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Supplemental information

Interpersonal synchronization of movement intermittency

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Supplemental Information (SI)

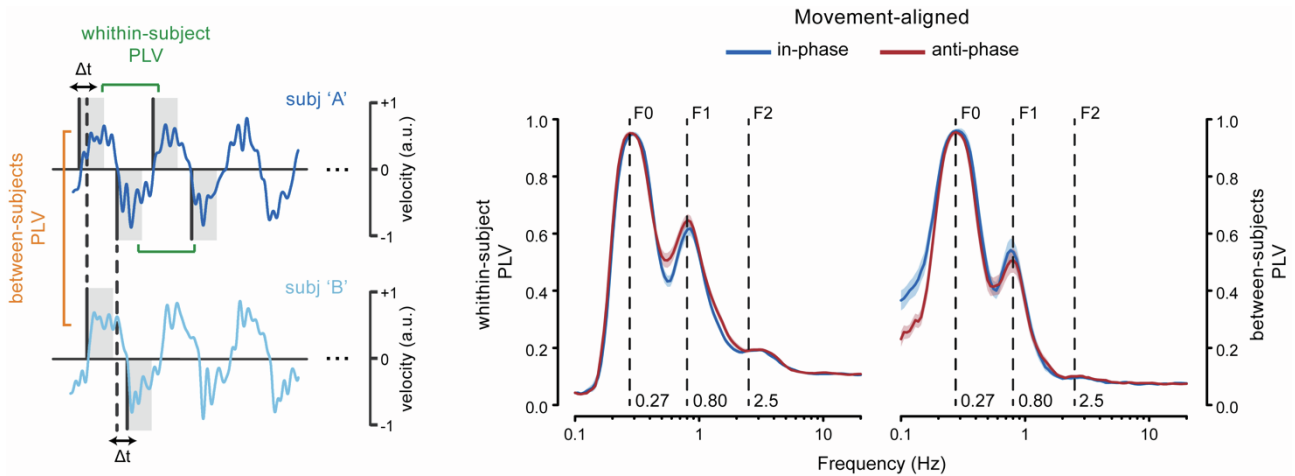


Figure S1. Movement-locked control analyses: submovement-level interpersonal synchronization is not explained by phase-locking of submovements to movement onset, related to Figure 3. The left panel shows example traces of two partners' finger velocity during in-phase synchronization ('Real partner') and a schematic of the data segmentation and analyses. Data are segmented in 2-s segments (corresponding to the instructed movement duration) locked to the onset of single movements performed by each partner. The phase-locking value (PLV) is computed either within-subject ($n = 60$) – i.e., across the movements performed by the same participant (separately for flexions and extensions and then averaged across movement types) – or between-subjects ($n = 30$) – i.e., between the two partners' movements. The right panels show the within-subject and between-subjects PLV spectra for both the in-phase and anti-phase conditions (mean \pm SEM).

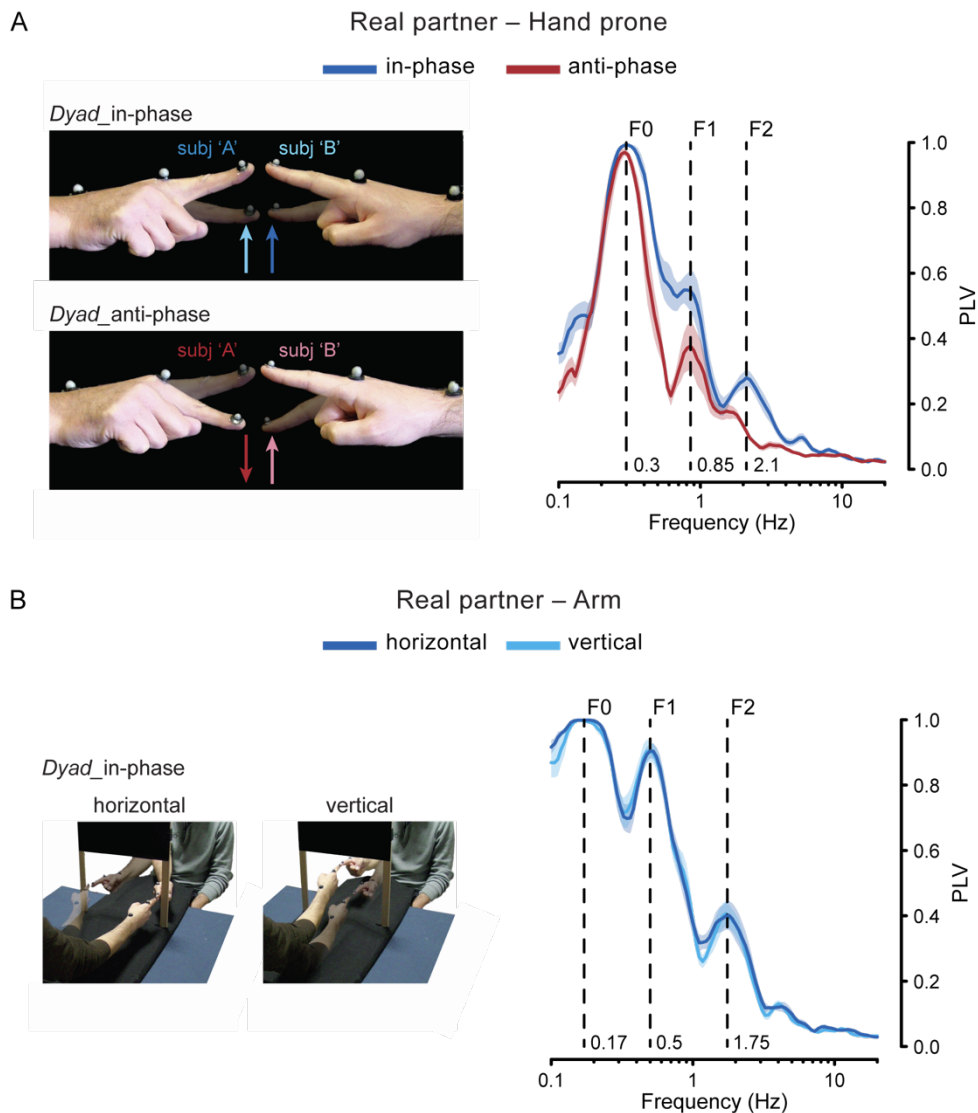


Figure S2. Secondary tasks: submovement-level interpersonal synchronization does not depend on movement congruency and generalizes to multi-joint actions, related to Figure 3. (A) left. Illustration of the ‘Real partner – Hand prone’ secondary task. Participants keep their right hand in a prone posture and move the index finger along the vertical axis. As opposed to the primary task (main Figure 1A, B), the two partners perform simultaneously the same type of movement (either flexion or extension) to attain in-phase coordination (i.e., move towards the same direction), whereas they perform different types of movements (as one performs flexion, the other performs extension and vice versa) to attain anti-phase coordination (i.e., move towards opposite directions). **right.** between-subjects PLV spectra for the in-phase and anti-phase condition ($n = 10$; mean \pm SEM). **(B) left.** Illustration of the ‘Real partner – Arm’ secondary task. Participants perform whole-arm movements (primarily around the elbow joint) along either the horizontal or vertical inner dimensions of the window ($\sim 40 \times 40$ cm) delimited by an interposed panel. The task involves tracking of each other’s movement to keep the respective fingertips spatially aligned (dyad-in-phase only). Given the larger movement amplitude compared to the primary task, the instructed movement rate is reduced to 10 bpm (i.e., ~ 0.17 Hz). **right.** between-subjects PLV spectra for the horizontal and vertical condition ($n = 10$; mean \pm SEM).

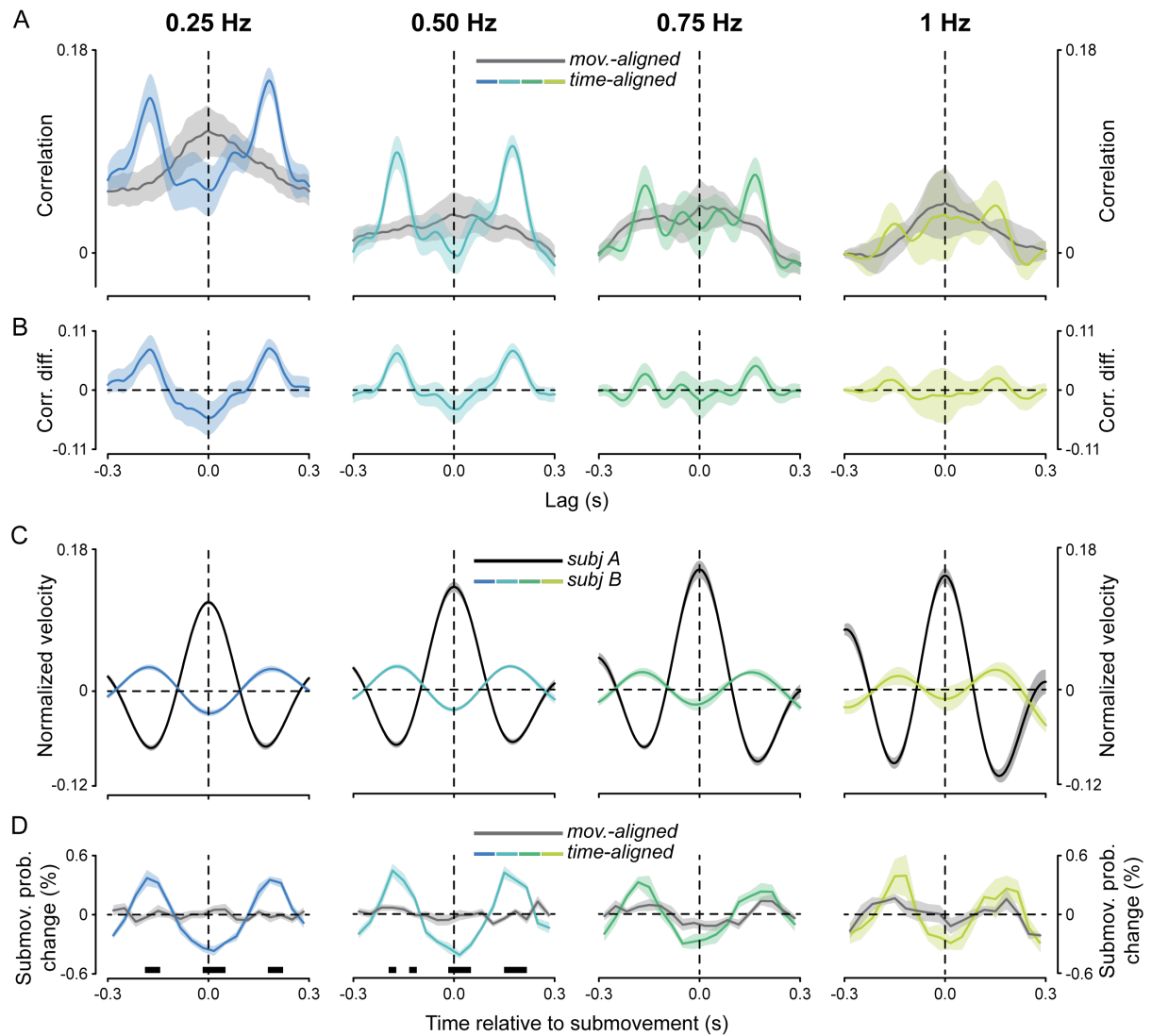


Figure S3. Control experiment: speed-dependency of submovement-level interpersonal synchronization, related to Figure 4. (A) Cross-correlation (same as in Figure 4A,B but for a restricted lag range to accommodate the shorter movement durations) computed between the finger velocities of two partners performing the 'Real partner' task at multiple movement paces (i.e., 0.25, 0.5, 0.75 Hz [$n=10$] and 1 Hz [$n=5$]). The cross-correlation is computed between velocity data segments (of length equal to average movement duration) that are either movement-aligned, i.e., aligned to each partner's movement onset, or time-aligned, i.e., aligned to one of the two partners (subject 'A' by convention) movement onset, thus preserving their real time alignment (mean \pm SEM; see Methods). (B) Difference between the time- and movement-aligned cross-correlation profiles (mean \pm SEM). (C) Velocity for both partners – subjects 'A' and 'B' – locked to submovements generated by one partner in the couple – i.e., subject 'A' by convention (same as in Figure 4E; mean \pm SEM). (D) Submovement probability (expressed as deviation from mean probability) for subject 'B' as a function of the actual time (time-aligned) or of time relative to movement onset (movement-aligned) from submovements generated by subject 'A' (same as shown in Figure 4F). The black horizontal bars indicate the time points that survive two-tailed t-test statistics on movement- vs. time-aligned data (Bonferroni-corrected for multiple comparisons across time).