Quantifying prevalence and risk factors of HIV multiple infection in Uganda from population-based deep-sequence data

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**MCMC trace plots for parameters in base model fit to simulated data with partial sequencing success and no false positive or false negative multiple subgraph windows.** Independent chains are shown in shades of grey. Warm-up iterations are excluded. MI = multiple infection. VL = viral load (log10 copies/mL) standardized to mean = 0 and std. dev = 1. Std. dev. = standard deviation.



**MCMC pairs plots for parameters in base model fit to simulated data with partial sequencing success and no false positive or false negative multiple subgraph windows.** Independent chains are shown in shades of grey. Warm-up iterations are excluded. Includes a sample of 250 iterations per chain. MI = multiple infection.



**Comparison of posterior and prior distributions of parameters in base model fit to simulated data with partial sequencing success and no false positive or false negative multiple subgraph windows.** Median is plotted as the central estimate and horizontal bars extend to the 95% and 50% HPD. Some horizontal bars do not extend beyond the central point. Warm-up iterations are excluded. MI = multiple infection. VL = viral load (log10 copies/mL) standardized to mean = 0 and std. dev = 1. Std. dev. = standard deviation.



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**MCMC trace plots for parameters in full model fit to simulated data with partial sequencing success and false positive and false negative multiple subgraph windows.** Independent chains are shown in shades of grey. Warm-up iterations are excluded.MI = multiple infection. VL = viral load (log10 copies/mL) standardized to mean = 0 and std. dev = 1. Std. dev. = standard deviation.



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**MCMC trace plots for parameters in extended model fit to simulated data with partial sequencing success, false positive and false negative multiple subgraph windows, and a binary risk factor for harboring multiple infection.** Independent chains are shown in shades of grey. Warm-up iterations are excluded. MI = multiple infection. VL = viral load (log10 copies/mL) standardized to mean = 0 and std. dev = 1. Std. dev. = standard deviation.



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**MCMC trace plots for parameters in full model fit to deep sequence data generated from ,029 Rakai Community Cohort Study participants living with viremic HIV.** Independent chains are shown in shades of grey. Warm-up iterations are excluded. MI = multiple infection. VL = viral load (log10 copies/mL) standardized to mean = 0 and std. dev = 1. Std. dev. = standard deviation.



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**MCMC trace plots for parameters in extended model with community type and lifetime sex partners as a risk factor for harboring multiple infections fit to deep sequence data generated from men living with viremic HIV who participated in the Rakai Community Cohort Study.** Independent chains are shown in shades of grey. Warm-up iterations are excluded. MI = multiple infection. VL = viral load (log10 copies/mL) standardized to mean = 0 and std. dev = 1. Std. dev. = standard deviation.



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**MCMC trace plots for parameters in extended model with variable selection to identify risk factor for harboring multiple infections fit to deep sequence data generated from ,970 Rakai Community Cohort Study participants living with viremic HIV.** Independent chains are shown in shades of grey. Warm-up iterations are excluded. MI = multiple infection. VL = viral load (log10 copies/mL) standardized to mean = 0 and std. dev = 1. Std. dev. = standard deviation.



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