

Structured Model for PHB Production (PHB)

- Growth and storage of PHB are described as functions of limiting substrate S (NH_4^+), residual biomass R and product P (PHB) concentrations.

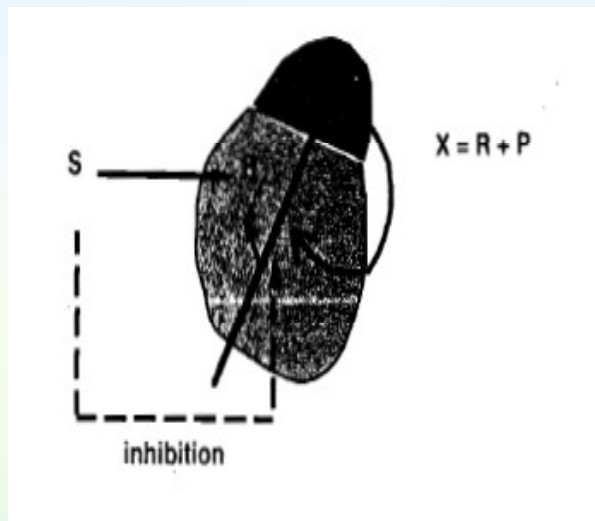


Fig. 7. Structured kinetic model for PHB synthesis.

PHB [Model]

- For the batch process,

$$\frac{dR}{dt} = r_R = \mu R$$

- Where r_R is the rate of synthesis of R and μ is the specific rate of synthesis of R, where

$$\mu = \mu_1 + \mu_2 = \mu_{m,1} \frac{S}{K_{s,1} + S} + \mu_{m,2} \frac{(S/K_{s,2})^n}{1 + (S/K_{s,2})^n}$$

PHB [Model]

- For substrate

$$\frac{dS}{dt} = r_s = -\frac{1}{Y_{R/S}} r_R$$

- The rate of synthesis of P(r_p) is assumed to be the sum of a growth associated term($r_{p,1}$) and a biomass associated term($r_{p,2}$) and is given by,

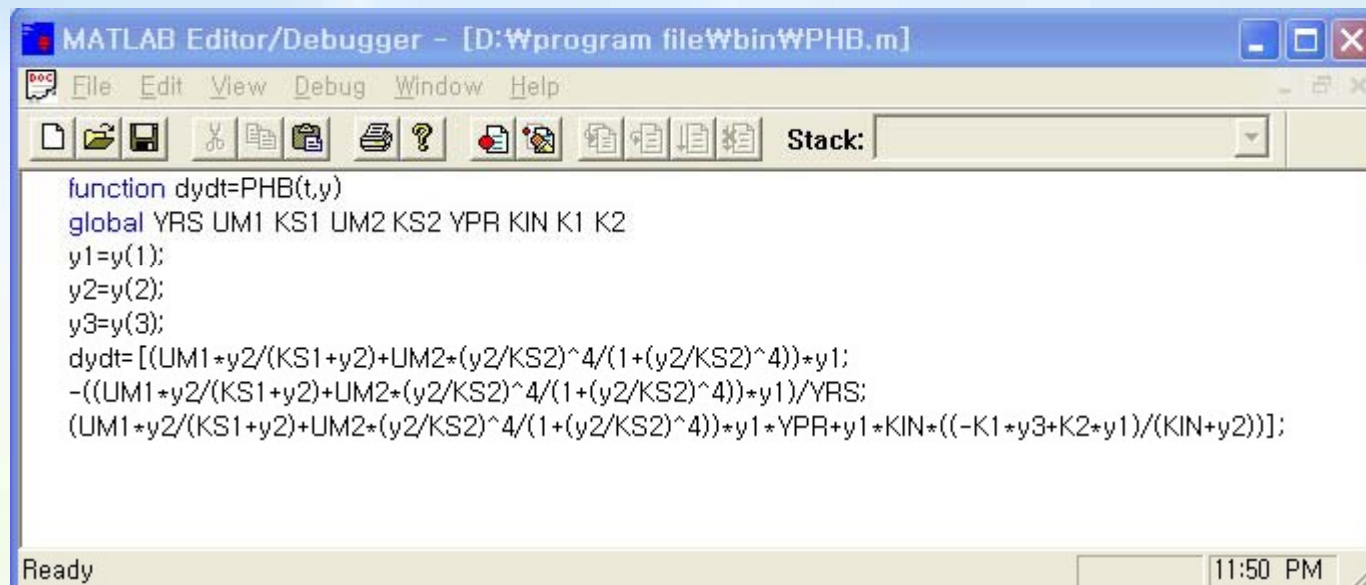
$$\frac{dP}{dt} = r = r_{p,1} + r_{p,2}$$

- The non-growth associated term of the synthesis of P($r_{p,2}$)

$$r_{p,2} = \frac{K_1}{(K_1 + S)} (-k_1 P + k_2 R)$$

PHB [Program]

M-file



The image shows a screenshot of the MATLAB Editor/Debugger window. The title bar reads "MATLAB Editor/Debugger - [D:\Wprogram file\Wbin\WPHB.m]". The menu bar includes "File", "Edit", "View", "Debug", "Window", and "Help". The toolbar contains various icons for file operations and editing. The main text area contains the following MATLAB code:

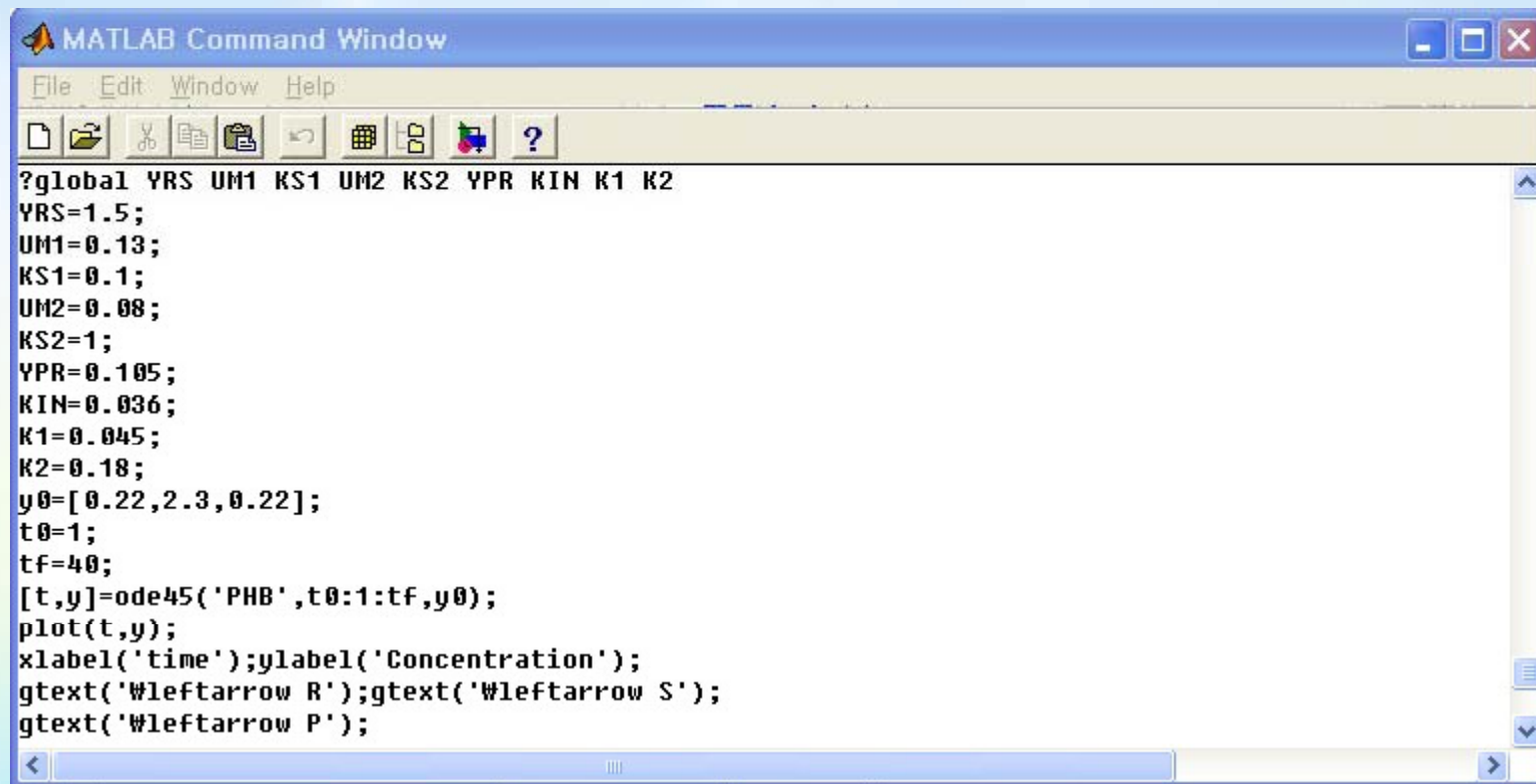
```
function dydt=PHB(t,y)
global YRS UM1 KS1 UM2 KS2 YPR KIN K1 K2
y1=y(1);
y2=y(2);
y3=y(3);
dydt=[(UM1+y2/(KS1+y2)+UM2+(y2/KS2)^4/(1+(y2/KS2)^4))+y1;
-((UM1+y2/(KS1+y2)+UM2+(y2/KS2)^4/(1+(y2/KS2)^4))+y1)/YRS;
(UM1+y2/(KS1+y2)+UM2+(y2/KS2)^4/(1+(y2/KS2)^4))+y1+YPR+y1*KIN+((-K1+y3+K2+y1)/(KIN+y2)]];

```

The status bar at the bottom left shows "Ready" and the bottom right shows "11:50 PM".

PHB [Program]

Command window

A screenshot of the MATLAB Command Window. The window title is "MATLAB Command Window". The menu bar includes "File", "Edit", "Window", and "Help". The toolbar contains icons for file operations (new, open, save, print, copy, paste), a grid, a zoom in/out icon, a run icon, and a help icon. The command window contains the following code:

```
?global YRS UM1 KS1 UM2 KS2 YPR KIN K1 K2
YRS=1.5;
UM1=0.13;
KS1=0.1;
UM2=0.08;
KS2=1;
YPR=0.105;
KIN=0.036;
K1=0.045;
K2=0.18;
y0=[0.22,2.3,0.22];
t0=1;
tf=40;
[t,y]=ode45('PHB',t0:1:tf,y0);
plot(t,y);
xlabel('time');ylabel('Concentration');
gtext('\leftarrow R');gtext('\leftarrow S');
gtext('\leftarrow P');
```

PHB [Nomenclature]

- C_1 Concentration kg/m_3
- K_1 Inhibition constant, for $(\text{NH}_4)_2\text{SO}_4$ kg/m_3
- K_S Saturation constant kg/m_3
- n Hill coefficient –
- P Product concentration (PHB) kg/m_3
- Prot Protein concentration kg/m_3
- R Residual biomass ($R=X-P$) kg/m_3
- r Reaction rate $\text{kg}/(\text{m}_3\text{h})$
- $r_{P,\text{red}}$ Reduced rate of synthesis of PHB –
- S Limiting substrate NH_4^+ as $(\text{NH}_4)_2\text{SO}_4$ kg/m_3
- X Biomass concentration kg/m_3
- $Y_{P/R}$ Yield coefficient kg/kg
- $Y_{R/S}$ Yield coefficient kg/kg
- μ Specific rate of synthesis of R (r_R/R) $1/\text{h}$
- μ_P Specific rate of synthesis of P (r_P/P) $1/\text{h}$

PHB [Result]

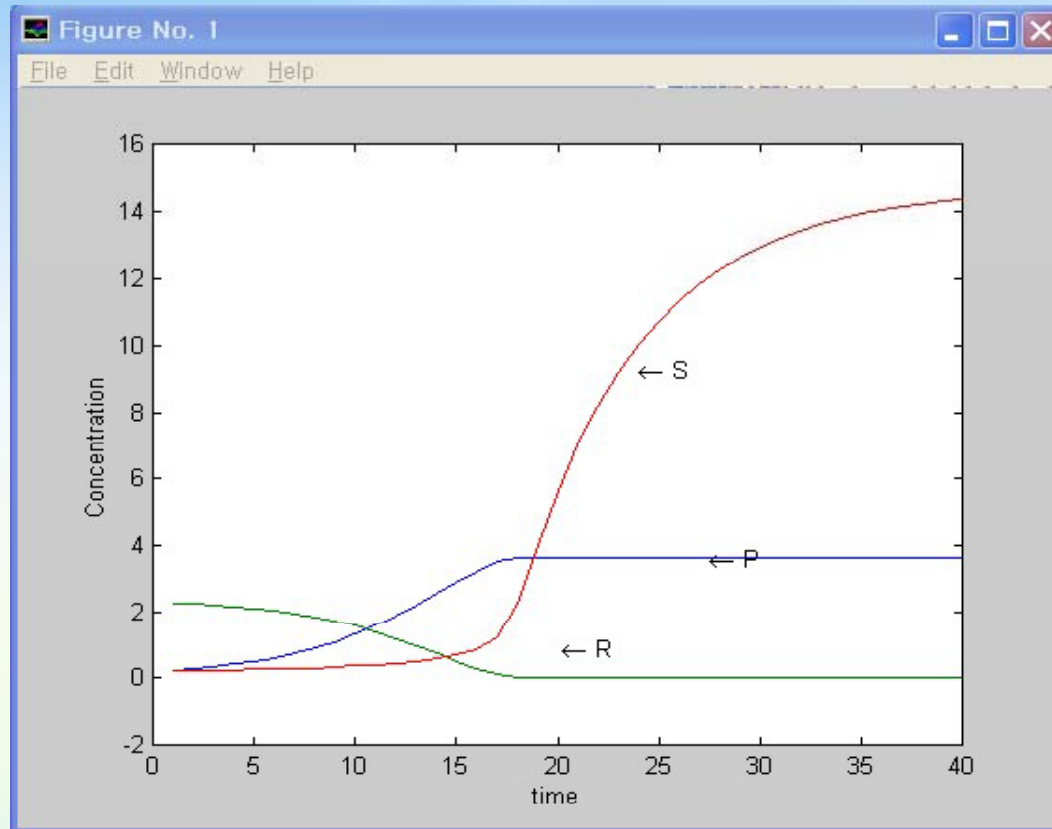


Fig. 8. Plots of R, S and P versus T during batch growth and production.