A biological interpretation of transient anomalous subdiffusion

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It is well known that if a particle diffuses in a suitable infinite hierarchy of traps, diffusion is anomalous at all times. But if the hierarchy is finite, diffusion is anomalous at short times and normal at long times. For a prescribed set of binding sites, Monte Carlo calculations yield the anomalous diffusion exponent and the average time over which diffusion is anomalous, and measure the effect on kinetics as the time required for a diffusing particle to reach a fixed target site from a random starting point. In this model if even a single trap is present there is a very short, almost artifactual, period of anomalous subdiffusion, but a hierarchy of traps extends the anomalous regime considerably. As is well known, an essential requirement for anomalous subdiffusion in a binding model is that the diffusing particle must not be in thermal equilibrium with the binding sites; an equilibrated particle diffuses normally at all times. This physical model can be translated directly into a biological model testable by single-particle tracking. The model is potentially applicable to observed cases of anomalous subdiffusion in the plasma membrane, nucleus, and cytoplasm. (Supported by NIH grant GM038133)