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CME compared with approximating Fokker-Planck equations via an analytic look at a birth-death process

Abundant mRNA, CME SS:

$$
\begin{aligned}
g &\xrightarrow{k_m} g + m \\
m &\xrightarrow{d_m} \varnothing
\end{aligned}
$$

CME (at steady state):

$$0 = k_m g\left[P(m-1) - P(m)\right] + d_m\left[(m+1)P(m+1) - mP(m)\right]$$

Solution (see for yourself via substitution):

$$P(m) = \frac{\left(\frac{k_m g}{d_m}\right)^m e^{-\frac{k_m g}{d_m}}}{m!} \ , \ m = 0, 1, 2, 3, \ldots$$

The mean and peak are (obviously)

$$\mu = \frac{k_m g}{d_m} \ ,$$

since the distribution is Poisson.

Abundant mRNA, FP SS w/ Gillespie noise:

Fokker-Planck (at steady state):

$$0 = -\frac{d}{dm}\left[\left(k_m g - d_m m\right)P(m)\right] + \frac{1}{2}\frac{d^2}{dm^2}\left[\left(k_m g + d_m m\right)P(m)\right]$$

Solution (via Mathematica)

$$P(m) = \frac{2^{4\mu}}{\Gamma(4\mu, 2\mu)} e^{-2(m+\mu)}\left(m+\mu\right)^{4\mu-1} \ , \ m \in [0, \infty)$$

where $\Gamma(a, x)$ is the incomplete gamma function defined via

$$\Gamma(a, x) := \int_x^\infty t^{a-1} e^{-t}\, dt \ .$$

The mean is

$$\langle m \rangle = \frac{4^{2\mu-1}e^{-2\mu}\mu^{4\mu}}{\Gamma(4\mu,2\mu)}\left[1+2e^{2\mu}\mu E_{-4\mu}(2\mu)\right] \ ,$$

where $E_n(x)$ (the function ExpIntegralE[n,x] in Mathematica) is defined via

$$E_n(x) := \int_1^\infty \frac{e^{-xt}}{t^n}\ dt \ .$$

The peak is

$$m = \mu - 1/2 \ .$$

Abundant mRNA, FP SS w/ additive noise:

Fokker-Planck (at steady state):

$$0 = -\frac{d}{dm}\left[\left(k_m g - d_m m\right)P(m)\right] + \frac{\sigma^2}{2}P''(m)$$

Solution (via Mathematica)

$$P(m) = \frac{2}{\sigma}\sqrt{\frac{d_m}{\pi}}\frac{1}{1+\operatorname{erf}\left(\frac{k_m g}{\sqrt{d_m}\sigma}\right)}\ \exp\left(-\frac{\left(\frac{k_m g}{\sqrt{d_m}} - \sqrt{d_m}m\right)^2}{\sigma^2}\right)\ ,\ m \in [0,\infty)\ ,$$

where $\operatorname{erf}(x)$, the error function (Erf[x] in Mathematica), is defined via

$$erf(x) := \frac{2}{\sqrt{\pi}}\int_0^z e^{-t^2}\ dt \ .$$

The peak is at

$$m = \frac{k_m g}{d_m} = \mu \ .$$

The mean is

$$\langle m \rangle = \frac{k_m g}{d_m} + \frac{\sigma \exp\left(-\frac{{k_m}^2 g^2}{d_m \sigma^2}\right)}{\sqrt{d_m \pi}\left[1+\operatorname{erf}\left(\frac{k_m g}{\sqrt{d_m}\sigma}\right)\right]} \ .$$

Abundant mRNA, FP SS w/ multiplicative noise:

Fokker-Planck (at steady state):

$$0 = -\frac{d}{dm}\left[\left(k_m g - d_m m\right)P(m)\right] + \frac{1}{2}\frac{d^2}{dm^2}\left[\sigma^2 m^2 P(m)\right]$$

Solution (via Mathematica)

$$P(m) = \left(\frac{2k_m g}{\sigma^2}\right)^{1+\frac{2d_m}{\sigma^2}} \frac{1}{\Gamma\left(1+\frac{2d_m}{\sigma^2}\right)}\, m^{-2\left(1+\frac{d_m}{\sigma^2}\right)} \exp\left(-\frac{2k_m g}{\sigma^2}\frac{1}{m}\right)$$

The peak is at

$$m = \frac{k_m g}{d_m+\sigma^2}\ .$$

The mean is (somewhat remarkably)

$$\langle m\rangle = \frac{k_m g}{d_m} = \mu\ .$$

Comparison between all distributions for small Poisson mean = 1:

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In[131]:= Plot[{Ppoiss[m, 1, 1, 1], PGill[m, 1, 1, 1], Padd[m, 1, 1, 1, 1.8], Pmult[m, 1, 1, 1, 3]},
  {m, 0, 10}, PlotRange → {0, 1}]
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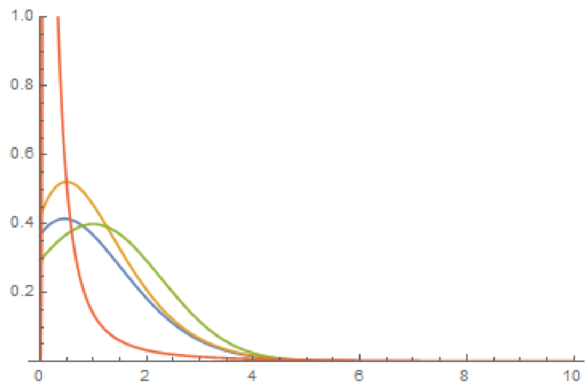
Out[131]=



Comparison between all distributions for large Poisson mean = 100:

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In[166]:= Plot[{Ppoiss[m, 100, 1, 1], PGill[m, 100, 1, 1], Padd[m, 100, 1, 1, 14.14],
  Pmult[m, 100, 1, 1, 0.1445]}, {m, 50, 150}, PlotRange → {0, 0.041}]
```

Out[166]=