Time scale separation in life-long ovarian follicles population dynamics model

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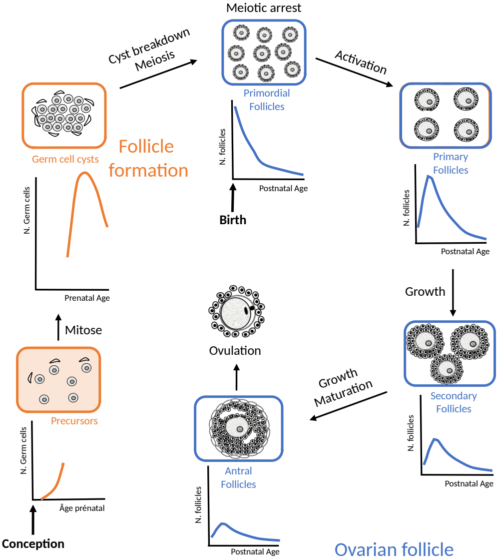
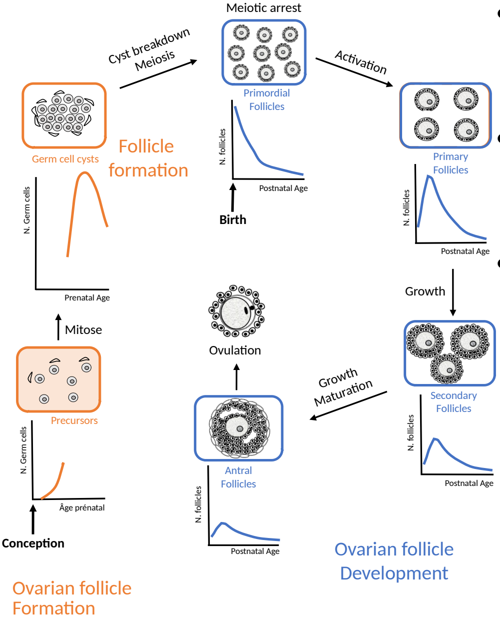


Ovarian follicle Development

Ovarian follicle Formation

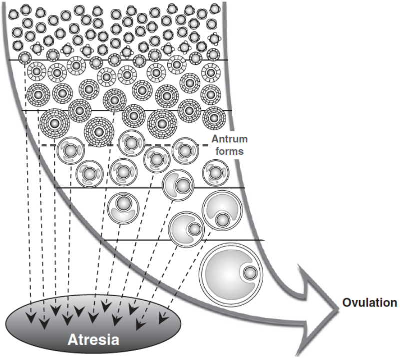


- Pool of Quiescent follicles
  static reserve (perinatal in most mammals)
  Slow activation
- Basal growth
  Dynamic reserve (starting at birth) Spanning over several ovarian cycles
- Terminal growth
  After puberty : ovulation within an ovarian cycle

Order of magnitude (in Women)

- Quiescent follicles

peri-natal	$\approx 5 \cdot 10^6$
At birth	$\approx 1 \cdot 10^6$
At puberty	$10^4 - 10^6$
At menopause	$< 10^3$
Activation rate	"A few per days"



Scaramuzzi et al., Reprod.Fert. Dev. 2011

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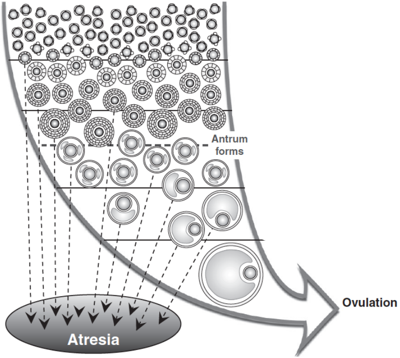
- Growing follicles

Maturation time	$120 - 180j$
Basal follicles	$10^3 - 10^4$
Terminal follicles	10^2
Pre-Ovulatory follicles	a few
Atresia	Most of ther



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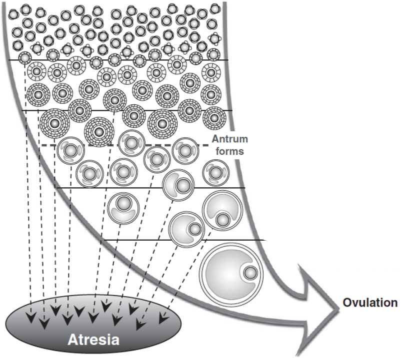
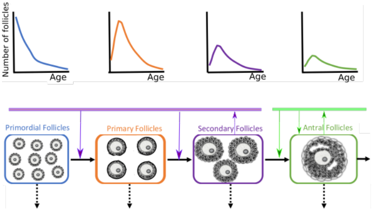
$>$**Only** 400 **follicles will ever reach the pre-ovulatory stage**

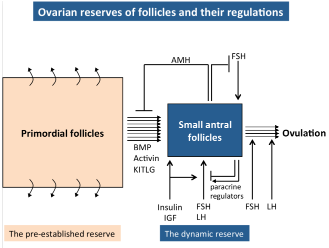


Scaramuzzi et al., Reprod.Fert. Dev. 2011

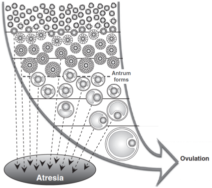
Population dynamics in female gametogenesis

- Asynchronous growth
- Several timescales : Ten of years / Months / Weeks
- Interactions between subpopulations





Monniaux, Theriogenology 2016



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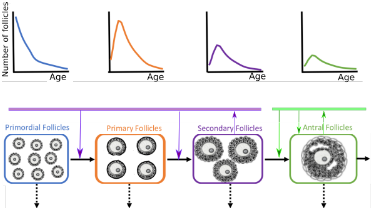
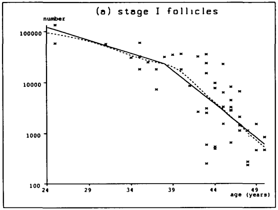
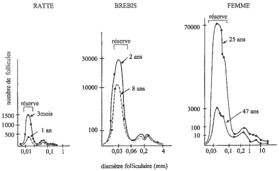


⇒ Irreversible (slow) decay of an initial pool of quiescent follicle

⇒ ”Stable” repartition of growing follicle

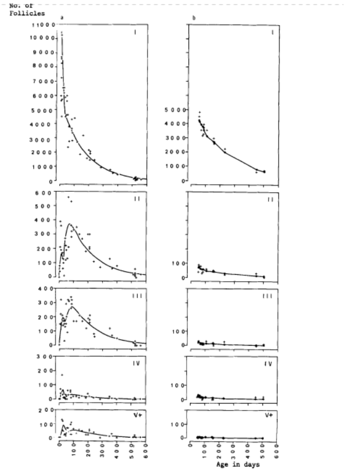


Faddy and Gosden 1995



Thibault and Levasseur, 2001

Previous compartmental model (mice data)

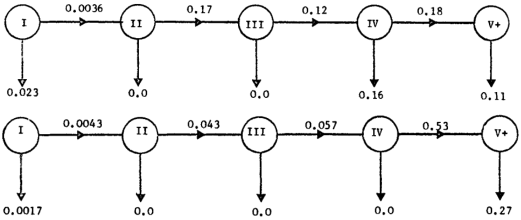


Faddy et al., J. Exp. Zool. 1976

An Analytical Model for Ovarian Follicle Dynamics

M. J. FADDY,[1] ESTHER C. JONES[2] AND R. G. EDWARDS[3]
[1] Department of Mathematical Statistics, University of Birmingham, Birmingham B15 2TT, U.K.; [2] Department of Anatomy, University of Birmingham, Birmingham B15 2TJ, U.K., and [3]Physiological Laboratory, University of Cambridge, Cambridge CB2 3EG, U. K.

- "Migration-death" model
- Linear Model



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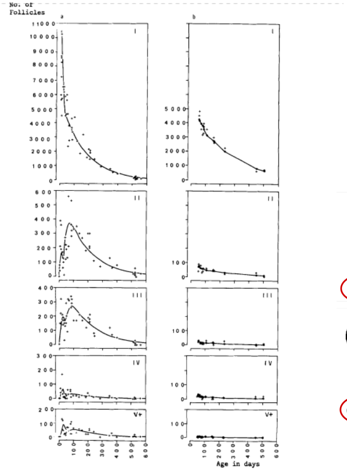

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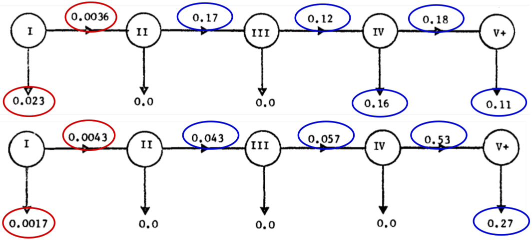
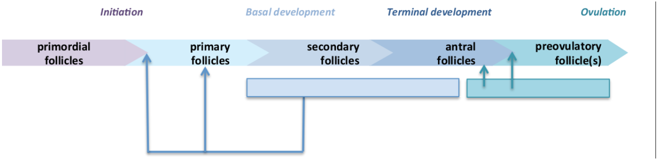


Lifespan follicle population model

- Structured Population in compartments
- Non linear interaction between follicles *via* $\lambda's$ and $\mu's$.

$$
\begin{array}{ccccccccc}
 & \lambda_0(\cdot) & & \lambda_1(\cdot) & & \lambda_2(\cdot) & & & \\
X & \rightarrow & Y_1 & \rightarrow & Y_2 & \rightarrow & \cdots & & Y_d \\
\downarrow \mu_0(\cdot) & & \downarrow \mu_1(\cdot) & & \downarrow \mu_2(\cdot) & & & & \downarrow \mu_d(\cdot) \\
\emptyset & & \emptyset & & \emptyset & & & & \emptyset
\end{array}
$$



Bonnet et al. *Multiscale population dynamics in reproductive biology : singular perturbation reduction in deterministic and stochastic models*, ESAIM : PROCEEDINGS AND SURVEYS, 2020.

Lifespan follicle population model

- Structured Population in compartments
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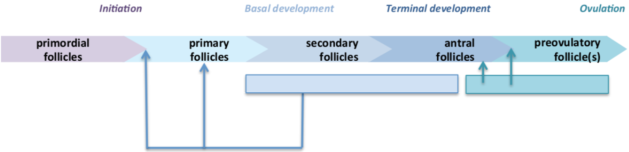
$$
\begin{array}{ccccccccc}
X & \xrightarrow{\lambda_0} & Y_1 & \xrightarrow{\lambda_1} & Y_2 & \xrightarrow{\lambda_2} & \cdots & & Y_d \\
\downarrow \mu_0 & & \downarrow \mu_1 & & \downarrow \mu_2 & & & & \downarrow \mu_d \\
\emptyset & & \emptyset & & \emptyset & & & & \emptyset
\end{array}
$$

Typical choice

$$
\begin{aligned}
\lambda_i(Y) &= m_i + \frac{f_i}{1 + K_{1,i} \sum_{j=1}^{d} \omega_{1,j} Y_j}, \\
\mu_i(Y) &= g_i \left(1 + K_{2,i} \sum_{j=0}^{d} \omega_{2,j} Y_j \right)
\end{aligned}
$$



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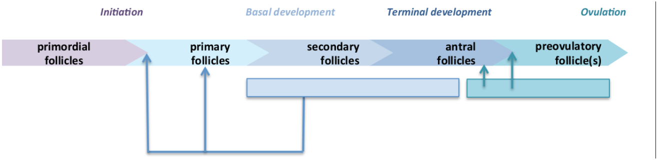
Lifespan follicle population model

- Structured Population in compartments
- Non linear interaction between follicles *via* $\lambda' s$ and $\mu' s$.
- Two time and abundance scales

- Quiescent Pool $\gg$ Growing Follicles
- Slow Activation $\ll$ Fast growth

$$
\begin{array}{ccccccccc}
\frac{1}{\varepsilon} X & \overset{\varepsilon\lambda_0}{\rightarrow} & Y_1 & \overset{\lambda_1}{\rightarrow} & Y_2 & \overset{\lambda_2}{\rightarrow} & \cdots & & Y_d \\
\downarrow \varepsilon\mu_0 & & \downarrow \mu_1 & & \downarrow \mu_2 & & & & \downarrow \mu_d \\
\emptyset & & \emptyset & & \emptyset & & & & \emptyset
\end{array}
$$



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Singular Perturbation Theory

$$\begin{array}{ccccccccc}
\frac{1}{\varepsilon}X & \overset{\varepsilon\lambda_0}{\rightarrow} & Y_1 & \overset{\lambda_1}{\rightarrow} & Y_2 & \overset{\lambda_2}{\rightarrow} & \cdots & & Y_d \\
\downarrow \varepsilon\mu_0 & & \downarrow \mu_1 & & \downarrow \mu_2 & & & & \downarrow \mu_d \\
\emptyset & & \emptyset & & \emptyset & & & & \emptyset
\end{array}$$

In the limit $\varepsilon \to 0$ We expect X and $Y = (Y_1, \cdots, Y_d)$ to converge to a differential-algebraic equation :

$$\begin{cases} \frac{dx}{dt}(t) & = & F(x(t), y(t)), \quad x(0) = x^{\mathrm{in}}, \\ 0 & = & G(x(t), y(t)), \quad t > 0 \end{cases}$$

$$
\begin{array}{ccccccccc}
\frac{1}{\varepsilon}X & \xrightarrow{\varepsilon\lambda_0} & Y_1 & \xrightarrow{\lambda_1} & Y_2 & \xrightarrow{\lambda_2} & \cdots & & Y_d \\
\downarrow \varepsilon\mu_0 & & \downarrow \mu_1 & & \downarrow \mu_2 & & & & \downarrow \mu_d \\
\emptyset & & \emptyset & & \emptyset & & & & \emptyset
\end{array}
$$

Theorem (G. Ballif, F. Clément, R.Y. SIAP 2022)

(...) $(X^\varepsilon, Y^\varepsilon)$ converges in $\mathcal{D}_{\mathbb{R}}[0,\infty[\times\mathcal{L}_m(\mathbb{N}^d)$ to the unique solution of

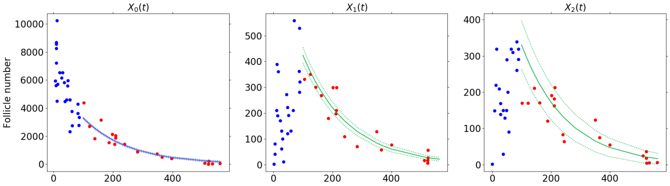
$$
\begin{cases}
\frac{dx}{dt}(t) = \Lambda_0\big(x(t)\big)x(t)\,, & x(0) = x^{\mathrm{in}}\,, \\
\Lambda_0\big(x(t)\big) = -\sum_{y\in\mathbb{N}^d}\Big(\lambda_0(y)+\mu_0(y)\Big)\pi_{x(t)}(y)\,,
\end{cases}
$$

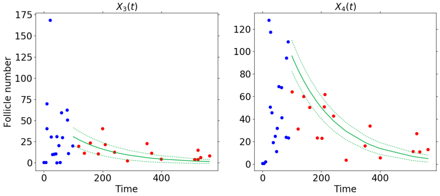
$$
\sum_{y\in\mathbb{N}^d} L_x\psi(y)\pi_x(y) = 0\,, \quad \forall\psi \textit{ bounded on } \mathbb{N}^d\,,
$$

$$
L_x\psi(y) = \lambda_0(y)x\Big[\psi(y+e_1)-\psi(y)\Big] + \sum_{i=1}^{d-1}\lambda_i(y)y_i\Big[\psi(y+e_{i+1}-e_i)-\psi(y)\Big]
$$

$$
+\sum_{i=1}^{d}\mu_i(y)y_i\Big[\psi(y-e_i)-\psi(y)\Big]\,.
$$

Does it works in practice ?



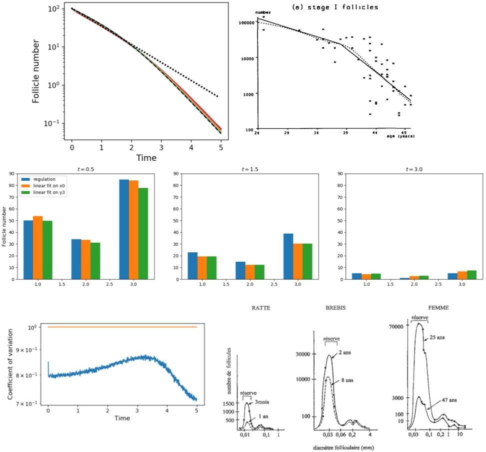


$$\begin{cases} x_0(t) & = X_0^{in} \exp\Big(-(\lambda_0+\mu_0)t \Big) \\ \pi_{x_0(t)}(y) & = \prod_{i=1}^{d} \frac{(x_0(t)\alpha_i)^{y_i}}{y_i!} e^{-x_0(t)\alpha_i} \end{cases}$$

$$\alpha_i = \prod_{j=0}^{i-1} \frac{\lambda_j}{\lambda_{j+1}+\mu_{j+1}}$$

- Timescale separation is coherent with published data on follicle counts in mice at the lifespan time scale, *away from a transient period*.

What is it useful for ?



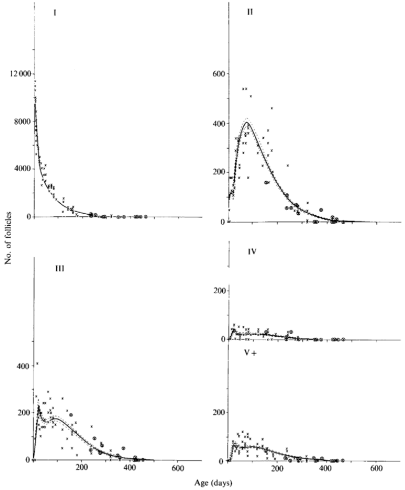
- ✓ acceleration of reserve decay with age : $\frac{dx}{dt} = -(a + \frac{b}{1+cx})x$ -> Mechanistic explanation of previously published statistical regression model (*Coxworth and Hawkes 2010*)
- ✓ "stable" evolution of growing follicles Y

Going further

- Can we infer the regulation mechanism that control follicle activation ?
- Can we refine the model to model the transient phase (reserve establishment / early post-natal dynamics) ?

"Time" course

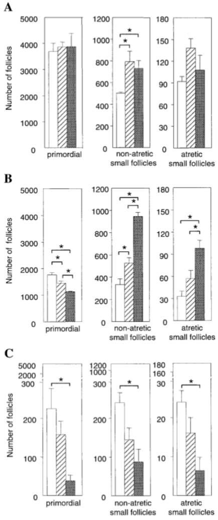
- Follicle count in mice from birth until 500 days.
- Reserve + 4 compartments (Faddy's classification)
- (Recovery of points by hand)



Faddy, Gosden and Edwards, J. Endo., 1983
Faddy, Telfer and Gosden, Cell Proliferation, 1987

Perturbation data : KO AMH

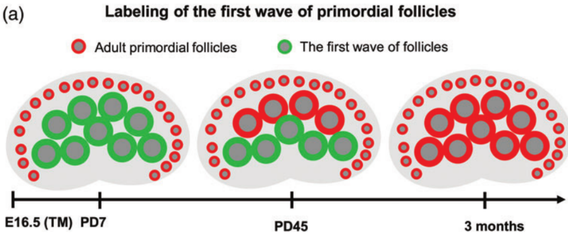
- AMH Inhibition *in vivo* on mice
- 3 genotypes : control group (+/+), heterozygous mice KO AMH (+/-) homozygous mice KO AMH (-/-).
- Follicle counts at 3 ages :
  - 25 days (A)
  - 120 days (B)
  - 390 days (C)



Durlinger and al, Endocrinology, 1999

Ovarian Reserve build-up

- Two distinct population of follicles are present initially
- Labelling of each population

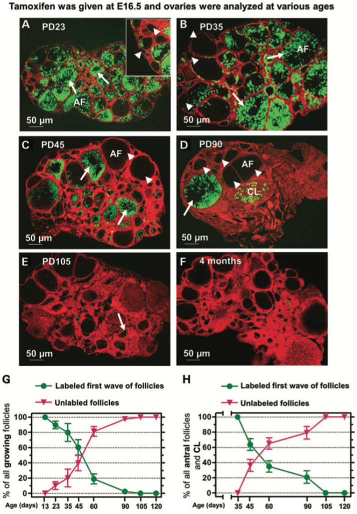


Zheng, Zhang and Liu, Hum. Mol. Reprod, 2014

Ovarian Reserve build-up

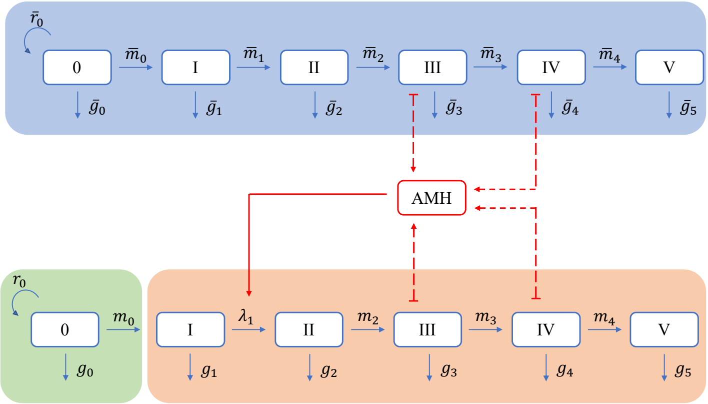
- Tracing follicles of the first wave of activated follicles.
- Proportion of first wave activated follicles among growing follicles.

$$p(t) = \frac{\sum_{i=1}^{4} X_i^1(t)}{\sum_{i=1}^{4} X_i^{tot}(t)}$$

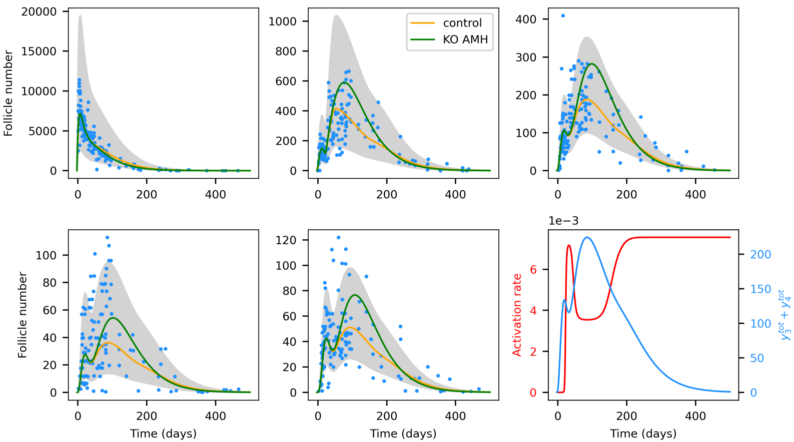


Zheng, Zhang and al, Hum. Mol. Gen, 2014

ODE model

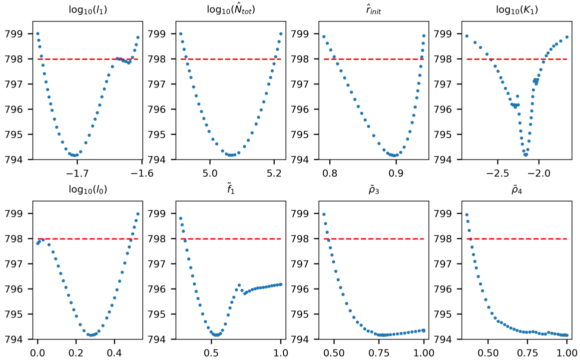

$\bar{r}_0$
0
$\bar{m}_0$
I
$\bar{m}_1$
II
$\bar{m}_2$
III
$\bar{m}_3$
IV
$\bar{m}_4$
V
$\bar{g}_0$
$\bar{g}_1$
$\bar{g}_2$
$\bar{g}_3$
$\bar{g}_4$
$\bar{g}_5$
AMH
r_0
0
m_0
I
λ_1
II
m_2
III
m_3
IV
m_4
V
g_0
g_1
g_2
g_3
g_4
g_5

Data fitting



Identifiability

Theoretical *(Structural Identifiability Julia package)* and practical identifiability *(Data2Dynamics Matlab package)* .



- 20 of 31 parameters are practically identifiable.
- Mean activation time is around 200 days, while growing time is around 50 days.

Identifiability

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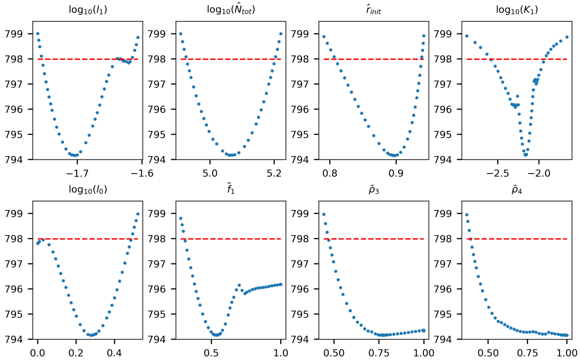
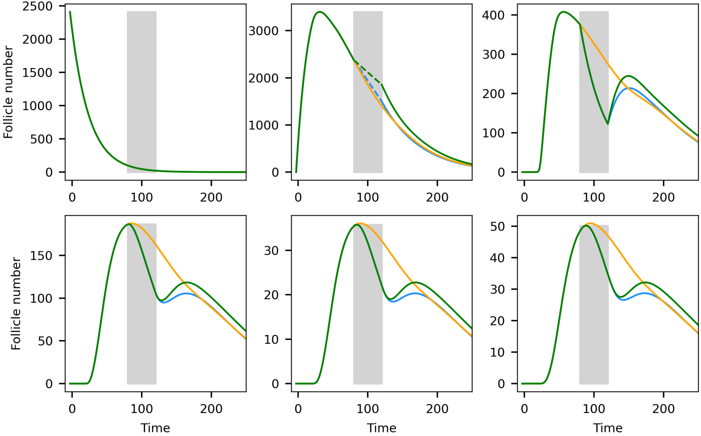
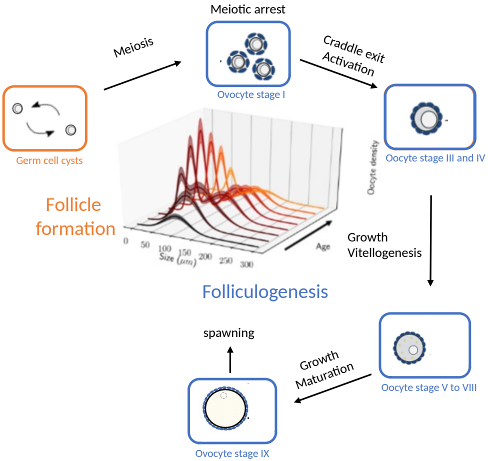


- 20 of 31 parameters are practically identifiable.
- Additional Data on germ cell dynamics would greatly improve identifiability

Prediction of AMH administration

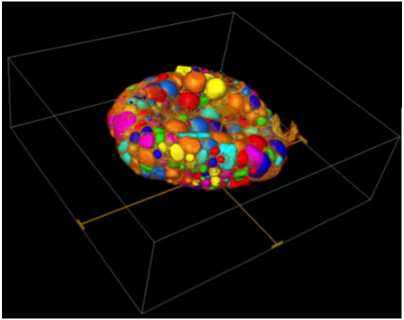


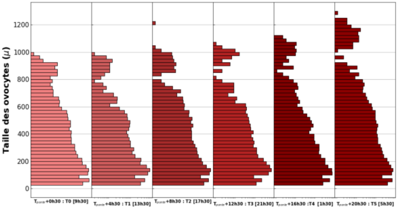
Comparison with fish oogenesis



Continuous structuring variable

3D imaging data : whole Follicle count and size measurement

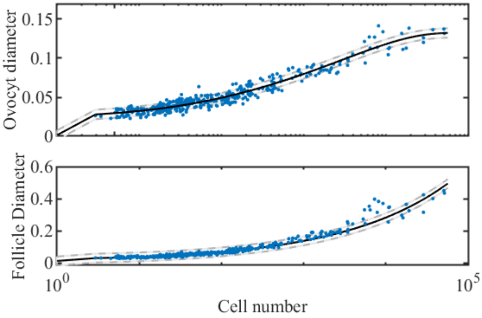


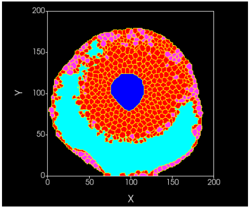


-> The bulk size distribution is ovarian-cycle independent (slow variable).

$$\begin{cases} \dfrac{d\rho_0(t)}{dt} &= -(\lambda_0(\rho(t,.)) + \mu_0(\rho(t,.)))\rho_0(t)\,, \\ \varepsilon\partial_t\rho(t,x) &= -\partial_x(\lambda(\rho(t,.),x)\rho(t,x)) - \mu(\rho(t,.),x)\rho(t,x)\,, \\ \lim\limits_{x\to 0}\lambda(\rho(t,.),x)\rho(t,x) &= \lambda_0(\rho(t,.))\rho_0(t)\,, \end{cases}$$

More than one structuring variable





Conclusion and perspective

- ✓ Lifespan ovarian follicle population dynamics model
- ✓ Separation of time scale explains slow decay of the reserve and quasi stable growing follicle repartition
- ✓ Follicle count data and perturbation experiments may reveal feedback mechanisms
- Extension to three timescale (reserve, basal growth and terminal growth)
- Extension to (several) continuous structuring variable
- Comparative physiology approach

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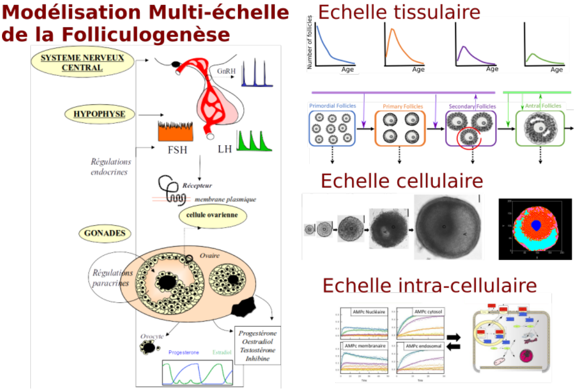
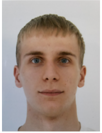
Open Post-position avalaible in 2023 !

Thanks for your attention !





Inria INRAE

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- ⋆ INRAE LPGP (Violette Thermes)
- ⋆ INSERM - Paris Cité (Céline Guigon)
- ⋆ CEMRACS 2018 (Céline Bonnet, Keltoum Chahour)