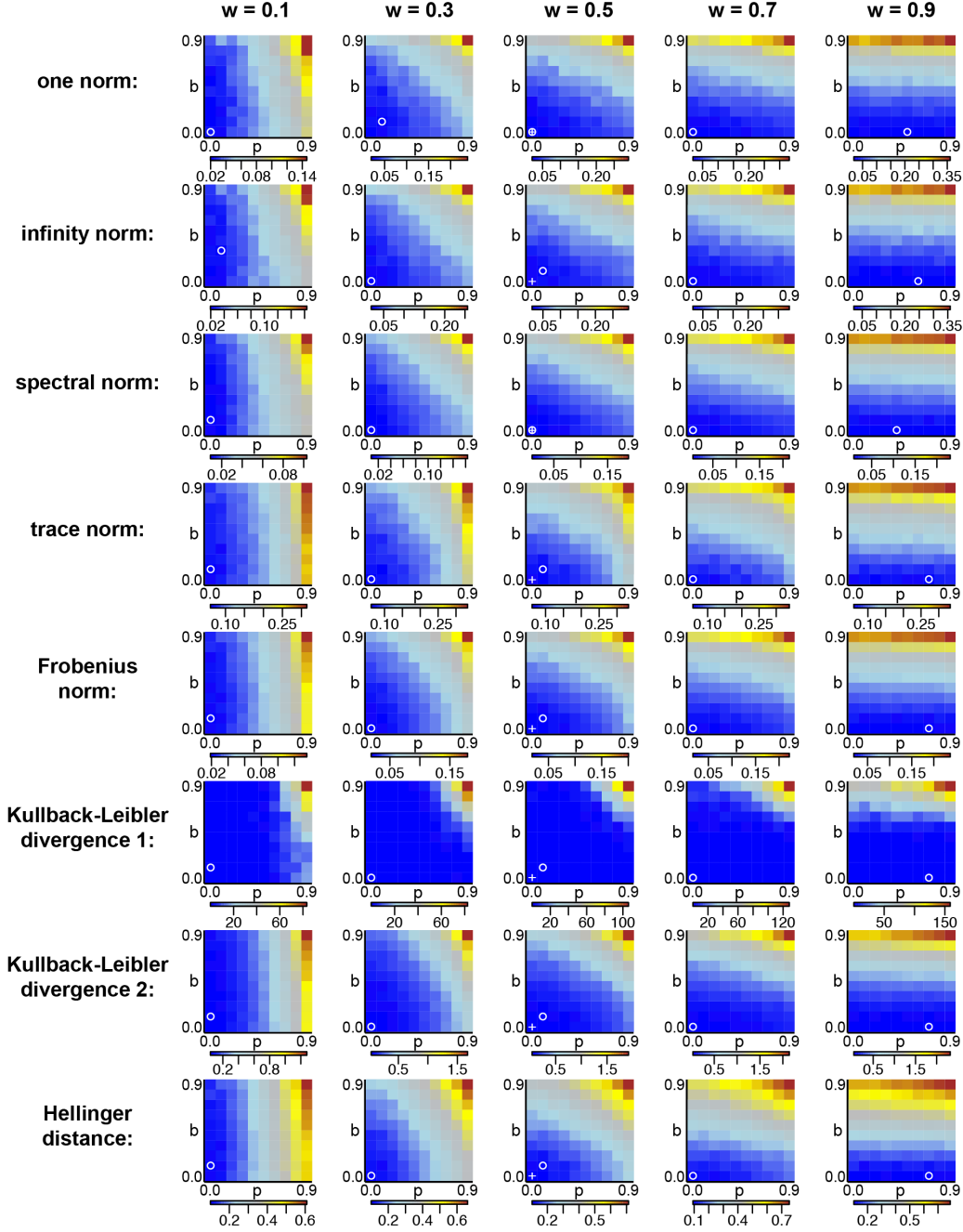


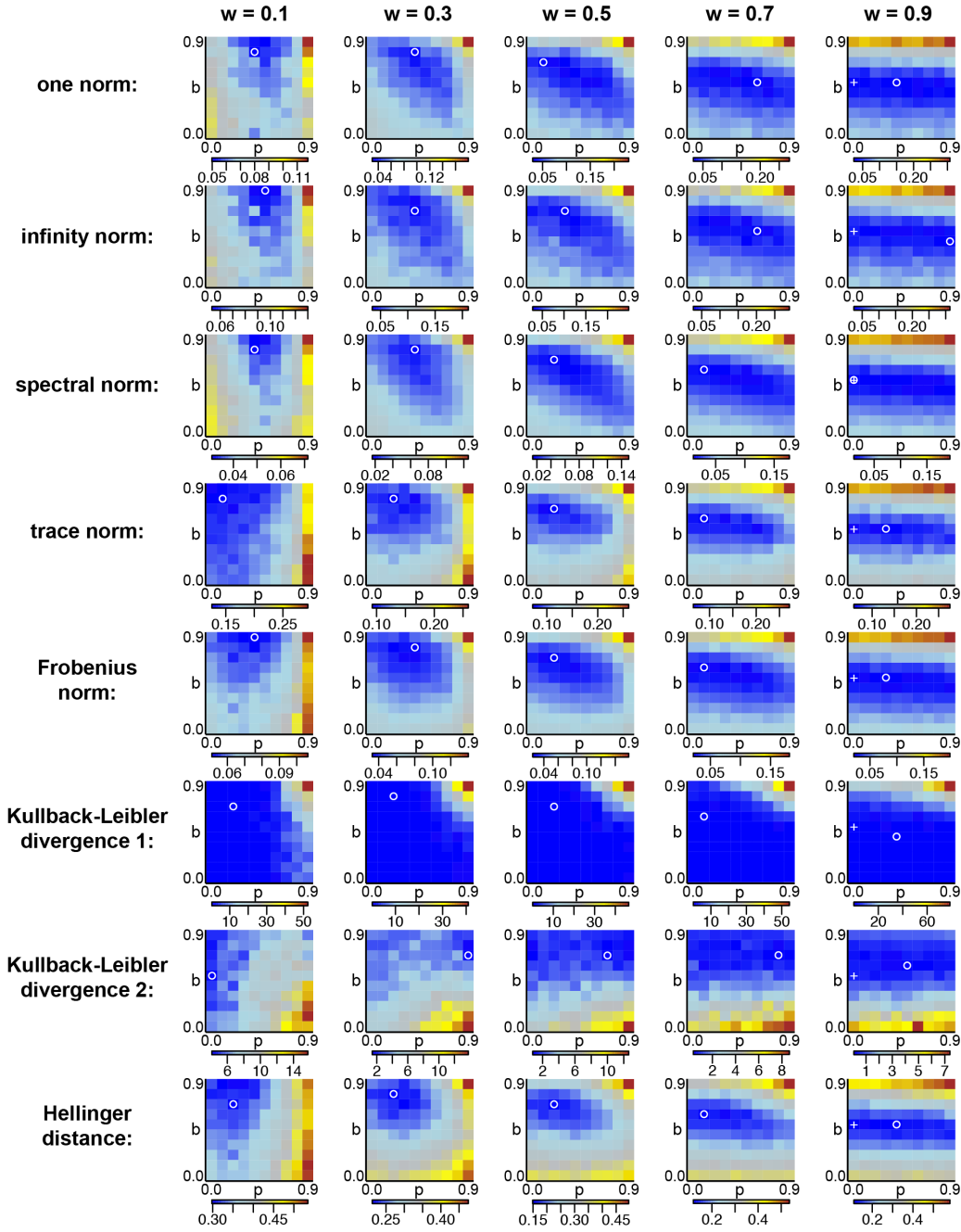
Supplementary Information: Inference of random walk models to describe leukocyte migration.

May 14, 2015

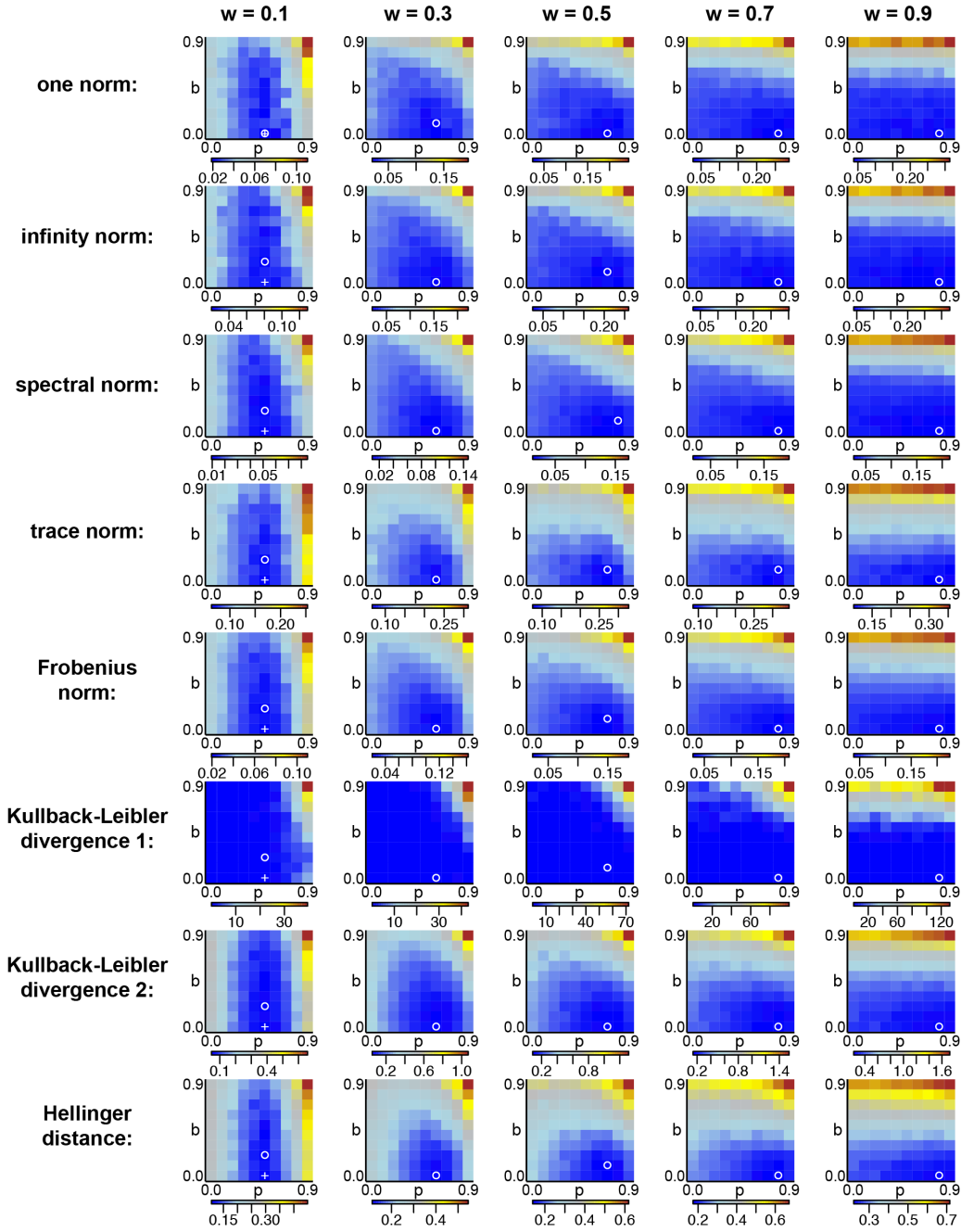
1 Supplementary Figures



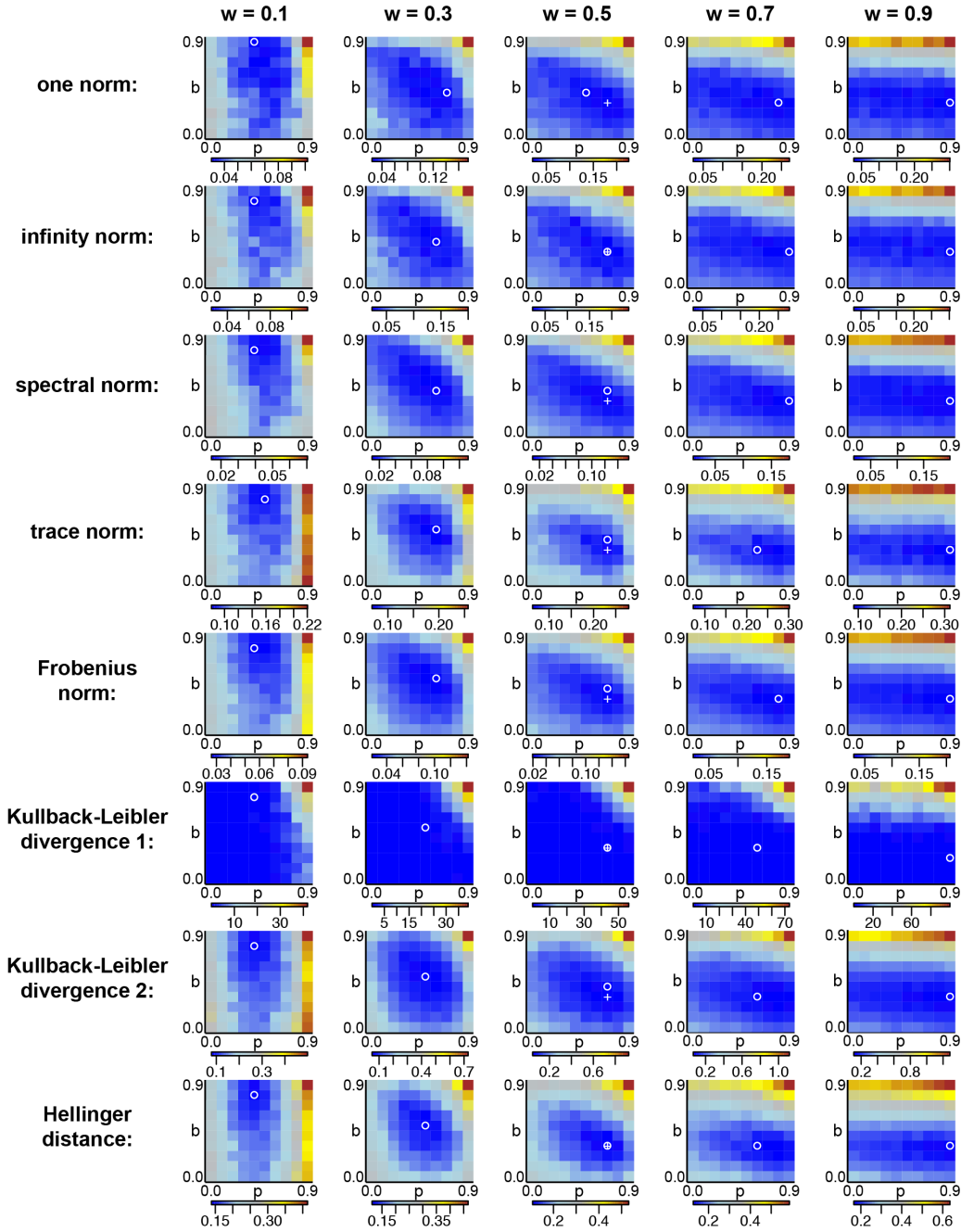
Supplementary Figure 1: **Heat atlases for Brownian motion (BM)**. 100 query transition matrices (TMs) were computed with various levels of b and p ranging from 0 to 0.9 in 0.1 increments, and 5 values of w . Each individual heat map is generated by calculating the distance from/to the query TMs with a certain value of w to/from the BM TM. The columns each use a different value of w in the query TMs (0.1 to 0.9 in 0.2 increments), and each row uses a different distance function to compute the distances. Persistence (p) increases along the x -axis of each graph while bias (b) increases along the y -axes.



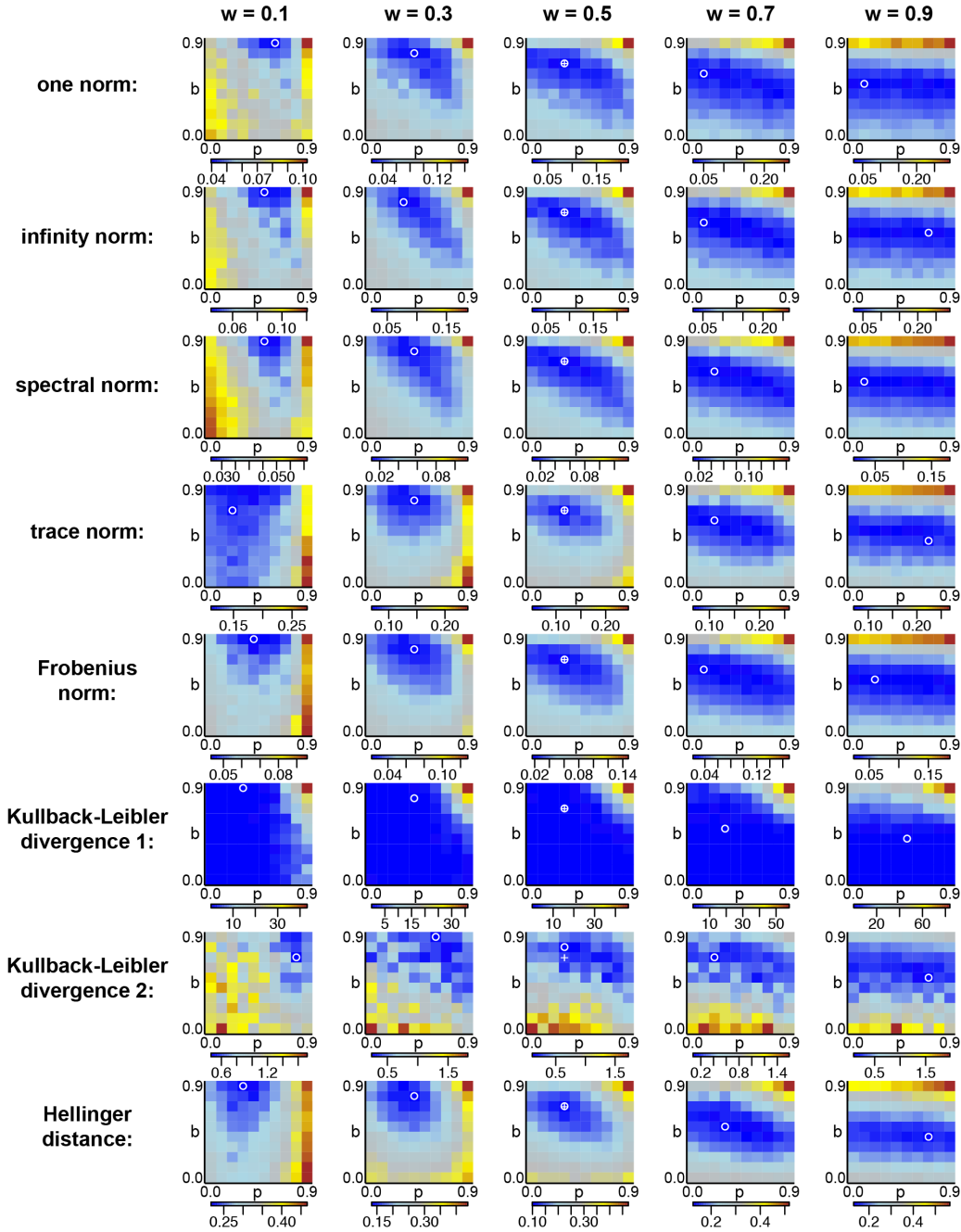
Supplementary Figure 2: **Heat atlases for Persistent Random Walk (PRW)**. 100 query transition matrices (TMs) were computed with various levels of b and p ranging from 0 to 0.9 in 0.1 increments, and 5 values of w . Each individual heat map is generated by calculating the distance from/to the query TMs with a certain value of w to/from PRW TM. The columns each use a different value of w in the query TMs (0.1 to 0.9 in 0.2 increments), and each row uses a different distance function to compute the distances. Persistence (p) increases along the x -axis of each graph while bias (b) increases along the y -axes.



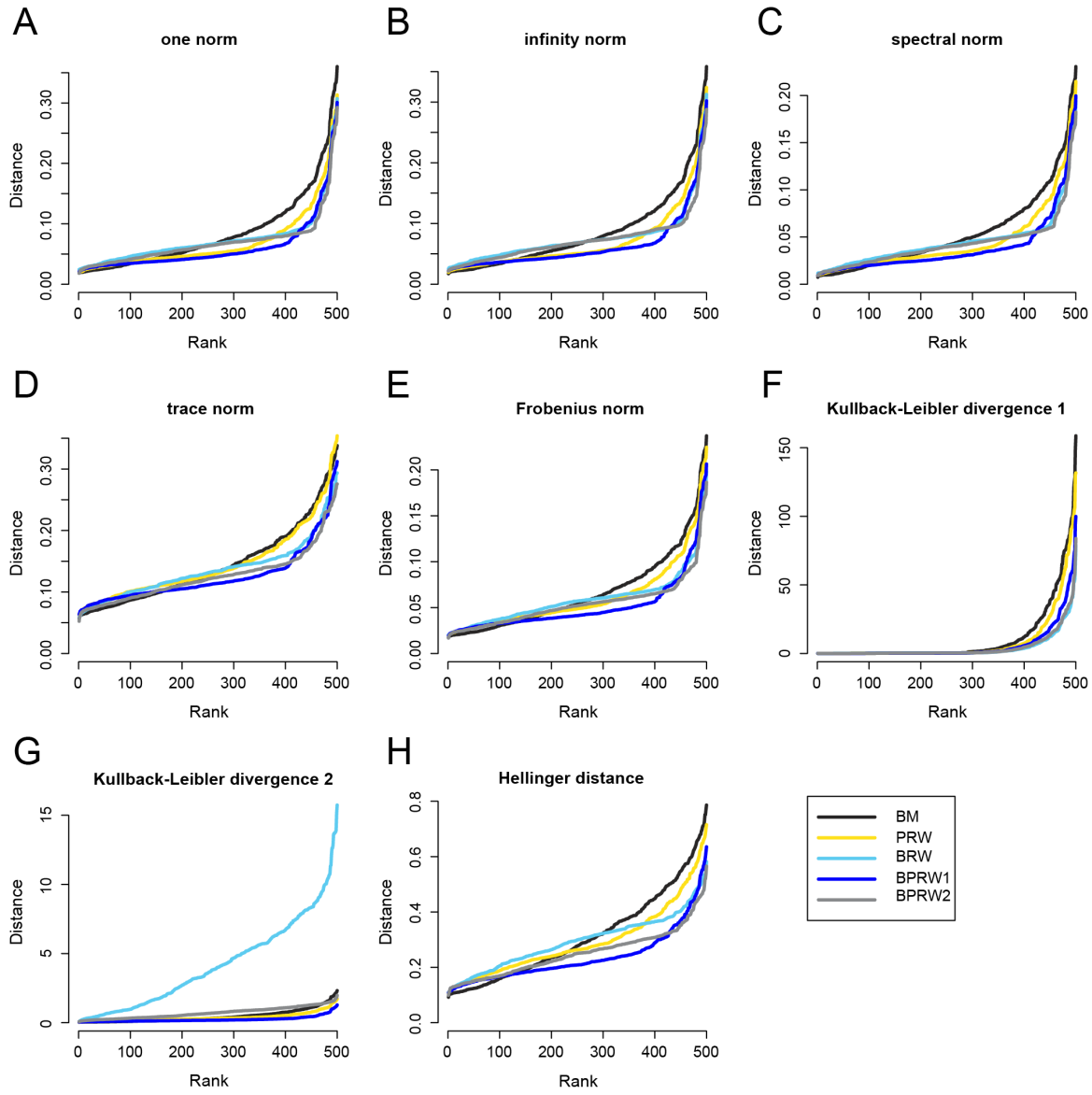
Supplementary Figure 3: **Heat atlases for Biased Random Walk (BRW).** 100 query transition matrices (TMs) were computed with various levels of b and p ranging from 0 to 0.9 in 0.1 increments, and 5 values of w . Each individual heat map is generated by calculating the distance from/to the query TMs with a certain value of w to/from BRW TM. The columns each use a different value of w in the query TMs (0.1 to 0.9 in 0.2 increments), and each row uses a different distance function to compute the distances. Persistence (p) increases along the x -axis of each graph while bias (b) increases along the y -axes.



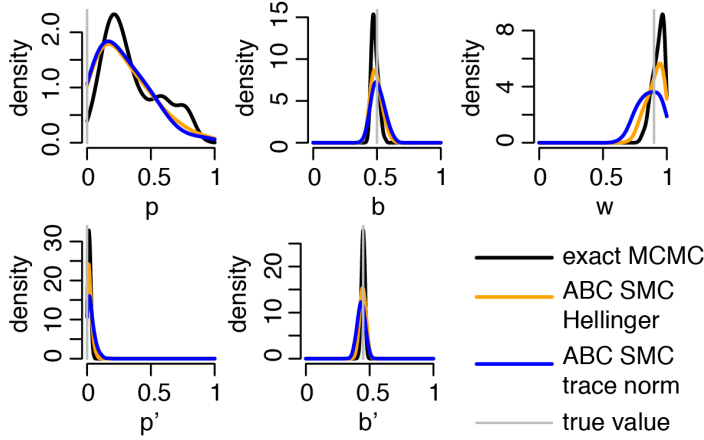
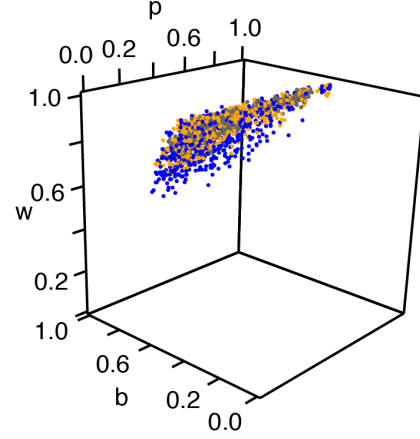
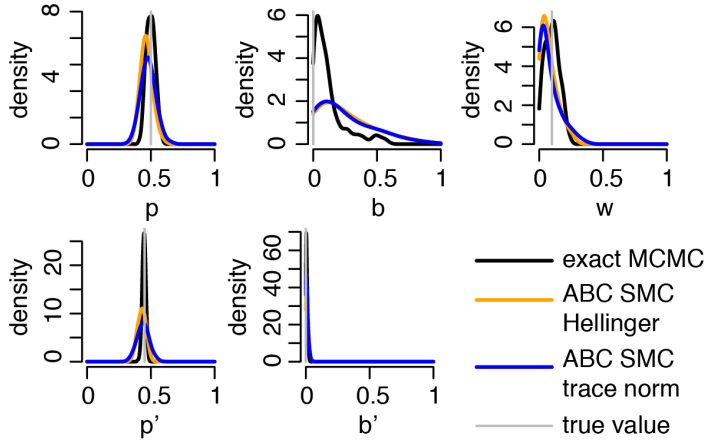
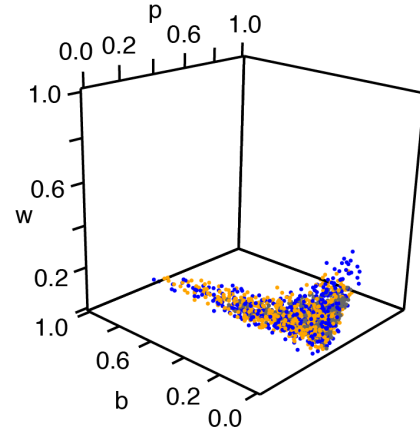
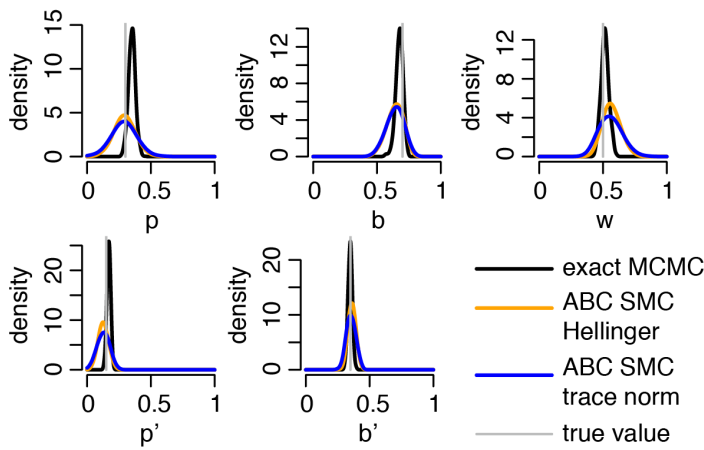
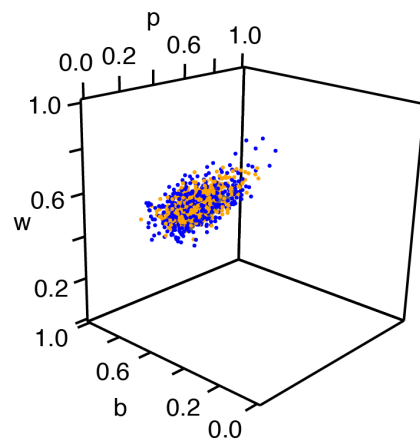
Supplementary Figure 4: **Heat atlases for Biased Persistent Random Walk (BPRW) example 1.** 100 query transition matrices (TMs) were computed with various levels of b and p ranging from 0 to 0.9 in 0.1 increments, and 5 values of w . Each individual heat map is generated by calculating the distance from/to the query TMs with a certain value of w to/from BPRW TM. The columns each use a different value of w in the query TMs (0.1 to 0.9 in 0.2 increments), and each row uses a different distance function to compute the distances. Persistence (p) increases along the x -axis of each graph while bias (b) increases along the y -axes.



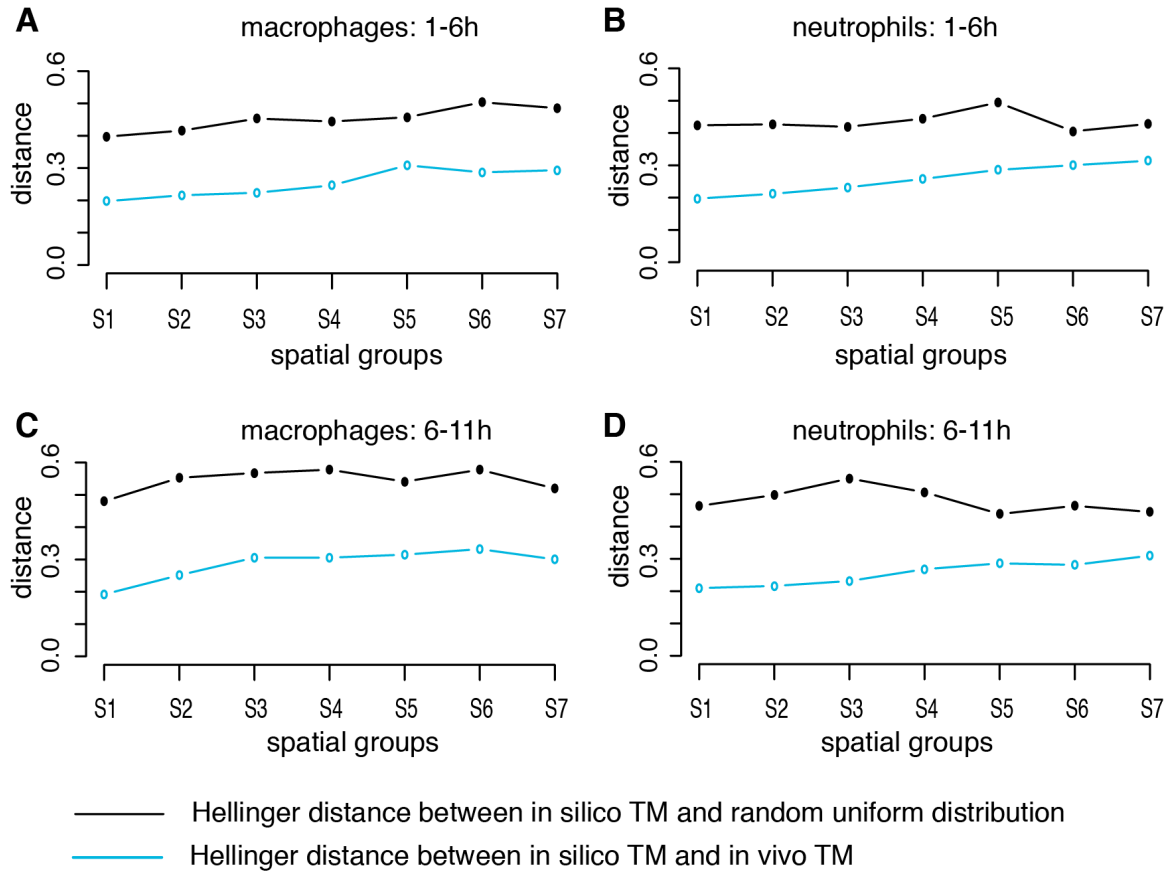
Supplementary Figure 5: **Heat atlases for Biased Persistent Random Walk (BPRW) example 2.** 100 query transition matrices (TMs) were computed with various levels of b and p ranging from 0 to 0.9 in 0.1 increments, and 5 values of w . Each individual heat map is generated by calculating the distance from/to the query TMs with a certain value of w to/from BPRW TM. The columns each use a different value of w in the query TMs (0.1 to 0.9 in 0.2 increments), and each row uses a different distance function to compute the distances. Persistence (p) increases along the x -axis of each graph while bias (b) increases along the y -axis.



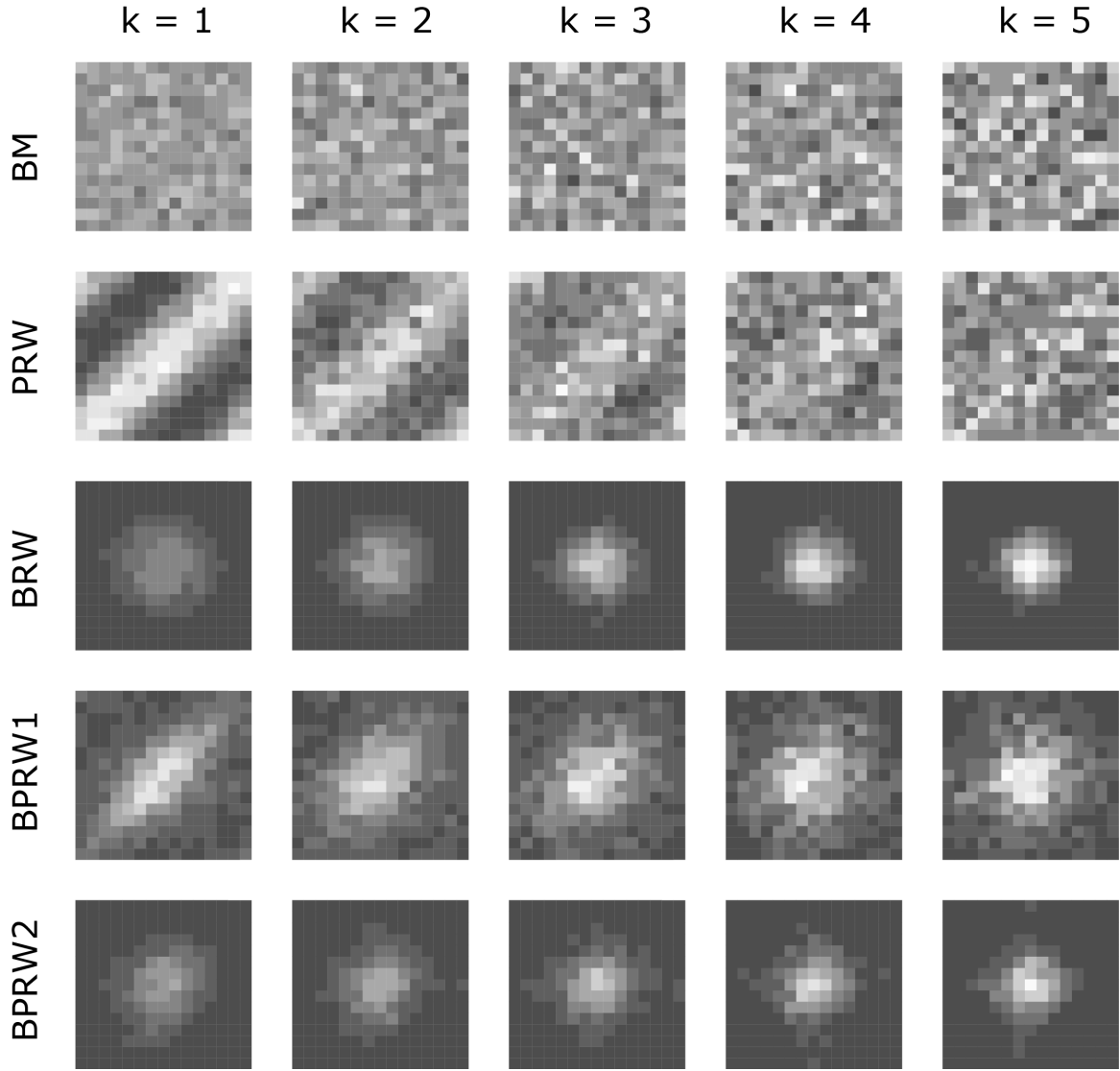
Supplementary Figure 6: **Rank plots.** 500 transition matrices (TMs) were generated from simulations with various values of w , p and b that spanned the parameter space. The distances from these 500 TMs to each of the 5 reference TMs given in Table ?? were calculated, and plotted in ascending order. Shown here are the results using a) the one norm, b) the infinity norm, c) the spectral norm, d) the trace norm, e) the Frobenius norm, f) Kullback-Leibler divergence 1, g) Kullback-Leibler divergence 2, and h) the Hellinger distance as the distance function.

A Biased random walk with $(p, b, w) = (0.0, 0.5, 0.9)$ **B****C Persistent random walk with $(p, b, w) = (0.5, 0.0, 0.1)$** **D****E Biased-persistent random walk with $(p, b, w) = (0.3, 0.7, 0.5)$** **F**

Supplementary Figure 7: **Inference results.** Results of parameter inference using ABC-SMC, with the Hellinger distance (orange) and trace norm (blue) as distance functions, performed on simulated data using the BRW (A-B), PRW (C-D) and BPRW2 (E-F) as reference TMs, respectively. Shown are the posterior parameter distributions as marginals for p , b and w and the marginal rescaled parameters p' and b' (A, C and E). The exact posterior distributions (using MCMC) are shown in black; the true values used for the simulation of the referenceTM are indicated by a red line. The 3D scatter plots of p , b and w are shown in B, D and F.



Supplementary Figure 8: **Distances between *in vivo* and *in silico* TMs.** Displayed are the Hellinger distances between the inferred in silico TMs and TMs extracted from *in vivo* data for macrophages (A and C) and neutrophils (B and D), respectively. As comparison we also display the Hellinger distance between the *in silico* TMs and a random uniform distribution.



Supplementary Figure 9: **Sampling effects on TMs.** To investigate the effect of low temporal resolution in observed data on the TMs we simulate trajectories for the 5 example models discussed (BM, PRW, BRW, BPRW1 and BPRW2), consider every k -th step as observed and compute the resulting TMs. We chose $k = 1$ (no sampling) till $k = 5$ (every 5th step is observed).