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Supporting Material

Inferring Diffusion Dynamics from FCS in Heterogeneous Nuclear Environments

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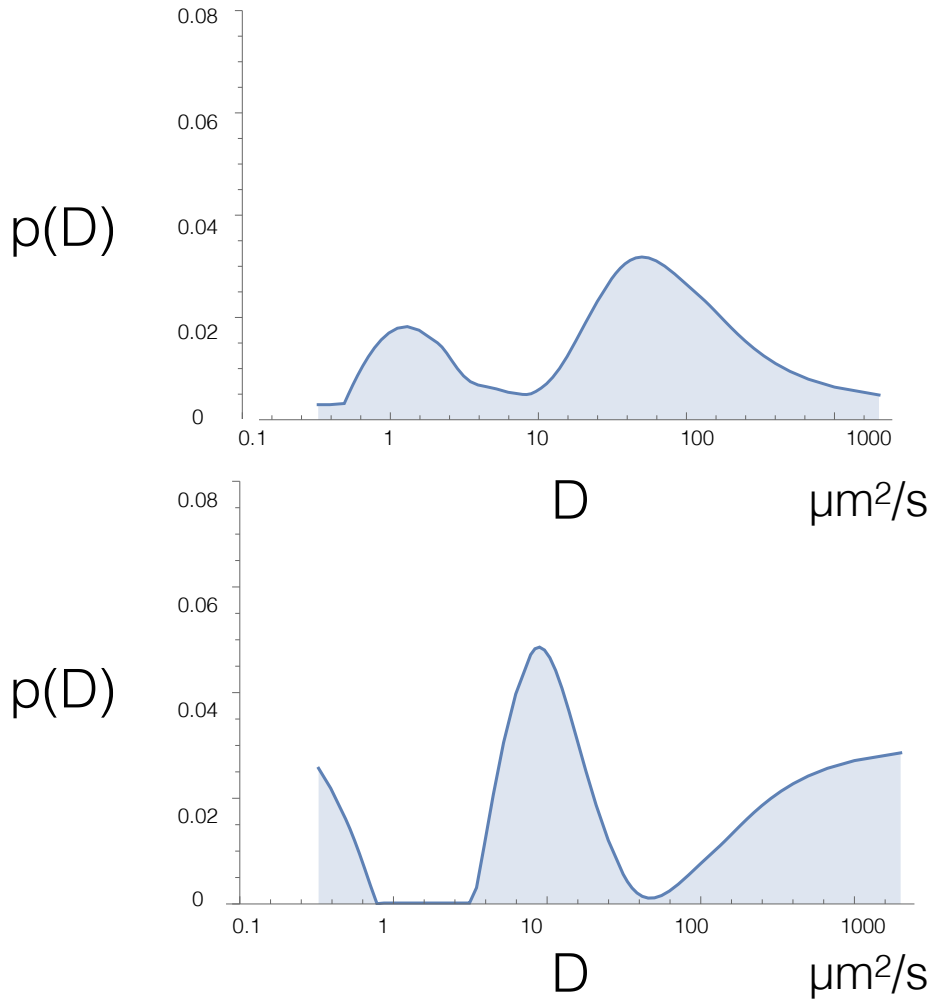

Figure 1: **Red fluorescent proteins (RFPs) diffusing in the nucleus without the BZip tag**. The $p(D)$'s for mCherry (top) and mRuby2 (bottom) diffusing in the nucleus without an attached BZip domain. These represent generic interactions such as molecular crowding, and look similar to the profiles of BZip in the cytosol, where, as with the RFPs without the BZip tag, there are no anticipated specific binding events. When processing data, these interactions can be subtracted from a p(D) of RFP-tagged transcription factors to help isolate the effect of specific binding sites.

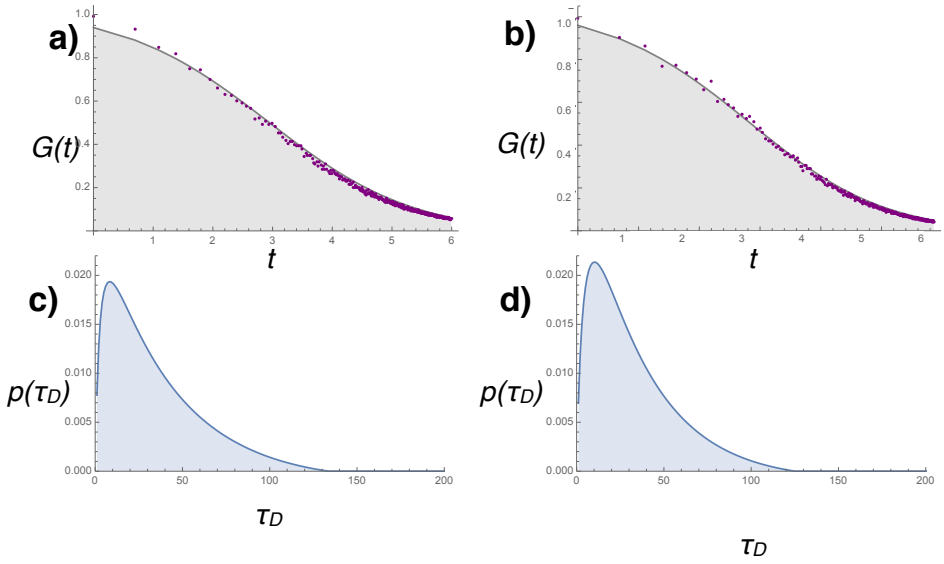

Figure 2: **More examples of theoretical $G(t)$'s that can be fit by anomalous exponents from which we extract distributions of diffusion times ($p(\tau_D)$).** $G(t)$ constructed using main text Eq. (3) with $\alpha = 0.7$ and $\alpha = 0.8$ plus 5% noise (respectively a and b, purple dots). A distribution of diffusion times $p(\tau_D)$ was extracted for each case (c,d) and used to reconstruct the $G(t)$ (a and b, red lines). The agreement suggests our method works across values of α. Our $G(t)$ reconstructions differ slightly more from the original $G(t)$'s compared to the $\alpha = 0.9$ case due to the fact that the original $G(t)$'s were truncated after the sixth decade.