Flour Power: Modeling the Growth and Decay of Sourdough Starters

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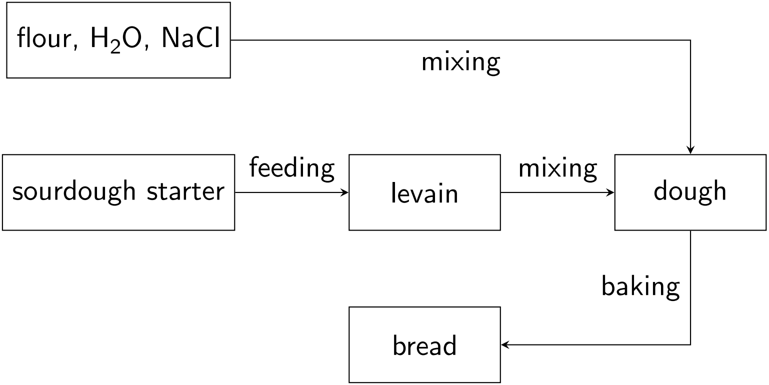
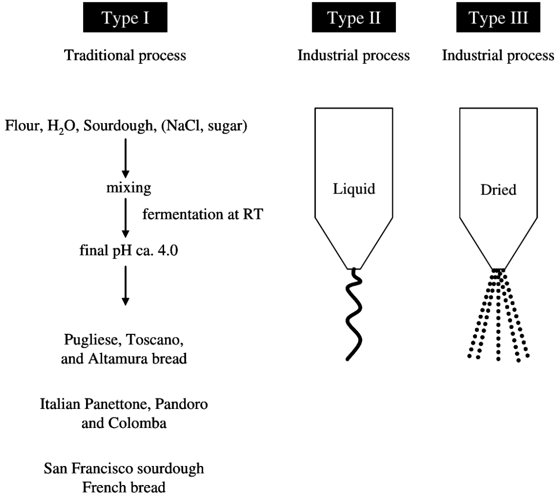
Outline

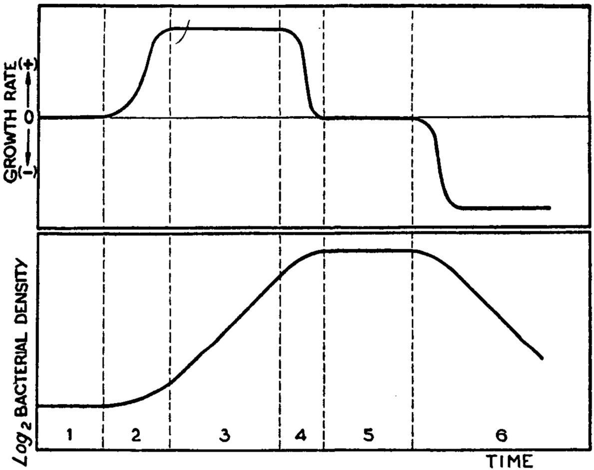
Focusing on sourdough within the context of baking and food production



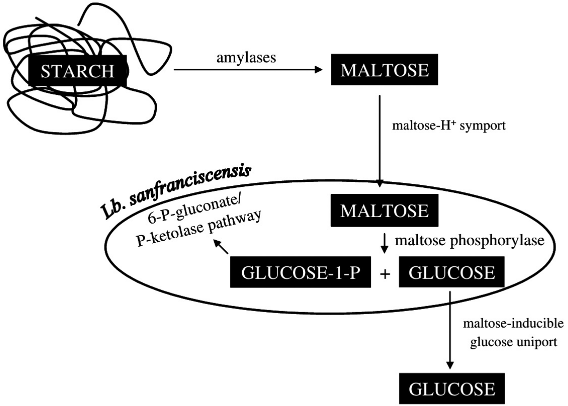
Type I sourdough is most mathematically interesting (Neysens and De Vuyst 2007)



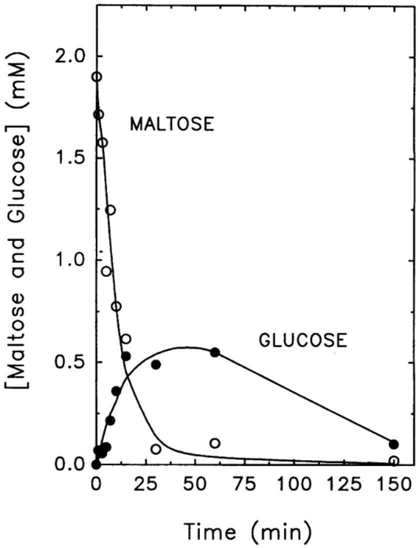
Monod's model introduces exponential growth and compartmental stages (Monod 1949)



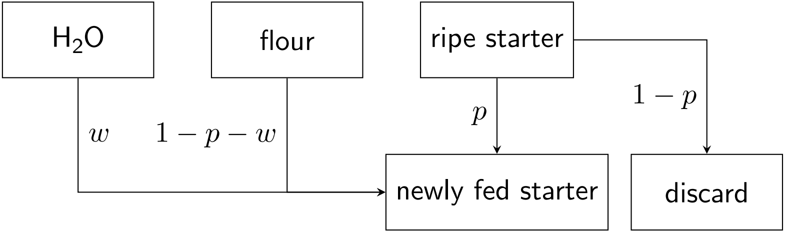
LAB “eat” maltose and “excrete” glucose (Neysens and De Vuyst 2007)



Maltose consumption follows exponential decay (Neubauer et al. 1994)



Back-slopping conserves mass, but not biomass



$$p \in (0,1)$$
$$w \in (0,1-p)$$

Exponential growth captures general shape of curve $(B, D, G, X, t \in \mathbb{R}_{\geq 0}; \alpha_B, \alpha_X \in \mathbb{R}_+)$

$$\frac{dB}{dt} = \alpha_B B$$

$$\frac{dD}{dt} = -\alpha_B D$$

$$\frac{dG}{dt} = \alpha_B B - \alpha_X X$$

$$\frac{dX}{dt} = \alpha_X X$$

Michaelis-Menten kinetics accurately describe nutrient consumption ($K_D, K_G \in \mathbb{R}_+$)

$$\frac{dB}{dt} = \alpha_B B \frac{D}{K_D + D}$$

$$\frac{dD}{dt} = -\alpha_B B \frac{D}{K_D + D}$$

$$\frac{dG}{dt} = \alpha_B B \frac{D}{K_D + D} - \alpha_X X \frac{G}{K_G + G}$$

$$\frac{dX}{dt} = \alpha_X X \frac{G}{K_G + G}$$

Steady state analysis at this point reveals the necessity of a decay term

$$\frac{dB}{dt} = \alpha_B B \frac{D}{K_D + D}$$

$$0 = \alpha_B B \frac{D}{K_D + D}$$

$$\alpha_B = 0 \quad \text{or} \quad B = 0 \quad \text{or} \quad D = 0$$

There could exist some $(\bar{B}, \bar{D}) = (0, d)$ where $d \neq 0$.

Adding a decay term "pushes" all solutions to 0 asymptotically ($\gamma_B, \gamma_X \in \mathbb{R}_+$)

$$\frac{dB}{dt} = \alpha_B B \frac{D}{K_D + D} - \gamma_B B$$

$$\frac{dD}{dt} = -\alpha_B B \frac{D}{K_D + D}$$

$$\frac{dG}{dt} = \alpha_B B \frac{D}{K_D + D} - \alpha_X X \frac{G}{K_G + G}$$

$$\frac{dX}{dt} = \alpha_X X \frac{G}{K_G + G} - \gamma_X X$$

Adding a yield term fixes dimension discrepancies in D and G equations ($Y_D, Y_G \in [1, \infty)$)

$$\frac{dB}{dt} = \alpha_B B \frac{D}{K_D + D} - \gamma_B B$$

$$\frac{dD}{dt} = -\frac{\alpha_B}{Y_D} B \frac{D}{K_D + D}$$

$$\frac{dG}{dt} = \frac{\alpha_B}{Y_D} B \frac{D}{K_D + D} - \frac{\alpha_X}{Y_G} X \frac{G}{K_G + G}$$

$$\frac{dX}{dt} = \alpha_X X \frac{G}{K_G + G} - \gamma_X X$$

An iterative process is best suited to describe back-slopping ($i \in \mathbb{N}; h \in \mathbb{R}_+$)

$$B_{i+1}(0) = pB_i(h)$$

$$D_{i+1}(0) = pD_i(h)$$

$$G_{i+1}(0) = pG_i(h)$$

$$X_{i+1}(0) = pX_i(h)$$

Adding another term accounts for nutrients and ambient organisms from flour

$$B_{i+1}(0) = pB_i(h) + (1 - p - w)B_0(0)$$

$$D_{i+1}(0) = pD_i(h) + (1 - p - w)D_0(0)$$

$$G_{i+1}(0) = pG_i(h) + (1 - p - w)G_0(0)$$

$$X_{i+1}(0) = pX_i(h) + (1 - p - w)X_0(0)$$

Acceptable variable values and dimensions

Variable List			
Variable	Range	Units	Biological Significance
t	$\mathbb{R}_{\geq 0}$	h	time since last feeding
B	$\mathbb{R}_{\geq 0}$	cfu	LAB density
D	$\mathbb{R}_{\geq 0}$	g kg^{-1}	disaccharide concentration
G	$\mathbb{R}_{\geq 0}$	g kg^{-1}	glucose concentration
X	$\mathbb{R}_{\geq 0}$	cfu	yeast density
i	$\mathbb{N}$	n/a	cycle counter

Acceptable parameter values and dimensions

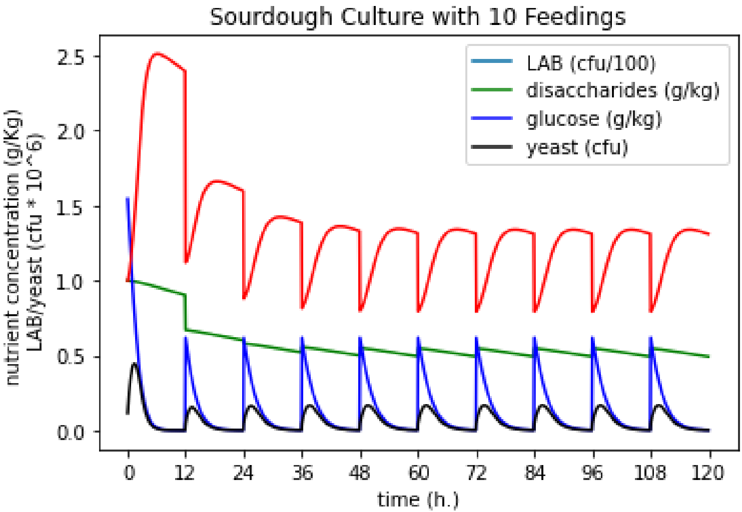
Parameter List

Parameter	Range	Units	Biological Significance
α_B	$\mathbb{R}_+$	h^{-1}	LAB growth
α_X	$\mathbb{R}_+$	h^{-1}	yeast growth
Y_D	$[1, \infty)$	g (cfu kg)$^{-1}$	disaccharide yield
Y_G	$[1, \infty)$	g (cfu kg)$^{-1}$	glucose yield
γ_B	$\mathbb{R}_+$	h^{-1}	LAB decay
γ_X	$\mathbb{R}_+$	h^{-1}	yeast decay
K_D	$\mathbb{R}_+$	g kg^{-1}	Michaelis-Menten for D
K_G	$\mathbb{R}_+$	g kg^{-1}	Michaelis-Menten for G
p	$(0, 1)$	1	inoculation/carryover
w	$(0, 1-p)$	1	hydration
h	$\mathbb{R}_+$	h	cycle length

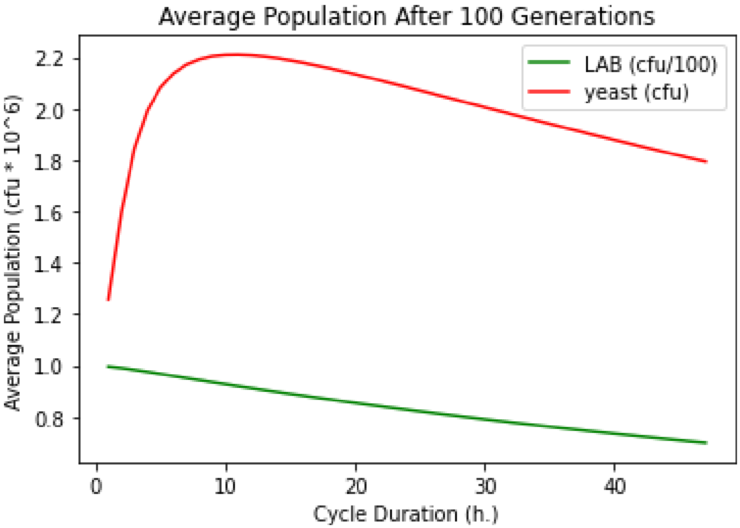
The only steady state is the trivial one! $((\bar{B}, \bar{D}, \bar{G}, \bar{X}) = \vec{0})$

- Baker "keeps starter alive" only through feeding (avoiding trivial steady state)
- Transience is most important property to study in this system
- This matches intuition: there can never be a non-zero bacteria or yeast population with an absence of nutrients

After a few generations, the maximum concentrations and shapes seem to even out



With these same parameter values, we can find the cycle length which maximizes LAB and yeast pop.



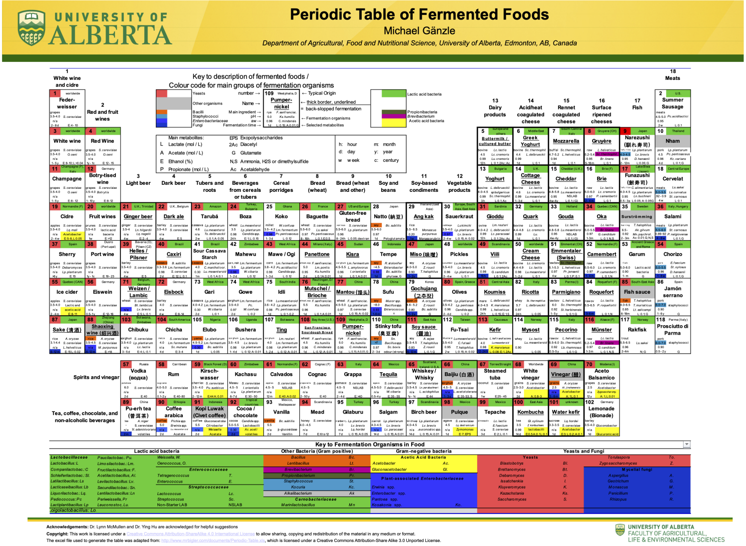
Shortcomings of the model: accuracy versus feasibility

- No pH control (Gänzle 2014)
- No temperature control (Gänzle 2014)
- Uncertainty Quantification (Tennøe 2018)
- (More) optimization

Where can we go from here?

- Good model for fermentation and symbiosis in other organisms (wine, cheese, etc.)
- Could apply to other models for species interactions
- Iterative model is also an interesting tool

The possibilities are endless (Gänzle, 2022)



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