my_nbviewer_forder (/github/zziioonnee/my_nbviewer_forder/tree/main)
/
바이오의료데이터구조_과제09_우송대학교_202110716_백지원.ipynb (/github/zziioonnee/my_nbviewer_forder/tree/main/바이오의료데이터구조_과제09_우송대학교_202110716

In [29]:

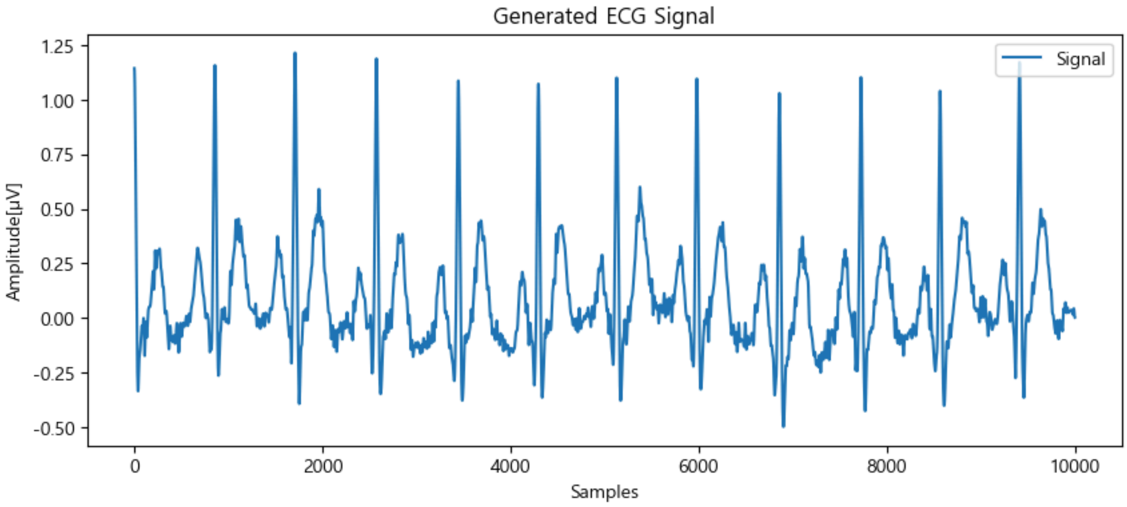
```
# NeuroKit2와 pandas 라이브러리 임포트
import neurokit2 as nk
import numpy as np
import pandas as pd

# ECG 데이터 생성
ecg_simulate = nk.ecg_simulate(
    duration=10,        # 10초간 데이터 생성
    heart_rate=70,      # 심박수 70bpm
    noise=0.1,          # 노이즈 정도
    random_state=42     # 재현성을 위한 시드값
)

# ECG 데이터 유형 확인
type(ecg_simulate)
```

Out[29]:

```
numpy.ndarray
```

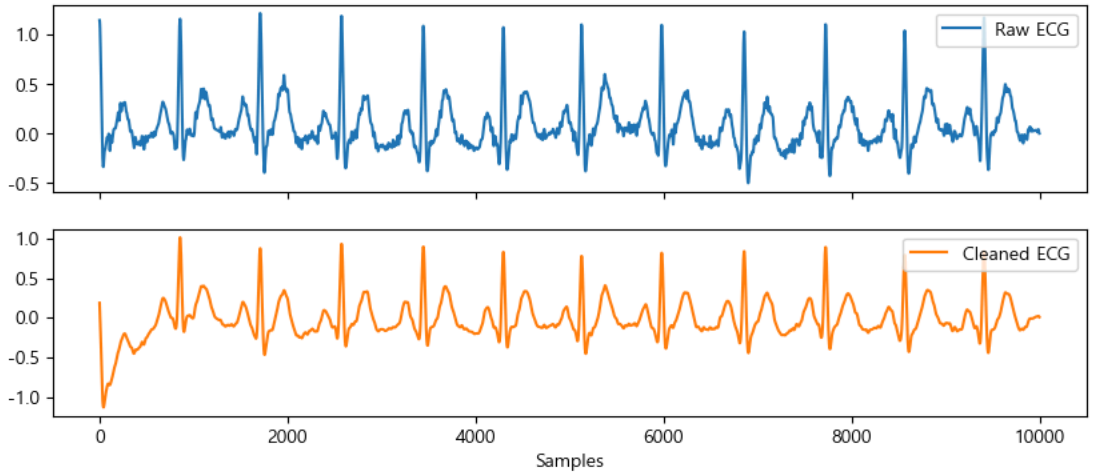
In [30]:

```
import matplotlib.pyplot as plt

#그래프 크기 설정 [width, height](inces)
plt.rcParams['figure.figsize']=[10, 4]

# ECG 데이터 플롯
nk.signal_plot(ecg_simulate)

# 제목, 축이름 추가, 그래프 출력
plt.title("Generated ECG Signal")
plt.xlabel("Samples")
plt.ylabel("Amplitude[μV]")
plt.show()
```



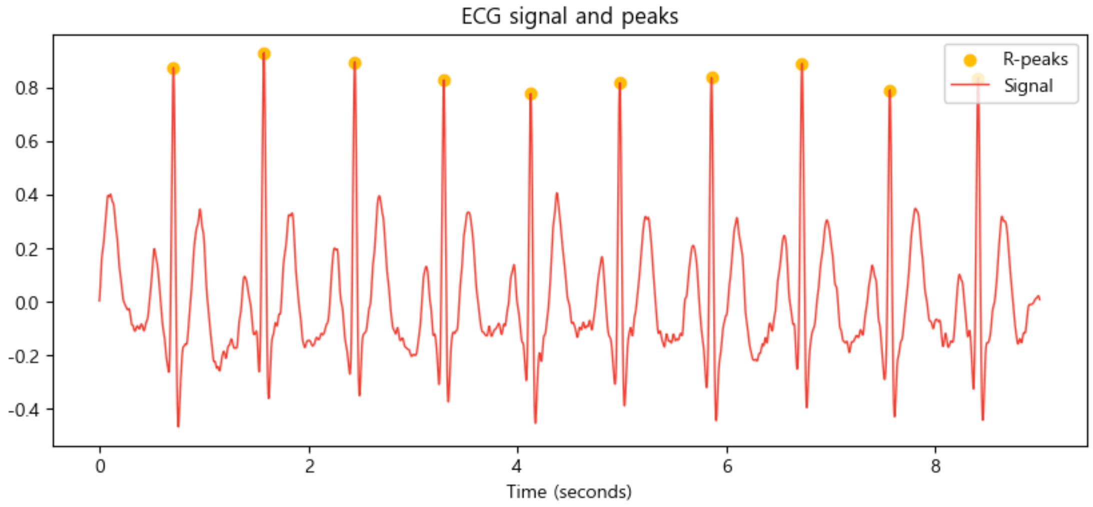
In [31]:

```
ecg_cleaned = nk.ecg_clean(
    ecg_simulate,
    sampling_rate=1000,
    method="neurokit"
)

# ECG 데이터 플롯
nk.signal_plot(
    [ecg_simulate, ecg_cleaned],
    labels=["Raw ECG", "Cleaned ECG"],
    subplots=True
)
```



In [32]:
```
# 정제된 이후의 신호는 시작 부분이 왜곡이 발생하므로 시작 부분을 제거
ecg_cleaned = ecg_cleaned[1000:]
```

In [33]:
```
rpeaks_instances, rpeaks_info = nk.ecg_peaks(
    ecg_cleaned,
    sampling_rate=1000,
    correct_artifacts=True,
    show=True
)
```



In [34]:
```
rpeaks_instances
```

Out[34]:

	ECG_R_Peaks
0	0
1	0
2	0
3	0
4	0
...	...
8995	0
8996	0
8997	0
8998	0
8999	0

9000 rows × 1 columns

In [35]:
```
# 반환된 신호 데이터 중에서 R-peak만 추출
rpeaks_instances[rpeaks_instances["ECG_R_Peaks"]!=0]
```

Out[35]:

	ECG_R_Peaks
709	1
1575	1
2445	1
3296	1
4129	1
4981	1
5858	1
6725	1
7566	1
8410	1

In [36]:

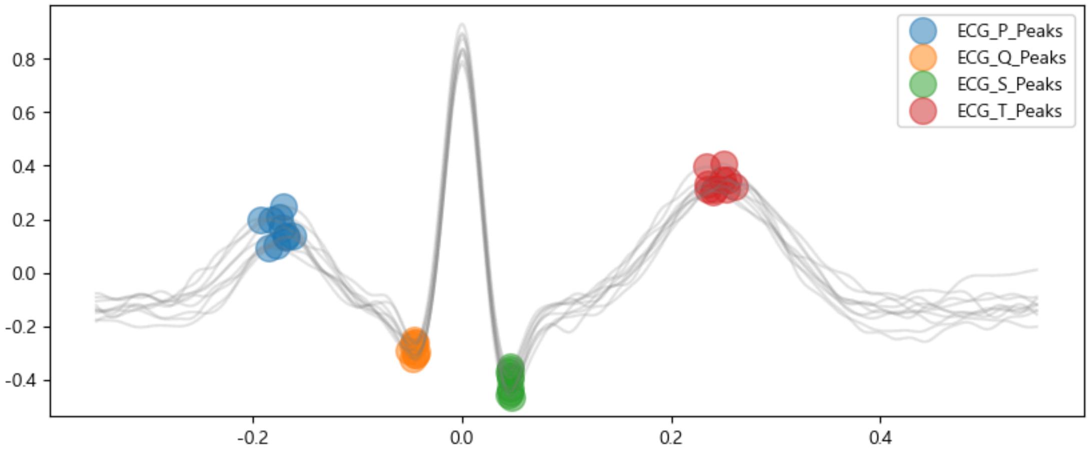
```
rpeaks_info
```

Out[36]:

```
{'method_peaks': 'neurokit',
 'method_fixpeaks': 'None',
 'ECG_R_Peaks': array([ 709, 1575, 2445, 3296, 4129, 4981, 5858, 6725, 7566, 8410]),
 'ECG_R_Peaks_Uncorrected': array([ 709, 1575, 2445, 3296, 4129, 4981, 5858, 6725, 7566, 8410]),
 'ECG_fixpeaks_ectopic': [],
 'ECG_fixpeaks_missed': [],
 'ECG_fixpeaks_extra': [],
 'ECG_fixpeaks_longshort': [],
 'ECG_fixpeaks_method': 'kubios',
 'ECG_fixpeaks_rr': array([0.85566667, 0.866     , 0.87      , 0.851     , 0.833     ,
        0.852     , 0.877     , 0.867     , 0.841     , 0.844     ]),
 'ECG_fixpeaks_drrs': array([-0.03693152,  0.29439696,  0.11396011, -0.54131054, -0.51282051,
         0.54131054,  0.71225071, -0.28490028, -0.74074074,  0.08547009]),
 'ECG_fixpeaks_mrrs': array([ 0.06662629,  0.37552998,  0.33313144, -0.33918837, -1.5142338 ,
        -0.13325257,  0.90854028,  0.56329497, -0.72683222, -0.29073289]),
 'ECG_fixpeaks_s12': array([ 0.29439696,  0.11396011,  0.29439696, -0.51282051, -0.54131054,
         0.71225071,  0.54131054, -0.74074074, -0.28490028, -0.74074074]),
 'ECG_fixpeaks_s22': array([ 0.29439696, -0.54131054, -0.54131054,  0.54131054,  0.71225071,
        -0.28490028, -0.74074074,  0.08547009,  0.08547009, -0.74074074]),
 'ECG_fixpeaks_c1': 0.13,
 'ECG_fixpeaks_c2': 0.17,
 'sampling_rate': 1000}
```

In [37]:

```
waves_data, waves = nk.ecg_delineate(
    ecg_cleaned,            # 정제된 신호 데이터
    rpeaks=rpeaks_info,     # R-peak 위치
    sampling_rate=1000,     # 샘플링 주파수
    show=True,              # 플롯 출력
    show_type='peaks'       # 모든 피크를 표시
)
```



In [38]:

```
# 각 파형의 피크, 시작, 끝 위치
waves_data.head()
```

Out[38]:

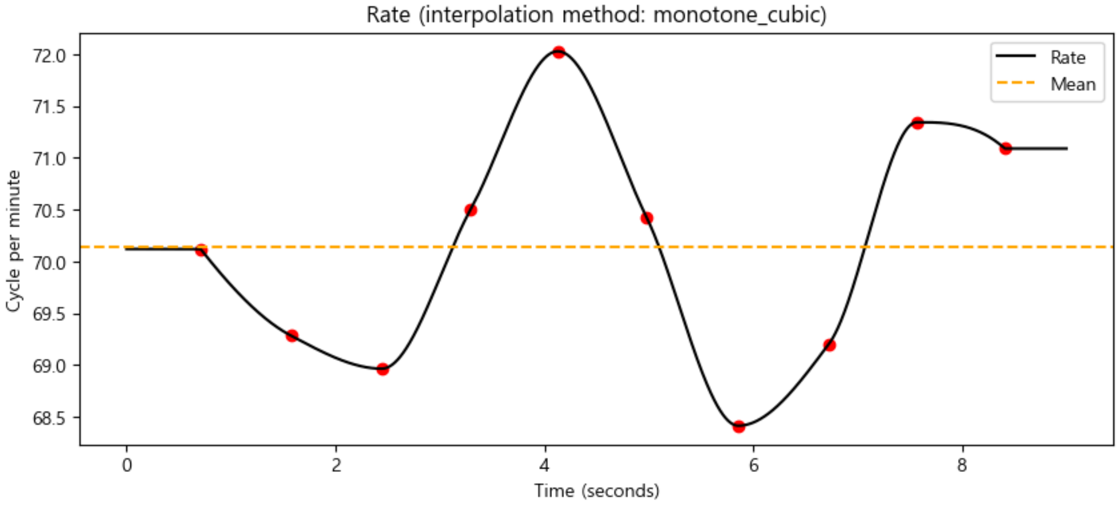
	ECG_P_Peaks	ECG_P_Onsets	ECG_P_Offsets	ECG_Q_Peaks	ECG_R_Onsets	ECG_R_Offsets	ECG_S_Peaks	ECG_T_Peaks	ECG_T_Onsets	ECG_T_Offsets
0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0

In [39]:

```
waves
```

```
Out[39]: {'ECG_P_Peaks': [526, 1390, 2252, 3127, 3966, 4809, 5683, 6554, 7397, 8232],
          'ECG_P_Onsets': [462, 1316, 2190, 3043, 3883, 4716, 5617, 6443, 7309, 8174],
          'ECG_P_Offsets': [661, 1477, 2263, 3195, 4003, 4871, 5807, 6607, 7513, 8312],
          'ECG_Q_Peaks': [664, 1529, 2397, 3251, 4085, 4936, 5811, 6679, 7515, nan],
          'ECG_R_Onsets': [529, 1507, 2277, 3219, 4059, 4898, 5779, 6654, 7469, nan],
          'ECG_R_Offsets': [793, 1649, 2516, 3370, 4204, 5059, 5932, 6799, 7638, 8483],
          'ECG_S_Peaks': [756, 1621, 2490, 3340, 4173, 5026, 5903, 6771, 7611, nan],
          'ECG_T_Peaks': [962, 1835, 2678, 3531, 4379, 5233, 6099, 6964, 7814, 8644],
          'ECG_T_Onsets': [942, 1782, 2631, 3424, 4273, 5136, 6002, 6846, 7683, 8575],
          'ECG_T_Offsets': [1093, 1912, 2813, 3649, 4484, 5240, 6249, 7045, 7910, 8656]}
```

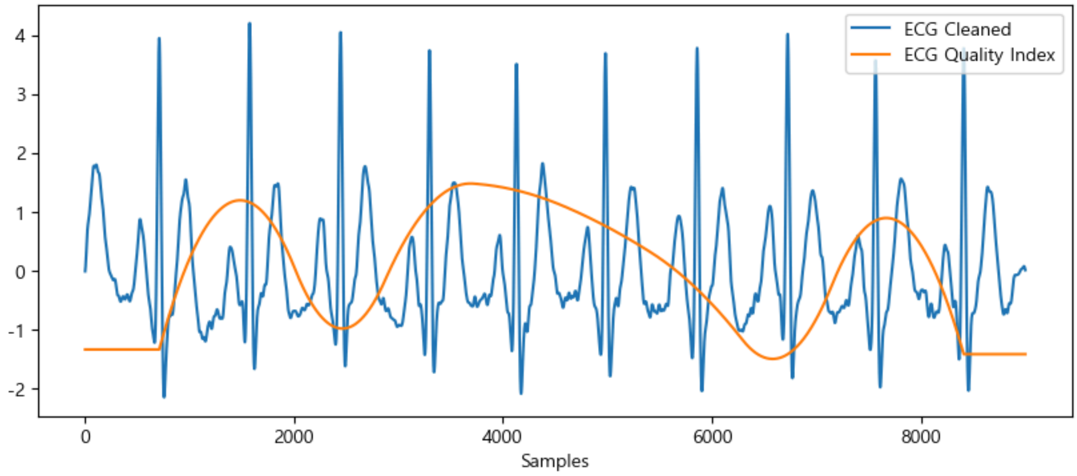
```
In [40]: rate = nk.signal_rate(
             peaks=rpeaks_info["ECG_R_Peaks"],       # R-peak 위치
             sampling_rate=1000,                     # 샘플링 주파수
             desired_length=len(ecg_cleaned),        # 신호 길이
             interpolation_method="monotone_cubic",  # 보간 방법
             show=True                               # 플롯 출력
         )
```



```
In [41]: # ECG 품질 지수 계산
         quality = nk.ecg_quality(
             ecg_cleaned,
             rpeaks=rpeaks_info["ECG_R_Peaks"],
             sampling_rate=1000,
             method='averageQRS'
         )

         quality
```

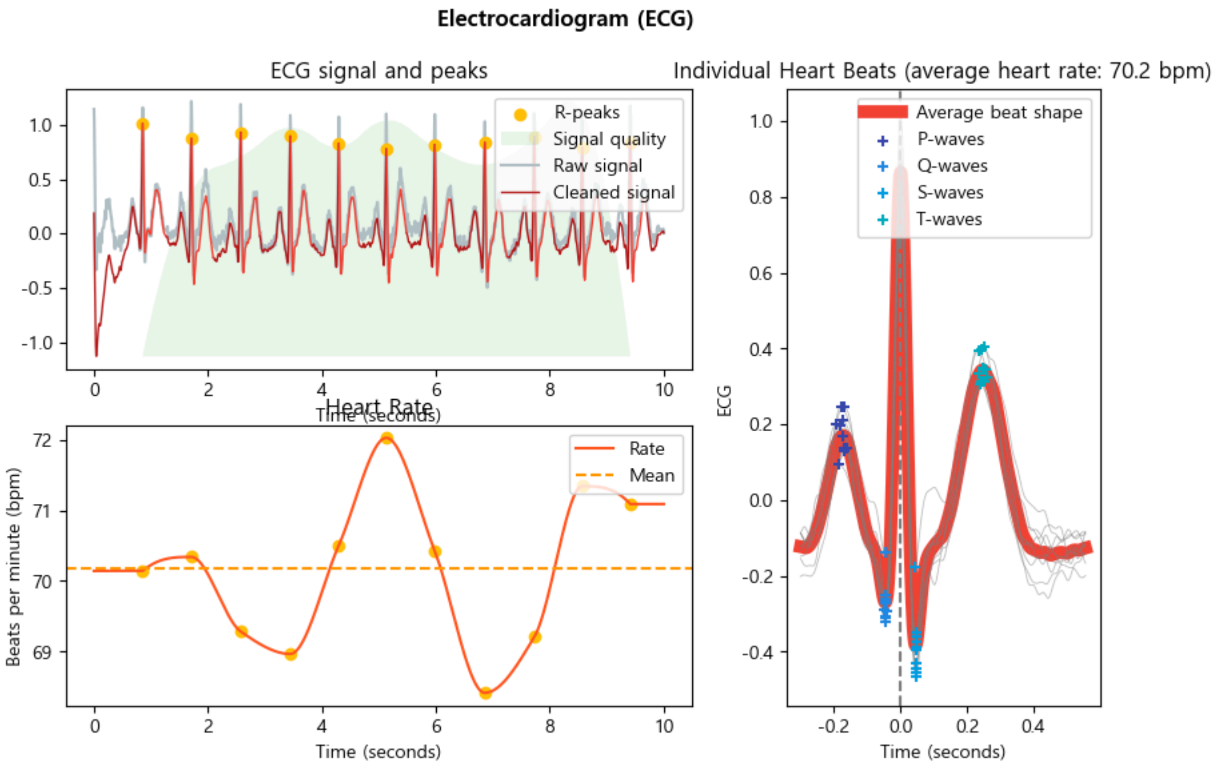
```
Out[41]: array([0.02861104, 0.02861104, 0.02861104, ..., 0.        , 0.        ,
                0.        ])
```

```
In [42]: # 품질 지수 플롯
         nk.signal_plot(
             [ecg_cleaned, quality],
             labels=["ECG Cleaned", "ECG Quality Index"],
             standardize=True
         )
```



In [43]:

```
# 전처리 파이프라인을 통한 ECG 데이터 처리
ecg_signals, info = nk.ecg_process(
    ecg_simulate,                   # 신호 데이터
    sampling_rate=1000,             # 샘플링 주파수
    method="neurokit"               # 전처리 방법
)

# 그래프 크기 설정
plt.rcParams['figure.figsize'] = [10, 6]

# 통합된 ECG 데이터 플롯
nk.ecg_plot(ecg_signals, info);
```



In [44]:

```
ecg_signals
```

Out[44]:

	ECG_Raw	ECG_Clean	ECG_Rate	ECG_Quality	ECG_R_Peaks	ECG_P_Peaks	ECG_P_Onsets	ECG_P_Offsets	ECG_Q_Peaks	ECG_R_Onsets	ECG_R_Offsets	ECG
0	1.144713	0.185982	70.142623	0.0	0	0	0	0	0	0	0	
1	1.140385	0.154798	70.142623	0.0	0	0	0	0	0	0	0	
2	1.130545	0.123352	70.142623	0.0	0	0	0	0	0	0	0	
3	1.115027	0.091415	70.142623	0.0	0	0	0	0	0	0	0	
4	1.093818	0.058787	70.142623	0.0	0	0	0	0	0	0	0	
...	...	...	...	...	...	...	...	...	...	...	...	
9995	0.014362	0.014388	71.090047	0.0	0	0	0	0	0	0	0	
9996	0.009472	0.012758	71.090047	0.0	0	0	0	0	0	0	0	
9997	0.005616	0.011069	71.090047	0.0	0	0	0	0	0	0	0	
9998	0.003197	0.009346	71.090047	0.0	0	0	0	0	0	0	0	
9999	0.002618	0.007612	71.090047	0.0	0	0	0	0	0	0	0	

10000 rows × 19 columns

In [45]:

```
info
```

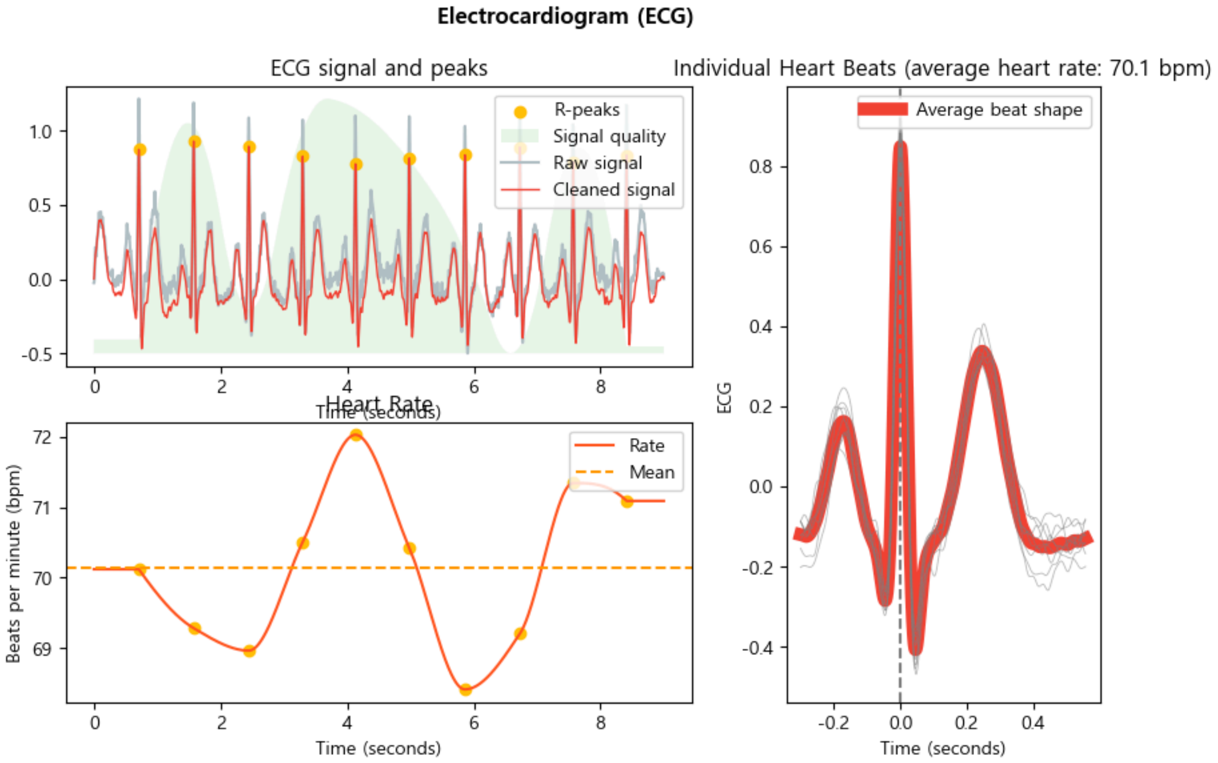
```
Out[45]: {'method_peaks': 'neurokit',
          'method_fixpeaks': 'None',
          'ECG_R_Peaks': array([ 856, 1709, 2575, 3445, 4296, 5129, 5981, 6858, 7725, 8566, 9410],
                dtype=int64),
          'ECG_R_Peaks_Uncorrected': array([ 856, 1709, 2575, 3445, 4296, 5129, 5981, 6858, 7725, 8566, 9410]),
          'ECG_fixpeaks_ectopic': [],
          'ECG_fixpeaks_missed': [],
          'ECG_fixpeaks_extra': [],
          'ECG_fixpeaks_longshort': [],
          'ECG_fixpeaks_method': 'kubios',
          'ECG_fixpeaks_rr': array([0.8554, 0.853 , 0.866 , 0.87  , 0.851 , 0.833 , 0.852 , 0.877 ,
                 0.867 , 0.841 , 0.844 ]),
          'ECG_fixpeaks_drrs': array([-0.02828784, -0.05955335,  0.32258065,  0.09925558, -0.47146402,
                 -0.44665012,  0.47146402,  0.62034739, -0.24813896, -0.64516129,
                  0.07444169]),
          'ECG_fixpeaks_mrrs': array([ 0.03308519,  0.        ,  0.32533774,  0.40253653, -0.17645437,
                 -1.10283981, -0.027571  ,  0.68927488,  0.42735043, -0.55141991,
                 -0.22056796]),
          'ECG_fixpeaks_s12': array([-0.05955335, -0.02828784,  0.09925558,  0.32258065, -0.44665012,
                 -0.47146402,  0.62034739,  0.47146402, -0.64516129, -0.24813896,
                 -0.64516129]),
          'ECG_fixpeaks_s22': array([ 0.32258065,  0.32258065, -0.47146402, -0.47146402,  0.47146402,
                  0.62034739, -0.24813896, -0.64516129,  0.07444169,  0.07444169,
                 -0.64516129]),
          'ECG_fixpeaks_c1': 0.13,
          'ECG_fixpeaks_c2': 0.17,
          'sampling_rate': 1000,
          'ECG_P_Peaks': [677,
           1526,
           2390,
           3252,
           4128,
           4966,
           5809,
           6683,
           7554,
           8397,
           9232],
          'ECG_P_Onsets': [591,
           1462,
           2316,
           3190,
           4043,
           4883,
           5716,
           6617,
           7443,
           8309,
           9174],
          'ECG_P_Offsets': [758,
           1661,
           2477,
           3263,
           4195,
           5003,
           5871,
           6808,
           7607,
           8513,
           9312],
          'ECG_Q_Peaks': [810,
           1665,
           2530,
           3398,
           4252,
           5086,
           5937,
           6812,
           7680,
           8516,
           nan],
          'ECG_R_Onsets': [780,
           1529,
           2507,
           3277,
           4219,
           5059,
           5898,
           6779,
           7654,
           8469,
           nan],
          'ECG_R_Offsets': [927,
           1793,
           2649,
           3516,
           4370,
           5204,
           6059,
           6932,
           7799,
           8638,
           9483],
          'ECG_S_Peaks': [899,
           1757,
           2622,
           3491,
           4341,
           5174,
           6027,
           6904,
           7772,
           8612,
           nan],
          'ECG_T_Peaks': [1099,
           1962,
           2835,
           3678,
           4531,
           5380,
           6233,
           7099,
           7964,
           8814,
           9644],
          'ECG_T_Onsets': [1034,
           1942,
           2782,
           3631,
           4424,
           5273,
           6137,
           7002,
           7847,
           8683,
           9575],
          'ECG_T_Offsets': [1264,
           2094,
           2912,
           3813,
           4649,
           5484,
           6240,
           7249,
           8045,
           8910,
           9656]}
```

In [46]:

```
# 전처리 파이프라인 함수 정의
def ecg_process_ha(ecg_signal):

    # 노이즈 제거
    ecg_cleaned = nk.ecg_clean(ecg_signal, sampling_rate=1000, method='neurokit')[1000:]
    rpeaks_instances, rpeaks_info = nk.ecg_peaks(ecg_cleaned, sampling_rate=1000)
    rate = nk.ecg_rate(rpeaks_info["ECG_R_Peaks"], sampling_rate=1000, desired_length=len(ecg_cleaned))
    quality = nk.ecg_quality(ecg_cleaned, rpeaks=rpeaks_info["ECG_R_Peaks"], sampling_rate=1000)

    # 출력할 데이터프레임 생성
    signals = pd.DataFrame({
        "ECG_Raw": ecg_signal[1000:],
        "ECG_Clean": ecg_cleaned,
        "ECG_Rate": rate,
        "ECG_Quality": quality
    })

    signals = pd.concat([signals, rpeaks_instances], axis=1)

    # Create info dict
    info = rpeaks_info
    info["sampling_rate"] = 1000

    return signals, info
```

In [47]:

```
# ECG 전처리 수행
signals, info = ecg_process_ha(ecg_simulate)

# ECG 데이터 플롯
nk.ecg_plot(signals, info)
```



In [48]:
```
import neurokit2 as nk

# 샘플 데이터 로드
df = nk.data("bio_resting_5min_100hz")

# 데이터 정보 확인
df.info()
```

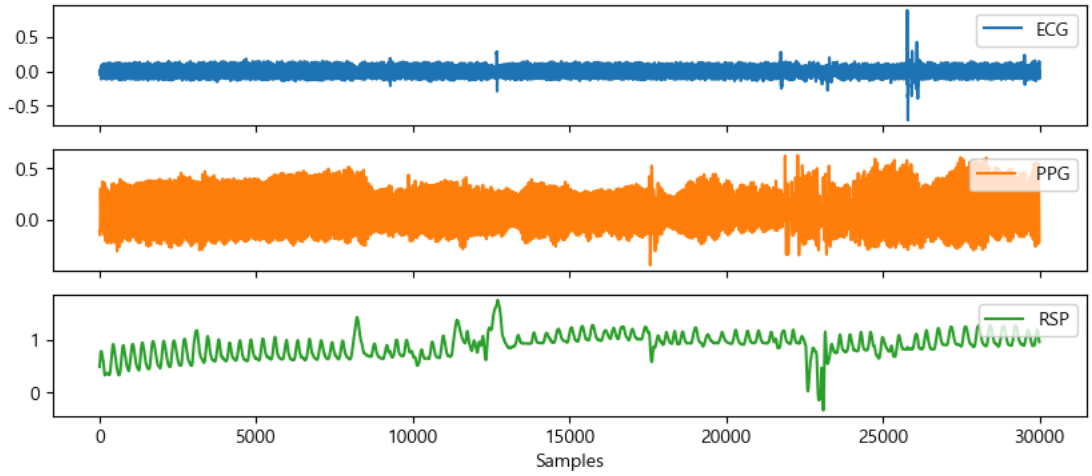
```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 30000 entries, 0 to 29999
Data columns (total 3 columns):
 #   Column  Non-Null Count  Dtype  
---  ------  --------------  -----  
 0   ECG     30000 non-null  float64
 1   PPG     30000 non-null  float64
 2   RSP     30000 non-null  float64
dtypes: float64(3)
memory usage: 703.3 KB
```

In [49]:
```
# 데이터 확인
df.head()
```

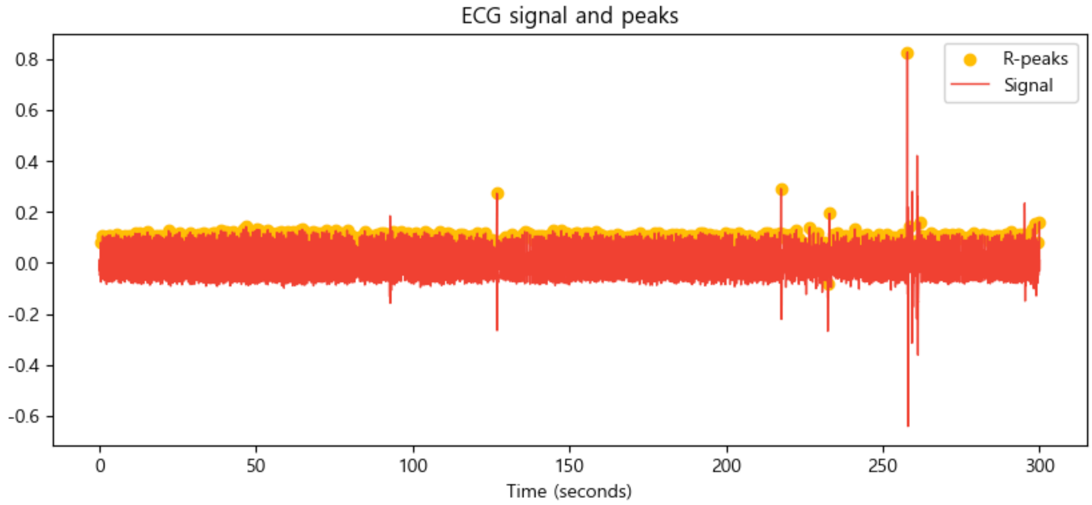
Out[49]:

	ECG	PPG	RSP
0	0.003766	-0.102539	0.494652
1	-0.017466	-0.103760	0.502483
2	-0.015679	-0.107422	0.511102
3	-0.001598	-0.110855	0.518791
4	0.002483	-0.112610	0.528669

In [50]:
```
# 데이터 시각화
plt.rcParams['figure.figsize'] = [10, 4]
nk.signal_plot(df, subplots=True, labels=["ECG", " PPG", "RSP"])
```



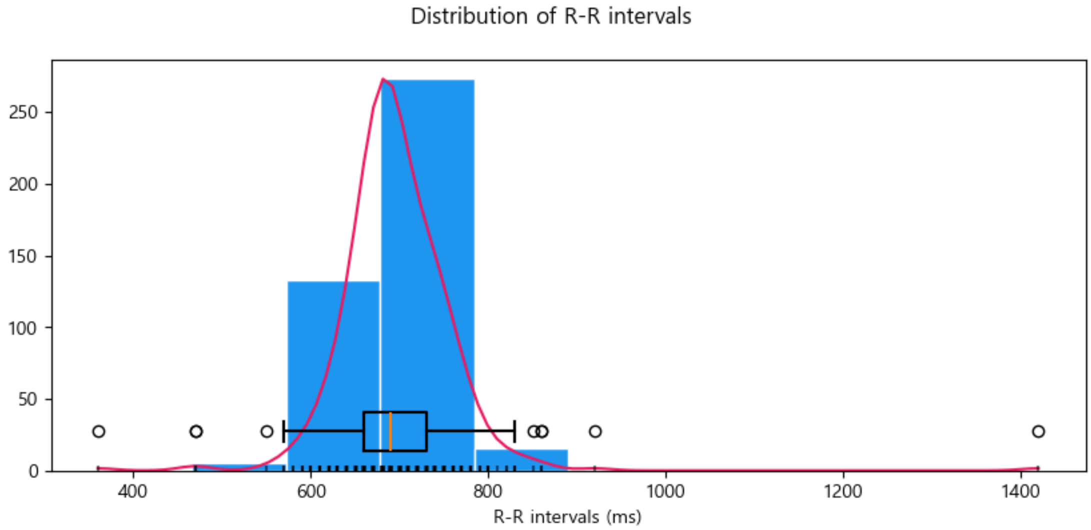
In [51]:
```
# ECG 데이터 추출
ecg_signal = df["ECG"]

# 노이즈 제거
ecg_cleaned = nk.ecg_clean(ecg_signal, sampling_rate=100, method="neurokit")

# R-peak 검출
rpeaks_instances, rpeaks_info = nk.ecg_peaks(ecg_cleaned, sampling_rate=100, show=True)

# R-peak 위치 저장
rpeaks = rpeaks_info["ECG_R_Peaks"]
```



In [52]:
```
# 시간 영역 분석
hrv_time = nk.hrv_time(rpeaks, sampling_rate=100, show=True)

# 사간 영역 분석 결과
hrv_time[['HRV_MeanNN', 'HRV_SDNN', 'HRV_RMSSD', 'HRV_pNN50']]
```

Out[52]:

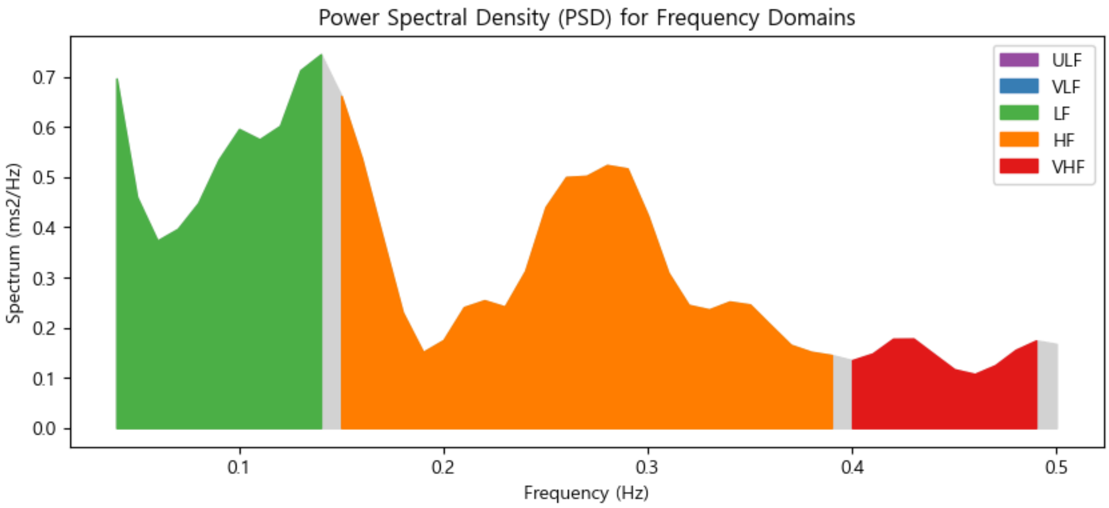
	HRV_MeanNN	HRV_SDNN	HRV_RMSSD	HRV_pNN50
0	696.372093	64.777555	76.484531	15.116279



In [53]:
```
# 주파수 영역 분석
hrv_freq = nk.hrv_frequency(rpeaks, sampling_rate=100, show=True, normalize=True)

hrv_freq
```

Out[53]:

	HRV_ULF	HRV_VLF	HRV_LF	HRV_HF	HRV_VHF	HRV_TP	HRV_LFHF	HRV_LFn	HRV_HFn	HRV_LnHF
0	NaN	0.017393	0.048824	0.064269	0.013135	0.143621	0.759686	0.339952	0.447491	-2.744677



In [54]:
```
# 주파수 영역 분석 결과
hrv_freq[['HRV_TP', 'HRV_VLF', 'HRV_HF', 'HRV_LFHF']]
```

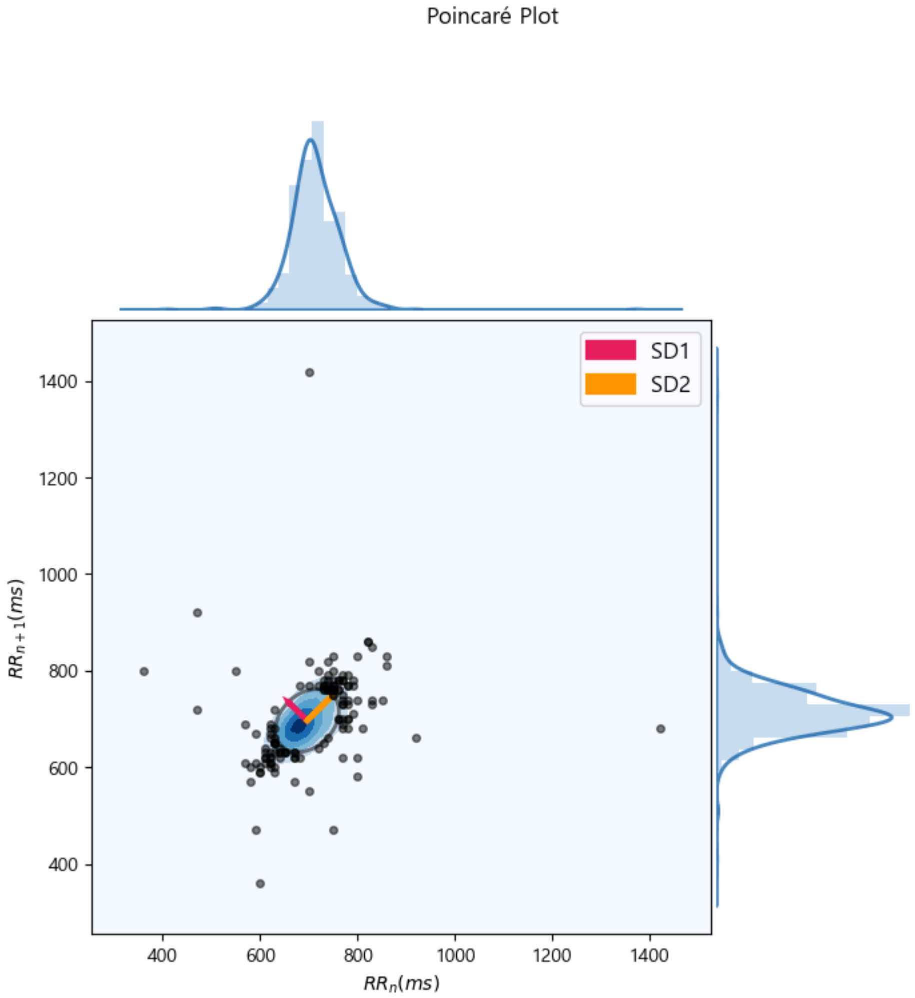
Out[54]:

	HRV_TP	HRV_VLF	HRV_HF	HRV_LFHF
0	0.143621	0.017393	0.064269	0.759686

In [55]:
```
plt.rcParams['figure.figsize'] = [6, 6]

# 푸엥카레 플롯을 통한 비선형 영역 분석
hrv_nonlinear = nk.hrv_nonlinear(rpeaks, sampling_rate=100, show=True)

# 비선형 영역 분석 결과
hrv_nonlinear[['HRV_SD1', 'HRV_SD2', 'HRV_SD1SD2']]
```

Out[55]:

	HRV_SD1	HRV_SD2	HRV_SD1SD2
0	54.145713	73.792275	0.733759

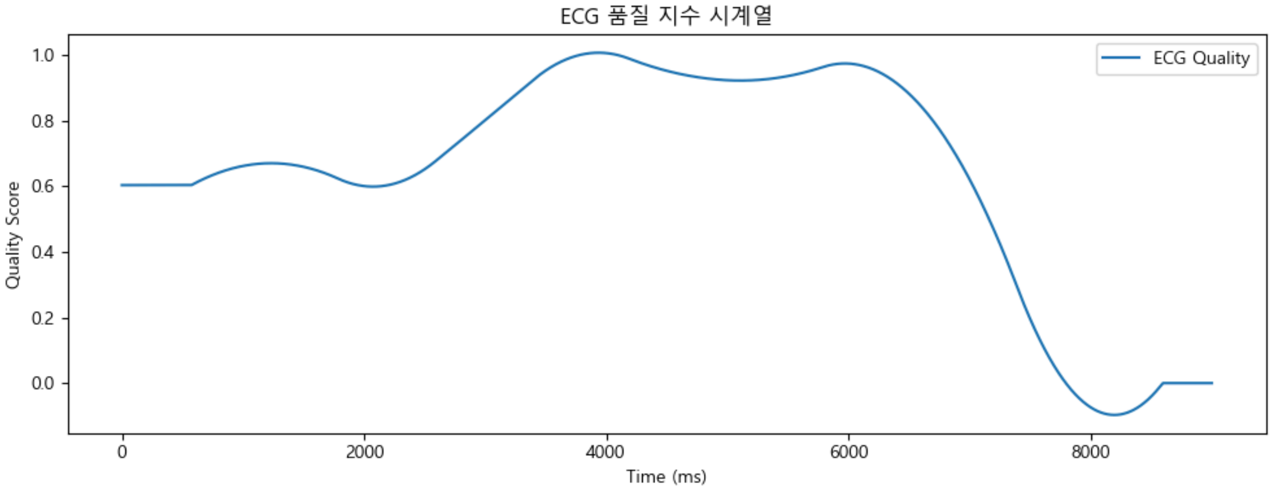


+ 심박수 통계 및 품질 시각화 추가

- 평균 심박수 및 품질 지수의 시각화를 통해 ECG 데이터의 전반적 특성을 보여줌.

In [56]:
```
# ECG 샘플 시계열 데이터 생성 (시뮬레이션용)
import neurokit2 as nk
import pandas as pd
import matplotlib.pyplot as plt

# 폰트
plt.rcParams['font.family'] = 'Malgun Gothic'
plt.rcParams['axes.unicode_minus'] = False

ecg_sim = nk.ecg_simulate(duration=10, noise=0.01, heart_rate=75, sampling_rate=1000)

# 전처리 실행
signals, info = ecg_process_ha(ecg_sim)

# 평균 심박수 출력
mean_hr = signals["ECG_Rate"].mean()
print(f"평균 심박수: {mean_hr:.2f} bpm")

# 품질 지수 시각화
plt.figure(figsize=(10, 4))
plt.plot(signals["ECG_Quality"], label="ECG Quality")
plt.title("ECG 품질 지수 시계열")
plt.xlabel("Time (ms)")
plt.ylabel("Quality Score")
plt.legend()
plt.tight_layout()
plt.show()
```

```
평균 심박수: 74.80 bpm
```

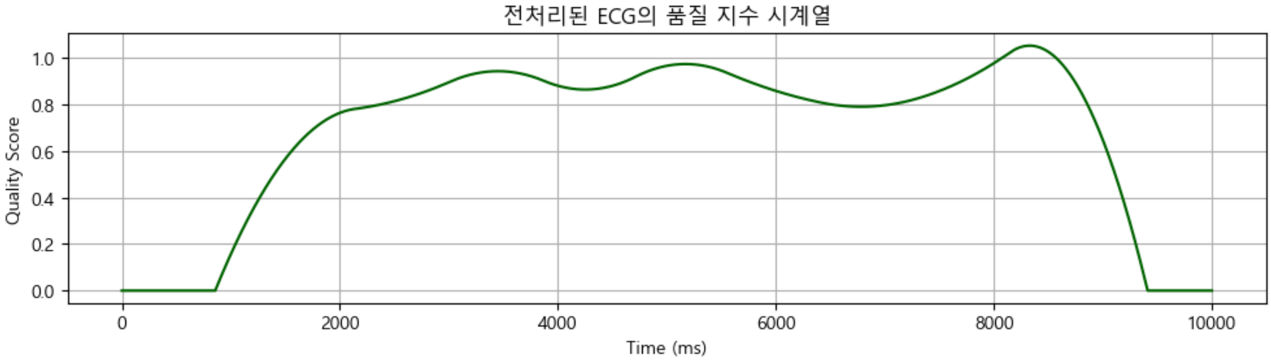


품질 지수 시각화 및 품질 평균 출력

- 전처리 후 ECG 품질 지수 시계열을 별도로 추출, 시각화.

In [57]:
```
# 품질 지수 평균 출력
mean_quality = ecg_signals["ECG_Quality"].mean()
print(f"평균 품질 지수: {mean_quality:.3f}")

# 품질 지수 시각화
plt.figure(figsize=(10, 3))
plt.plot(ecg_signals["ECG_Quality"], color='darkgreen')
plt.title("전처리된 ECG의 품질 지수 시계열")
plt.xlabel("Time (ms)")
plt.ylabel("Quality Score")
plt.grid(True)
plt.tight_layout()
plt.show()
```

```
평균 품질 지수: 0.688
```


전처리된 ECG의 품질 지수 시계열
Quality Score
Time (ms)