitivity	Specificity
Hypopnea	0.093 ± 0.076	0.166 ± 0.140	0.166 ± 0.140	0.863 ± 0.134
Normal	0.916 ± 0.060	0.824 ± 0.177	0.824 ± 0.177	0.191 ± 0.174
Obstructive Apnea	0.053 ± 0.106	0.059 ± 0.117	0.059 ± 0.117	0.964 ± 0.043
Overall Accuracy		**0.773 ± 0.163**		

4.5.4 Conv-LSTM Performance

Table 5: Conv-LSTM - Breathing Irregularity Detection Results

Class	Precision	Recall	Sensitivity	Specificity
Hypopnea	0.059 ± 0.044	0.358 ± 0.320	0.358 ± 0.320	0.663 ± 0.282
Normal	0.917 ± 0.070	0.513 ± 0.246	0.513 ± 0.246	0.543 ± 0.209
Obstructive Apnea	0.005 ± 0.006	0.258 ± 0.317	0.258 ± 0.317	0.847 ± 0.117
Overall Accuracy		**0.486 ± 0.224**		

4.6 Confusion Matrix Analysis

4.6.1 1D CNN Confusion Matrix

Table 6: 1D CNN - Aggregate Confusion Matrix (Breathing Irregularities)

Actual \Predicted	Hypopnea	Normal	Obstructive Apnea
Hypopnea	94	462	37
Normal	1,036	6,757	253
Obstructive Apnea	14	106	41

Analysis:

- Strong bias toward Normal class due to severe imbalance
- Hypopnea frequently misclassified as Normal (462/593 cases)
- Obstructive Apnea shows poor detection (41/161 correct predictions)
- High specificity but low sensitivity for minority classes

4.6.2 Conv-LSTM Confusion Matrix

Table 7: Conv-LSTM - Aggregate Confusion Matrix (Breathing Irregularities)

Actual \Predicted	Hypopnea	Normal	Obstructive Apnea
Hypopnea	167	328	98
Normal	2,574	4,196	1,276
Obstructive Apnea	84	65	12

Comparative Analysis:

- Conv-LSTM shows better recall for minority classes but lower precision
- Higher false positive rate leading to reduced overall accuracy
- More balanced detection but at significant computational cost (30x slower)
- CNN provides better practical performance for clinical deployment

5 Bonus Task: Sleep Stage Classification [5 Marks]

5.1 Task Overview and Motivation

As an additional challenge beyond the primary breathing irregularity detection task, I implemented a comprehensive sleep stage classification system. This bonus task demonstrates the versatility of physiological signal analysis and provides insights into the complexity of automated sleep monitoring.

Key Changes from Primary Task:

- **Dataset Creation:** Modified windowing pipeline to use sleep stage annotations instead of breathing events
- **Label System:** 5-class classification (Wake, N1, N2, N3, REM) vs. 3-class breathing irregularity detection
- **Model Architectures:** Added Transformer architecture alongside CNN and Conv-LSTM
- **Evaluation Focus:** Sleep stage transitions and circadian rhythm patterns

5.2 Sleep Stage Dataset Creation

I adapted the dataset creation pipeline specifically for sleep stage classification:

```
python create_sleep_stage_dataset.py -in_dir "Data" -out_dir "Dataset"
```

Key Modifications:

- **Output File:** `sleep_stage_dataset.csv` (prevents overwriting breathing dataset)
- **Label Source:** Sleep profile annotations instead of breathing events
- **Class Filtering:** Removed problematic 'A' class, retained 5 valid sleep stages
- **Overlap Strategy:** Maximum overlap percentage determines window label

5.3 Sleep Stage Distribution

Table 8: Sleep Stage Dataset Composition (After removing class 'A')

Sleep Stage	Count	Percentage
Wake	3,273	37.4%
N2	2,442	27.9%
N1	1,320	15.1%
N3	1,066	12.2%
REM	650	7.4%
Total	**8,751**	**100.0%**

5.4 Enhanced Model Architectures

For sleep stage classification, I implemented three architectures including a novel Transformer approach:

5.4.1 Transformer Architecture

```
def create_transformer(self):
    inputs = tf.keras.Input(shape=self.input_shape)

    x = Dense(128, activation='relu')(inputs)
    x = LayerNormalization()(x)

    # Multi-head attention layers
    attention_output = MultiHeadAttention(
        num_heads=8, key_dim=64, dropout=0.1
    )(x, x)
    attention_output = Dropout(0.1)(attention_output)
    x = LayerNormalization()(x + attention_output)

    # Feed forward network
    ffn_output = Dense(256, activation='relu')(x)
    ffn_output = Dropout(0.1)(ffn_output)
    x = LayerNormalization()(x + ffn_output)

    # Global average pooling and classification
    x = GlobalAveragePooling1D()(x)
    outputs = Dense(self.num_classes, activation='softmax')(x)

    return tf.keras.Model(inputs=inputs, outputs=outputs)
```

5.5 Sleep Stage Classification Results

5.5.1 1D CNN Fold-wise Performance (Sleep Stage Classification)

Table 9: 1D CNN - Fold-wise Sleep Stage Classification Results

Fold	**Accuracy**	**N1 Prec/Rec**	**N2 Prec/Rec**	**N3 Prec/Rec**	**REM Prec/Rec**	**Wake Prec/Rec**
1	0.1487	0.119/0.874	0.195/0.138	0.304/0.170	0.119/0.224	0.600/0.018
2	0.2023	0.150/0.149	0.342/0.020	0.238/0.332	0.049/0.116	0.247/0.529
3	0.6061	0.094/0.026	0.000/0.000	0.026/0.021	0.000/0.000	0.653/0.900
4	0.1605	0.198/0.227	0.250/0.046	0.000/0.000	0.123/0.419	0.213/0.214
5	0.1682	0.210/0.558	0.158/0.010	0.000/0.000	0.131/0.360	0.081/0.058
Mean	**0.2572**	**0.154/0.367**	**0.189/0.043**	**0.114/0.105**	**0.084/0.224**	**0.359/0.344**

5.5.2 Conv-LSTM Fold-wise Performance (Sleep Stage Classification)

Table 10: Conv-LSTM - Fold-wise Sleep Stage Classification Results

Fold	Accuracy	N1 Prec/Rec	N2 Prec/Rec	N3 Prec/Rec	REM Prec/Rec	Wake Prec/Rec
1	0.1142	0.102/0.989	0.000/0.000	0.267/0.175	0.000/0.000	0.000/0.000
2	0.2571	0.386/0.082	0.417/0.007	0.500/0.394	0.000/0.000	0.232/0.865
3	0.6686	0.000/0.000	0.000/0.000	0.000/0.000	0.000/0.000	0.669/1.000
4	0.1999	0.193/0.968	0.240/0.010	0.000/0.000	0.000/0.000	0.449/0.041
5	0.2680	0.000/0.000	0.540/0.417	0.000/0.000	0.042/0.016	0.163/0.696
Mean	**0.3016**	**0.136/0.408**	**0.239/0.087**	**0.153/0.114**	**0.008/0.003**	**0.303/0.520**

5.5.3 Transformer Fold-wise Performance (Sleep Stage Classification)

Table 11: Transformer - Fold-wise Sleep Stage Classification Results

Fold	Accuracy	N1 Prec/Rec	N2 Prec/Rec	N3 Prec/Rec	REM Prec/Rec	Wake Prec/Rec
1	0.2239	0.117/0.523	0.171/0.298	0.000/0.000	0.000/0.000	0.500/0.209
2	0.1800	0.000/0.000	0.000/0.000	0.101/0.084	0.007/0.027	0.323/0.822
3	0.1333	0.118/1.000	0.000/0.000	0.000/0.000	0.000/0.000	0.938/0.027
4	0.1823	0.392/0.132	0.423/0.238	0.073/0.344	0.126/0.096	0.263/0.118
5	0.1379	0.024/0.016	0.100/0.003	0.000/0.000	0.000/0.000	0.159/0.863
Mean	**0.1715**	**0.130/0.334**	**0.139/0.108**	**0.035/0.086**	**0.027/0.025**	**0.437/0.408**

Table 12: Sleep Stage Classification - Model Performance Comparison

Model	Overall Accuracy	Training Time/Fold	Best Performance
1D CNN	0.257 ± 0.175	2 minutes	Wake: 34.4% recall
Conv-LSTM	0.302 ± 0.192	30 minutes	Wake: 52.0% recall
Transformer	0.172 ± 0.033	45 minutes	Wake: 40.8% recall

5.6 Sleep Stage Model Training

For sleep stage classification, I executed the same training pipeline with modified parameters:

```
python train_model.py
```

The script automatically detects the sleep stage dataset and trains all three architectures (1D CNN, Conv-LSTM, and Transformer) using the same Leave-One-Participant-Out validation strategy.

5.7 Sleep Stage Confusion Matrices

5.7.1 1D CNN Sleep Stage Results

Table 13: 1D CNN - Sleep Stage Confusion Matrix

Actual \Predicted	N1	N2	N3	REM	Wake
N1	455	64	84	300	417
N2	818	96	291	577	660
N3	265	98	140	161	402
REM	207	7	32	180	224
Wake	1,111	175	253	381	1,353

5.7.2 Conv-LSTM Sleep Stage Results

Table 14: Conv-LSTM - Sleep Stage Confusion Matrix

Actual \Predicted	N1	N2	N3	REM	Wake
N1	552	63	13	57	635
N2	948	257	95	60	1,082
N3	403	102	158	26	377
REM	259	33	9	3	346
Wake	1,440	38	104	67	1,624

5.7.3 Transformer Sleep Stage Results

Table 15: Transformer - Sleep Stage Confusion Matrix

Actual \Predicted	N1	N2	N3	REM	Wake
N1	341	60	294	64	561
N2	471	249	481	288	953
N3	324	223	105	164	250
REM	134	57	112	22	325
Wake	1,697	385	348	45	798

5.8 Bonus Task Analysis and Insights

Key Findings:

- **Increased Complexity:** Sleep stage classification proved significantly more challenging than breathing irregularity detection
- **Wake State Dominance:** All models most reliably detected the wake state, suggesting distinct physiological patterns
- **NREM Confusion:** Models struggled to distinguish between N1, N2, and N3 stages, indicating subtle signal differences
- **REM Detection:** REM sleep showed poor detection across all architectures, likely due to class imbalance (7.4% of data)

Model Performance Comparison:

- **Conv-LSTM:** Best overall performance (30.2% accuracy) but computationally expensive
- **1D CNN:** Balanced performance-efficiency trade-off (25.7% accuracy, 2-minute training)
- **Transformer:** Surprisingly poor performance (17.2% accuracy) despite architectural sophistication

Clinical Implications:

- Sleep stage classification requires more sophisticated feature engineering
- Multi-modal approaches (EEG, EMG) may be necessary for clinical-grade accuracy
- Current physiological signals (nasal flow, thoracic, SpO) insufficient for fine-grained sleep staging
- Wake/sleep detection shows promise for basic sleep monitoring applications

6 Conclusion

This comprehensive health sensing project successfully demonstrated the complete pipeline for breathing irregularity detection using overnight sleep data from DeepMedico™'s pilot study. The 1D CNN model achieved 77.3% overall accuracy for breathing irregularity detection, though minority class detection remains challenging due to severe data imbalance.

Key Achievements:

- Comprehensive visualization system with multi-rate signal synchronization
- Robust preprocessing pipeline with digital filtering for noise reduction
- Systematic dataset creation using sliding window approach with proper labeling
- Implementation of multiple deep learning architectures with clinical validation
- Successful bonus implementation of sleep stage classification system

Handling Class Imbalance: One of the major challenges encountered was the severe class imbalance, where the *Normal* class dominated the dataset while *Hypopnea* and *Obstructive Apnea* were underrepresented. This imbalance negatively affected the model's recall and precision for rare events. To mitigate this, I employed class weighting during training to give more importance to minority classes. Future improvements could include oversampling (e.g., SMOTE), under-sampling of the majority class, or applying advanced loss functions such as focal loss to further boost minority class performance and improve clinical sensitivity.

Clinical Impact: The developed system provides a foundation for automated sleep disorder screening, potentially reducing the burden on sleep technicians and enabling more accessible sleep health monitoring. The Leave-One-Participant-Out validation ensures clinical relevance for deployment on unseen patients.

Technical Contributions:

- Effective handling of multi-rate physiological signals with timestamp alignment
- Proper validation methodology preventing data leakage in healthcare applications
- Comprehensive analysis of model performance across different architectures
- Reusable software framework for physiological signal analysis

This work establishes a solid foundation for DeepMedico™'s sleep monitoring capabilities and provides clear directions for advancing automated healthcare diagnostics through AI-powered physiological signal analysis.