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| **Variables and parameters**  d = 1/gametocyte lifespan in density model (logd = natural logarithm of d)  G0 = gametocyte density on day 0 (logG0 = natural logarithm of G0)  loggam\_m = natural logarithm of density of male gametocytes  loggam\_f = natural logarithm of density of female gametocytes  zero\_m = indicator variable for censored observation for male gametocyte density– ie male gametocyte density measured as zero so assumed below detection threshold.  zero\_f = indicator variable for censored observation for female gametocyte density– ie female gametocyte density measured as zero so assumed below detection threshold.  varre = variance of subject level random effect (logvarre = its natural logorathm)  varloggamd = variance of log gametocyte density around predicted value (logvarloggamd = its natural logarithm)  sdloggamd = standard deviation of variance of log gametocyte density around predicted value (ie square root of varloggamd)  lg0 = mean predicted log gametocyte density  e = subject level random effect  loggamd = subject specific predicted log gametocyte density  ll = log likelihood  **Model code**  proc nlmixed data=**’datasetname’** alpha=0.05;  parms logd=-2 logvarre=0 logG0=5 logvarloggamd=0 ;  d = exp(logd);  G0=exp(logG0);  varre = exp(logvarre);  varloggamd=exp(logvarloggamd);  sdloggamd = sqrt(varloggamd);  lg0= log(exp(-d\*day)\*G0);  loggamd = e + lg0;  if (zero\_m=0) then ll=-0.5\*logvarloggamd-(1/(2\*varloggamd))\*(loggam\_m-loggamd)\*\*2;  else ll=log(probnorm((loggam\_m-loggamd)/sdloggamd));  model loggam\_m~general(ll);  random e ~normal(0, varre) subject=id;  estimate "mean male gct circulation time" 1/exp(logd);  run;  proc nlmixed data=**’datasetname**’ alpha=0.05;  parms logd=-2 logvarre=0 logG0=5 logvarloggamd=0 ;  d = exp(logd);  G0=exp(logG0);  varre = exp(logvarre);  varloggamd=exp(logvarloggamd);  sdloggamd = sqrt(varloggamd);  lg0= log(exp(-d\*day)\*G0);  loggamd = e + lg0;  if (zero\_f=0) then ll=-0.5\*logvarloggamd-(1/(2\*varloggamd))\*(loggam\_f-loggamd)\*\*2;  else ll=log(probnorm((loggam\_f-loggamd)/sdloggamd));  model loggam\_f~general(ll);  random e ~normal(0, varre) subject=id;  estimate "mean female gct circulation time" 1/exp(logd);  run; |

**Supplementary File 7. SAS code used for estimation of gametocyte half-life for gametocytes**