Table 1. Plummer's Model

| Quantity | Symbol | Expression or value |
|---|---|---|
| Distribution function | $f$ | $\dfrac{3.2^{7/2}}{7\pi^3}\dfrac{a^2}{G^5M^4m}(-E)^{7/2}$ |
| Mass density | $\rho$ | $\dfrac{3M}{4\pi a^3}\left(1+\dfrac{r^2}{a^2}\right)^{-5/2}$ |
| Projected mass density | $\Sigma$ | $\dfrac{M}{\pi a^2}\left(1+\dfrac{d^2}{a^2}\right)^{-2}$ |
| Mass within radius $r$ | $M(r)$ | $M\left(1+\dfrac{a^2}{r^2}\right)^{-3/2}$ |
| Mass within projected radius $d$ | $M(d)$ | $M\left(1+\dfrac{a^2}{d^2}\right)^{-1}$ |
| (Specific) Potential | $\phi$ | $-\dfrac{GM}{a}\left(1+\dfrac{r^2}{a^2}\right)^{-1/2}$ |
| One-dimensional velocity dispersion | $\sigma^2$ | $-\dfrac{1}{6}\phi(r)$ |
| Projected velocity dispersion | $\sigma_z^2$ | $\dfrac{3\pi}{64}\dfrac{GM}{a}\left(1+\dfrac{d^2}{a^2}\right)^{-1/2}$ |
| Potential energy | $W$ | $-\dfrac{3\pi}{32}\dfrac{GM^2}{a}$ |
| Kinetic energy | $T$ | $-\dfrac{W}{2}$ |
| Total energy | $E$ | $\dfrac{W}{2}$ |
| Core radius | $r_c$ | $\dfrac{a}{\sqrt{2}}$ |
| Virial radius | $R_v$ | $\dfrac{16}{3\pi}a$ |
| Half-mass radius | $R_h$ | $\dfrac{a}{\sqrt{2^{2/3}-1}}, \simeq 1.305a$ |
| Half-mass relaxation time | $t_{rh}$ | $\dfrac{0.206Na^{3/2}}{\sqrt{GM}\ln\Lambda}$ |

turning a distribution function into a surface density is a sequence of integrations, and these tend to iron out differences between quite disparate models. (From $f$ we integrate to get $\rho(\phi)$, integrate again to obtain $\phi(r)$ and hence $\rho(r)$, and integrate yet again to construct $\Sigma$.) Another reason may be that the profile of a star cluster is a lot simpler than that of an elephant.

An alternative approach is to attempt to invert this series of integrations more-or-less directly, and in principle this can be done. In other words, from $\Sigma$ it is possible to invert the appropriate integral equation