

# Inference of transmission network structure from HIV phylogenetic trees

Federica Giardina<sup>1,2\*</sup>, Ethan Obie Romero-Severson<sup>2</sup>, Jan Albert<sup>3,4</sup>, Tom Britton<sup>1</sup>, Thomas Leitner<sup>2</sup>

**1 Department of Mathematics, Stockholm University, Stockholm, Sweden**

**2 Theoretical Biology and Biophysics Group, Los Alamos National Laboratory, Los Alamos, NM**

**3 Department of Microbiology, Tumor and Cell Biology, Karolinska Institute, Stockholm, Sweden**

**4 Department of Clinical Microbiology, Karolinska University Hospital, Stockholm, Sweden**

\* E-mail: federica@math.su.se

## Supplementary information

**S1 Tab. Effect of increased rewiring probability ( $\rho$ ) on network identification.**

$\rho = 0.01$	WS	ER	BA
WS	0.99	0.01	0.00
ER	0.03	0.76	0.21
BA	0.01	0.21	0.78
$\rho = 0.1$	WS	ER	BA
WS	0.95	0.05	0.00
ER	0.11	0.70	0.19
BA	0.01	0.19	0.80
$\rho = 0.25$	WS	ER	BA
WS	0.75	0.16	0.09
ER	0.16	0.63	0.21
BA	0.06	0.15	0.79
$\rho = 0.5$	WS	ER	BA
WS	0.65	0.17	0.18
ER	0.19	0.57	0.24
BA	0.10	0.21	0.69