Supplementary Information for

Interpersonal autonomic coupling profiles distinguish social transmission from common-input synchrony

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This PDF file includes:
Figure S1 to S6
Tables S1 to S9

Index

Introduction

This document provides supplementary information to support the findings of the article entitled "Interpersonal autonomic coupling profiles distinguish social transmission from common-input synchrony".
We report below the formal expressions for the two Linear Mixed-Effects Models (LMER) employed in this study. Model 1 (Equation1) was fitted to assess differences in IPCC across experimental conditions (Hp 1-3), while Model 2 (Equation 2) was designed to investigate whether IPCC varies as a function of the emotional dimensions of arousal and valence (Hp 4).

$$IPCC = \text{Condition} + \text{Genders} + \text{Frequency} + (1 \mid \text{ID}) \tag{1}$$

$$IPCC = \text{Condition} * (\text{Arousal} + \text{Valence}) + \text{Genders} + \text{Frequency} + (1 \mid \text{ID}) \tag{2}$$

All statistical tests reported in the Supplementary Tables section were performed using the parametric bootstrap method ($n_{\text{sim}} = 1000$ simulations) described in the Methods section ("Parametric Bootstrap") of the main text. P values in bold indicate significant effects at $\alpha = 0.05$.

Supplementary Figures

Model Selection

Model Order Selection - EDA

This figure illustrates the mean model order selected using the AIC criterion, for EDA signals. For each dyad, model orders were averaged across temporal windows and experimental conditions. The overall mean model order was 3.73 ± 1.95.

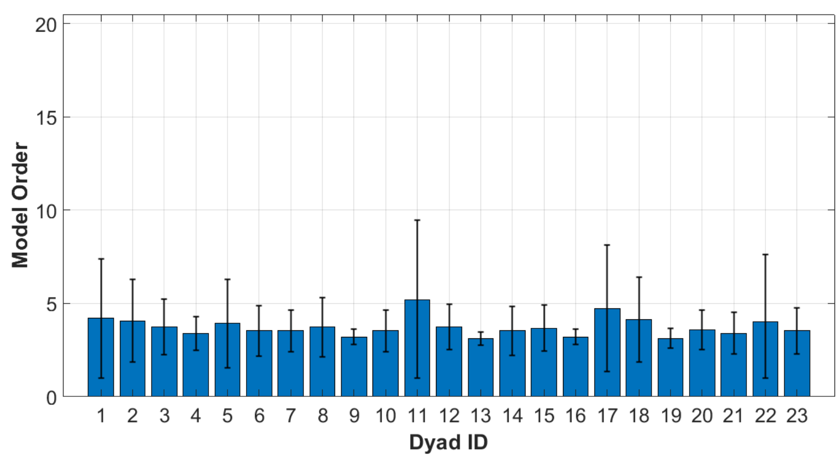

Figure S1: Mean selected model order for EDA signals across dyads. On the x-axis, dyad IDs are shown, and on the y-axis, the model order ranging from 1 to the maximum allowed value ($pmax = 20$). For each dyad, the figure illustrates the mean selected model order (blue bars) and its standard deviation (black bars).

Model Order Selection - HRV

This figure illustrates the mean model order selected using the AIC criterion, for HRV signals. For each dyad, model orders were averaged across temporal windows and experimental conditions. The overall mean model order was 13.61 $\pm$ 4.01.

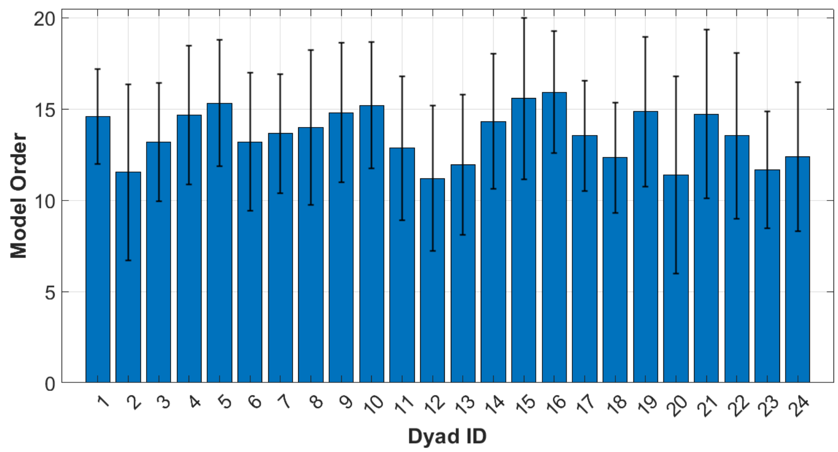

Figure S2: Mean selected model order for HRV signals across dyads. On the x-axis, dyad IDs are shown, and on the y-axis, the model order ranging from 1 to the maximum allowed value ($pmax = 20$). For each dyad, the figure illustrates the mean selected model order (blue bars) and its standard deviation (black bars).

Condition Plot

EDA Condition Plot

Figure S3 illustrates how IPCC for EDA signals varies across the experimental conditions.

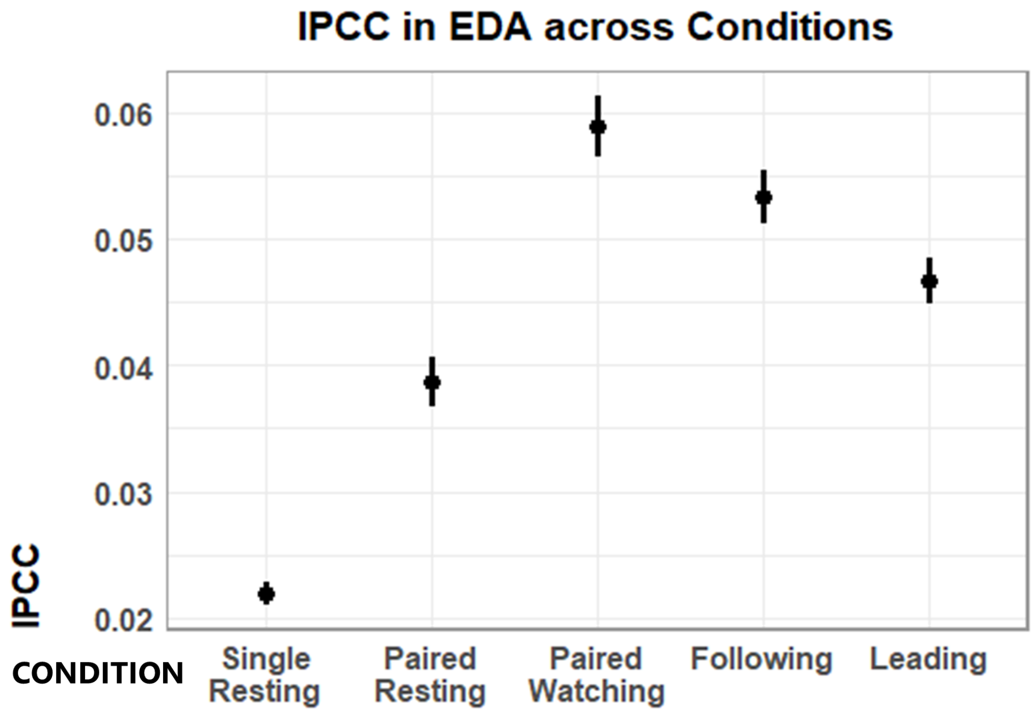

Figure S3: IPCC values for EDA signals across different experimental conditions (Single Resting, Paired Resting, Paired Watching, Following, Leading).
Dots represent the mean IPCC values, with error bars indicating the standard error (SE) of the mean.

HRV Condition Plot

Figure S4 illustrates how IPCC for HRV signals varies across the experimental conditions.

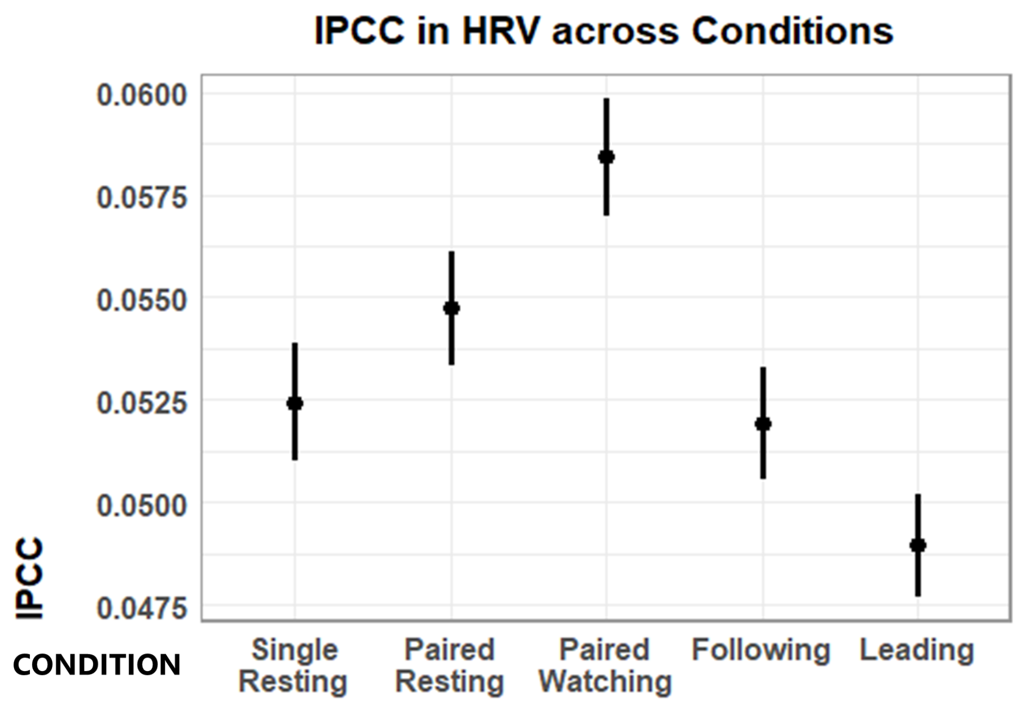

Figure S4: IPCC values for HRV signals across different experimental conditions (Single Resting, Paired Resting, Paired Watching, Following, Leading).
Dots represent the mean IPCC values, with error bars indicating the standard error (SE) of the mean.

Arousal Plot

Figure S5 illustrates the relationship between IPCC and Arousal, for EDA and HRV signals, across experimental conditions.

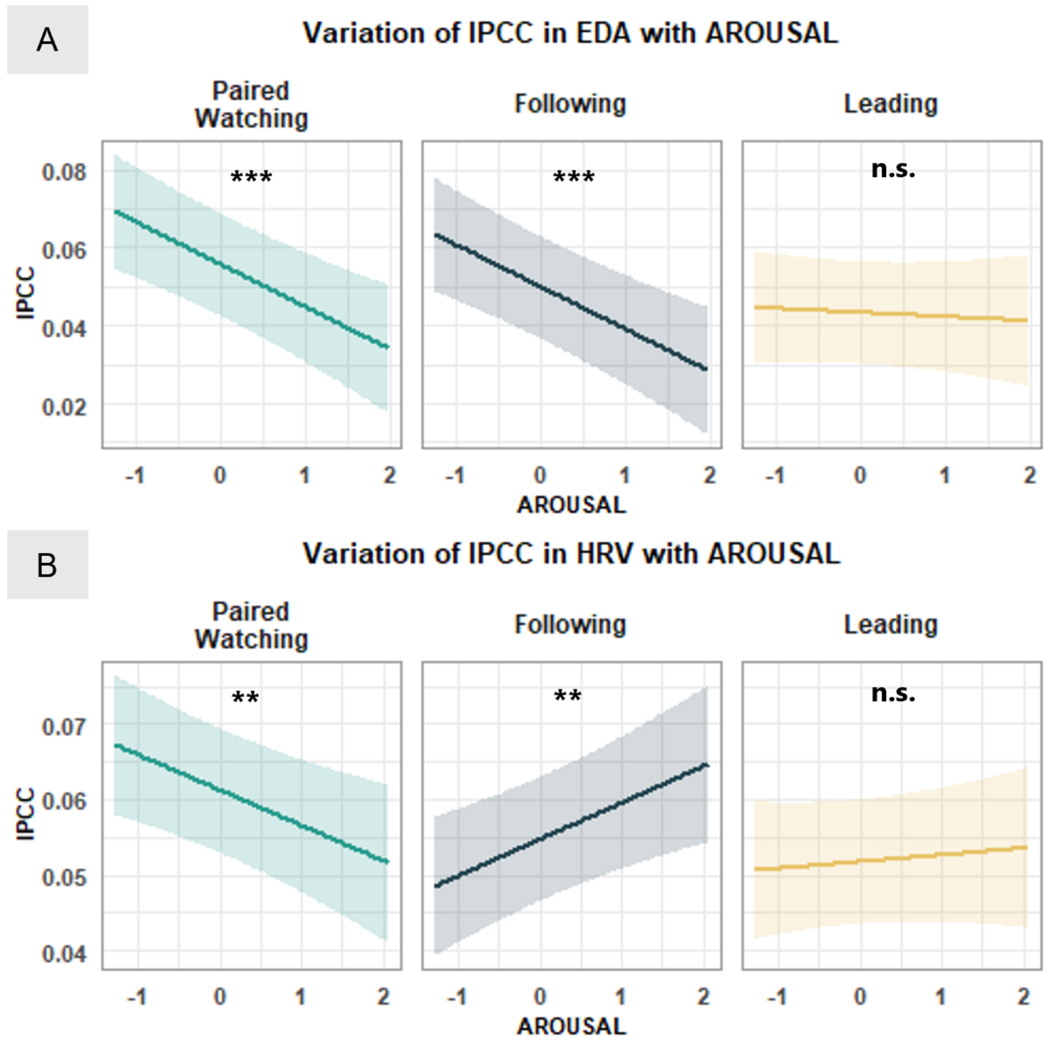

Figure S5: IPCC as a function of images' arousal. (A) IPCC obtained from EDA signals. (B) IPCC obtained from HRV signals. Results are shown for the three experimental conditions: Paired Watching, Following, and Leading. *Note:* Asterisks indicate statistical significance of the slopes: $***P < 0.001$, $**P < 0.01$, and n.s. for non-significant results.

HRV Genders Comparisons Plot

Figure S6 illustrates how IPCC for HRV signals varies across different gender combinations.

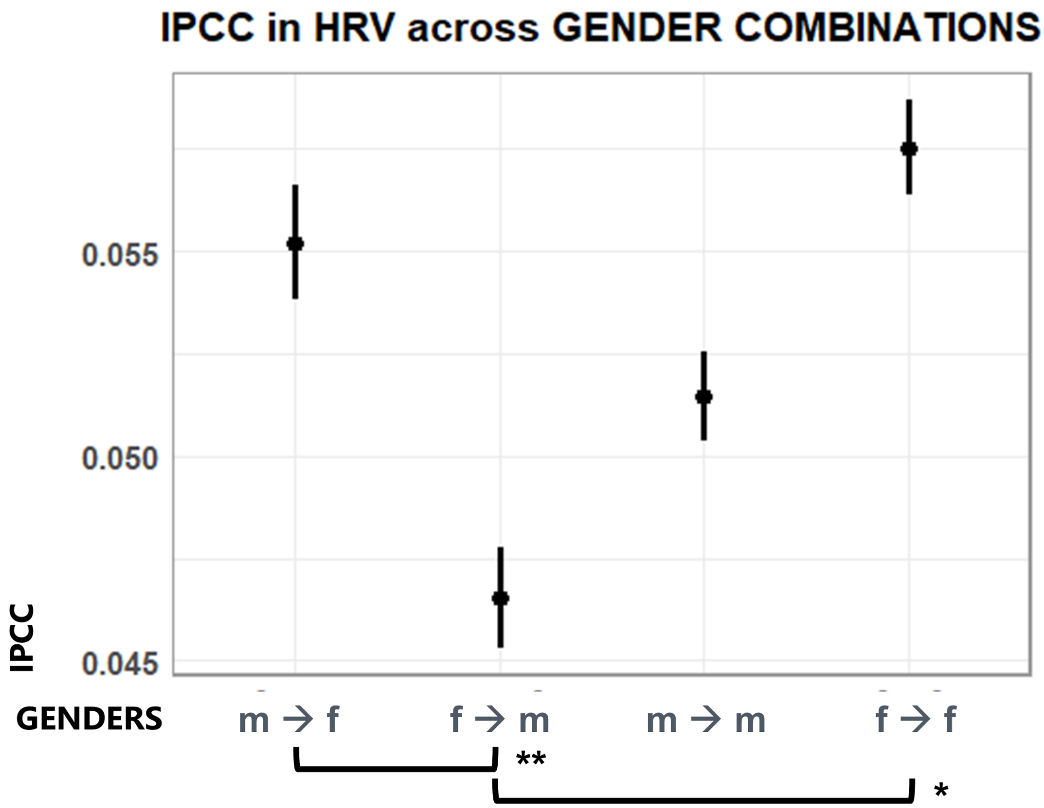

Figure S6: IPCC values for different gender combinations.
The y-axis represents the IPCC values, while the x-axis shows the specific gender pairs. The symbol → denotes the direction of influence (e.g., m → f indicates that the male Granger-causes the female). Dots represent the mean IPCC values, with error bars indicating the standard error (SE) of the mean.
Note: Asterisks denote the statistical significance of pairwise comparisons: (**) $p < 0.01$.

Supplementary Tables

EDA Statistical Analysis

LMER Model 1 Diagnostics

Table S1: Summary of fixed effects significance of EDA IPCC prediction in

Linear Mixed Model 1. Each predictor was tested using parametric bootstrapping. The table reports the T statistic[1] (Stat), the degrees of freedom (df), and the corresponding p-value[2].

Predictor	**Stat**	**df**	**p-value**
Condition	232.36	4	**0.0010**
Genders	3.16	3	0.4186
Frequency	57.87	1	**0.0010**

[1] $T = 2(\log(L_{\text{full}}) - \log(L_{\text{null}}))$ represents the Likelihood Ratio Test statistic.

[2] Bolded p-values indicate significant predictors ($p < 0.05$).

Post-hoc pairwise comparisons across conditions

Table S2: Post-hoc pairwise comparisons across conditions for the EDA IPCC prediction in

Model 1. The table displays the raw p-value (P_{raw}), the T statistic[1] (Stat), degrees of freedom (df), and the adjusted p-value[2] (P_{FDR}).

Comparison	$\mathbf{P_{raw}}$	**Stat**	**df**	$\mathbf{P_{FDR}}$
Single Resting vs Paired Resting	0.0010	39.90	1	**0.0014**
Single Resting vs Paired Watching	0.0010	192.00	1	**0.0014**
Single Resting vs Following	0.0010	139.00	1	**0.0014**
Single Resting vs Leading	0.0010	86.90	1	**0.0014**
Paired Resting vs Paired Watching	0.0010	57.80	1	**0.0014**
Paired Resting vs Following	0.0010	30.40	1	**0.0014**
Paired Resting vs Leading	0.0030	9.17	1	**0.0038**
Paired Watching vs Following	0.0300	4.43	1	**0.0300**
Paired Watching vs Leading	0.0010	21.10	1	**0.0014**
Following vs Leading	0.0090	6.19	1	**0.0100**

[1] $T = 2(\log(L_{\text{full}}) - \log(L_{\text{null}}))$ represents the Likelihood Ratio Test statistic.

[2] Bolded p-values indicate significant comparisons after FDR correction ($p < 0.05$).

LMER Model 2 Diagnostics

Table S3: Summary of Linear Mixed Model 2 fixed effects significance of EDA IPCC prediction in Linear Mixed Model 2. The table reports the T statistic[1] (Stat), the degrees of freedom (df) and the corresponding p-value[2].

Predictor	**Stat**	**df**	**p-value**
Arousal × Condition	10.77	2	**0.0040**
Valence × Condition	4.52	2	0.1019
Arousal	49.56	5	**0.0010**
Valence	25.96	5	**0.0010**
Genders	0.96	3	0.8282
Frequency	29.82	1	**0.0010**

[1] $T = 2(\log(L_{\text{full}}) - \log(L_{\text{null}}))$ represents the Likelihood Ratio Test statistic.

[2] Bolded p-values indicate significant predictors ($p < 0.05$).

Arousal x Condition Post-hoc Analysis

Table S4: Post-hoc analysis of Arousal trends across experimental conditions for EDA signals (Model 2). The table reports the estimated slopes (Trend), the T statistic[1] (Stat), the degrees of freedom (df) and the corresponding p-value[2].

Condition	**Trend**	**Stat**	**df**	**p-value**
Paired Watching	-0.011	17.12	1	**0.0010**
Following	-0.011	17.95	1	**0.0010**
Leading	-0.001	0.16	1	0.6953

[1] $T = 2(\log(L_{\text{full}}) - \log(L_{\text{null}}))$ represents the Likelihood Ratio Test statistic.

[2] Bolded p-values indicate slopes significantly different from zero ($p < 0.05$).

HRV Statistical Analysis

LMER model 1 Diagnostics

Table S5: Summary of Linear Mixed Model 1 predicting HRV IPCC. Each predictor was tested using parametric bootstrapping. The table reports the T statistic[1] (Stat), the degrees of freedom (df), and the corresponding p-value[2].

Predictor	Stat	df	p-value
Condition	27.38	4	**0.0010**
Genders	21.19	3	**0.0010**
Frequency	162.99	1	**0.0010**

[1] $T = 2(\log(L_{\text{full}}) - \log(L_{\text{null}}))$ represents the Likelihood Ratio Test statistic.
[2] Bolded p-values indicate significant predictors ($p < 0.05$).

Post-hoc pairwise comparisons across conditions

Table S6: Post-hoc pairwise comparisons across conditions for the HRV IPCC Model 1. The table displays the raw p-value (P_{raw}), the T statistic[1] (Stat), degrees of freedom (df), and the adjusted p-value[2] (P_{FDR}).

Comparison	$\mathbf{P_{raw}}$	Stat	df	$\mathbf{P_{FDR}}$
Single Resting vs Paired Resting	0.2408	1.45	1	0.2675
Single Resting vs Paired Watching	0.0010	9.84	1	**0.0033**
Single Resting vs Following	0.7982	0.08	1	0.7982
Single Resting vs Leading	0.0529	3.35	1	0.0882
Paired Resting vs Paired Watching	0.0410	3.74	1	0.0819
Paired Resting vs Following	0.1369	2.18	1	0.1711
Paired Resting vs Leading	0.0040	9.19	1	**0.0100**
Paired Watching vs Following	0.0010	11.64	1	**0.0033**
Paired Watching vs Leading	0.0010	24.63	1	**0.0033**
Following vs Leading	0.1199	2.42	1	0.1711

[1] $T = 2(\log(L_{\text{full}}) - \log(L_{\text{null}}))$ represents the Likelihood Ratio Test statistic.
[2] Bolded p-values indicate significant comparisons ($p < 0.05$).

Post-hoc pairwise comparisons across genders

Table S7: Post-hoc pairwise comparisons across genders for the HRV IPCC prediction in Model 1. The table displays the raw *p*-value (P_{raw}), the T statistic[1] (Stat), degrees of freedom (df), and the adjusted *p*-value[2] (P_{FDR}).

Comparison	$\mathbf{P_{raw}}$	Stat	df	$\mathbf{P_{FDR}}$
f → m vs m → f	0.0010	17.16	1	**0.0060**
f → m vs m → m	0.3716	1.03	1	0.4460
f → m vs f → f	0.5584	0.40	1	0.5584
m → f vs m → m	0.2147	1.74	1	0.3222
m → f vs f → f	0.0130	7.77	1	**0.0390**
m → m vs f → f	0.1109	2.81	1	0.2218

[1] $T = 2(\log(L_{\text{full}}) - \log(L_{\text{null}}))$ represents the Likelihood Ratio Test statistic.

[2] Bolded *p*-values indicate significant comparisons after FDR correction ($p < 0.05$).

LMER model 2 Diagnostics

Table S8: Summary of Linear Mixed Model 2 predicting HRV IPCC based on arousal, valence, experimental condition, genders, and frequency bin. Each predictor was tested using parametric bootstrapping. The table reports the T statistic[1] (Stat), the degrees of freedom (df), and the corresponding *p*-value[2].

Predictor	Stat	df	*p*-value
Arousal × Condition	19.17	1	**0.0020**
Valence × Condition	1.87	1	0.3866
Arousal	45.90	3	**0.0010**
Valence	31.59	3	**0.0010**
Genders	11.06	3	**0.0210**
Frequency	65.50	1	**0.0010**

[1] $T = 2(\log(L_{\text{full}}) - \log(L_{\text{null}}))$ represents the Likelihood Ratio Test statistic.

[2] Bolded *p*-values indicate significant predictors ($p < 0.05$).

Arousal x Condition Post-hoc Analysis

Table S9: Post-hoc analysis of Arousal trends across experimental conditions for HRV signals (Model 2). The table reports the estimated slopes (Trend), the T statistic[1] (Stat), the degrees of freedom (df) and the corresponding *p*-value[2].

Condition	Trend	Stat	df	*p*-value
Paired Watching	-0.005	8.28	1	**0.0030**
Following	0.005	8.92	1	**0.0020**
Leading	0.001	0.29	1	0.5884

[1] $T = 2(\log(L_{\text{full}}) - \log(L_{\text{null}}))$ represents the Likelihood Ratio Test statistic.

[2] Bolded *p*-values indicate slopes significantly different from zero ($p < 0.05$).