

Predictive modeling of microbial growth under dynamic conditions

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<http://www.ifr.ac.uk/safety/comicro/>

Predictive Microbiology

Quantitative Microbial Ecology of Food

In vitro

environment



microbial response

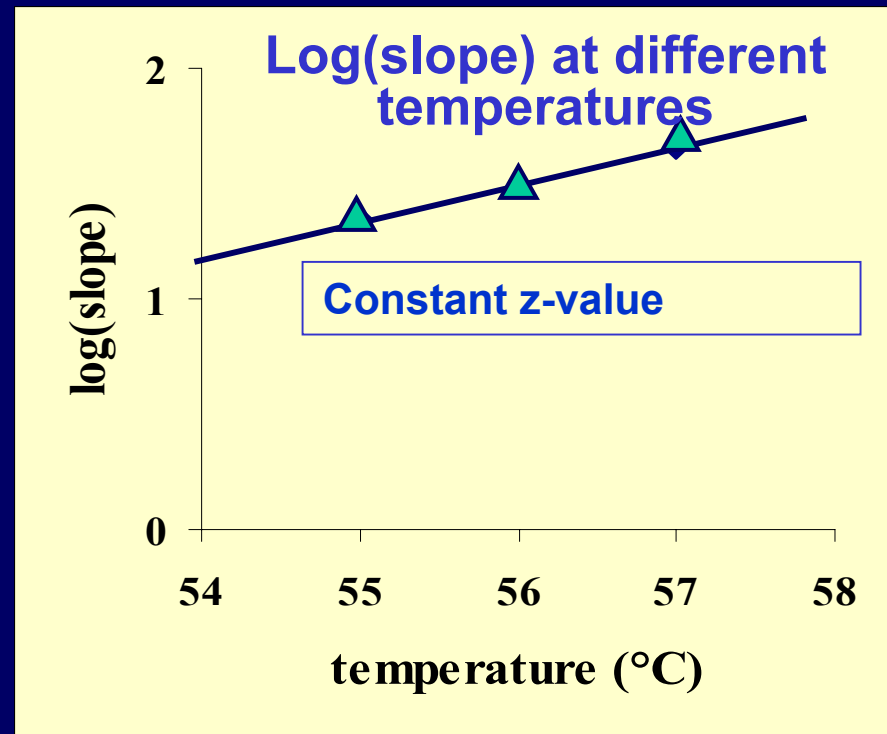
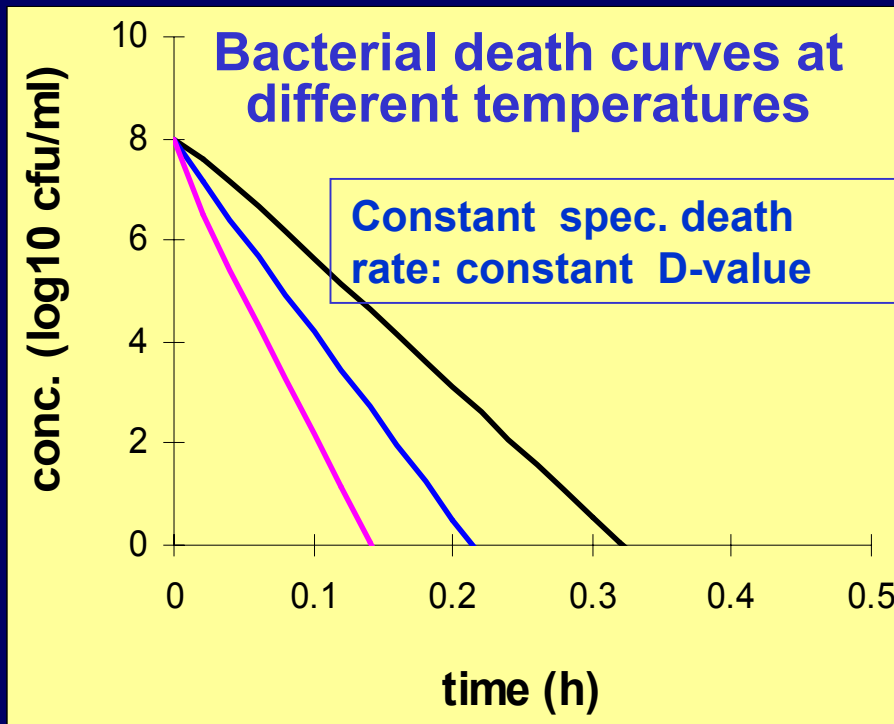
In vivo

*temperature, pH, water activity,
atmosphere composition,
additives, food structure
competition among organisms*

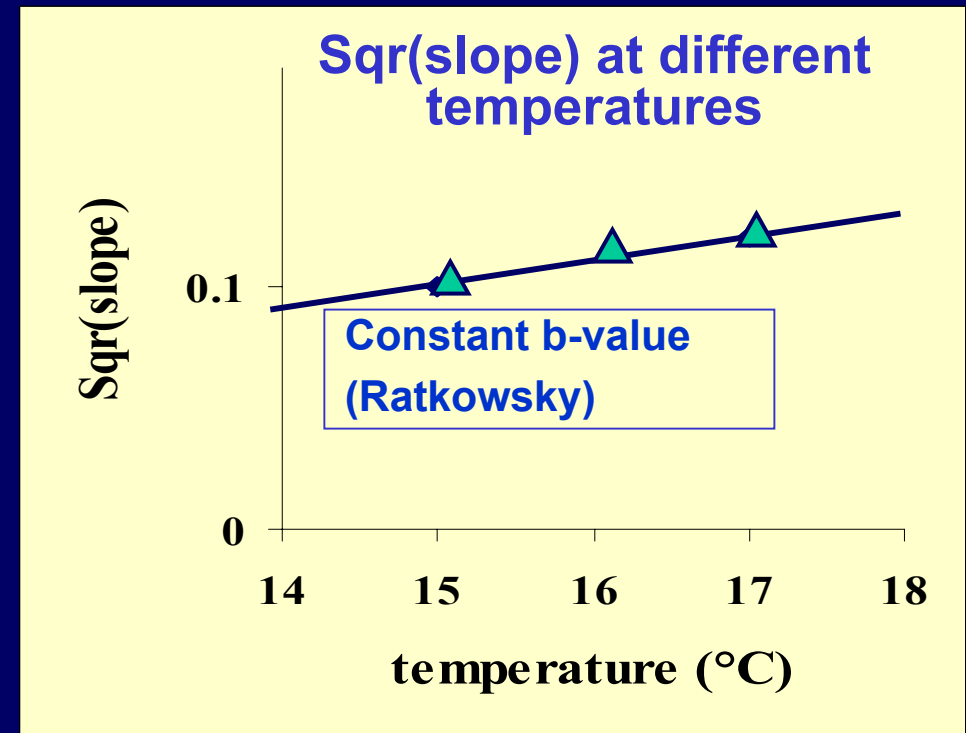
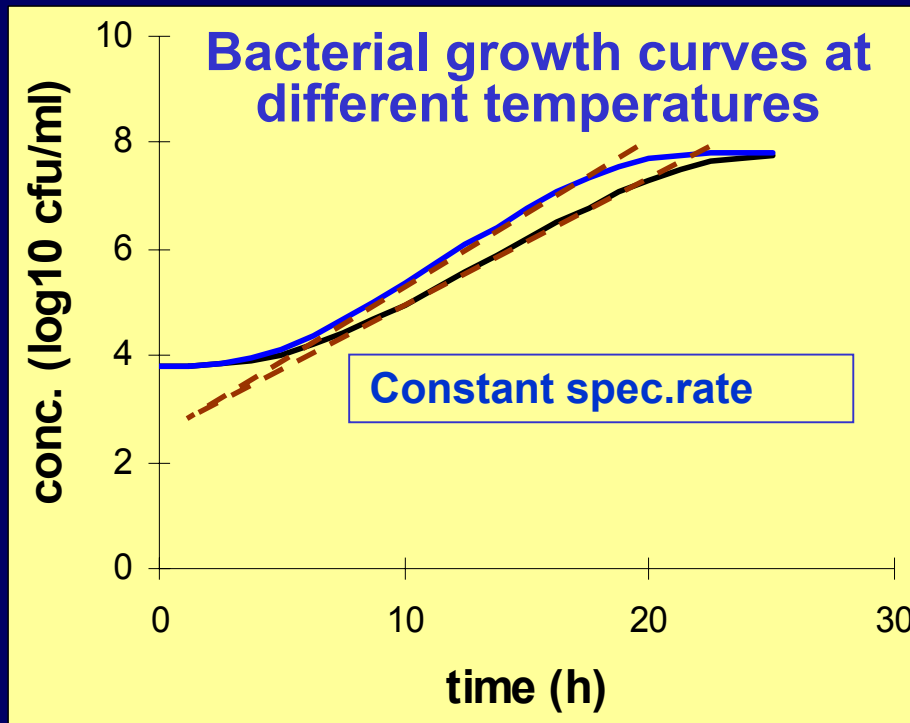
*growth / no growth,
probability of growth,
lag time, doubling time,
time to reach a certain conc.
full growth / survival curves
(dynamic response)
metabolic production*

“Classical” Predictive Models I.

Linear thermal death model

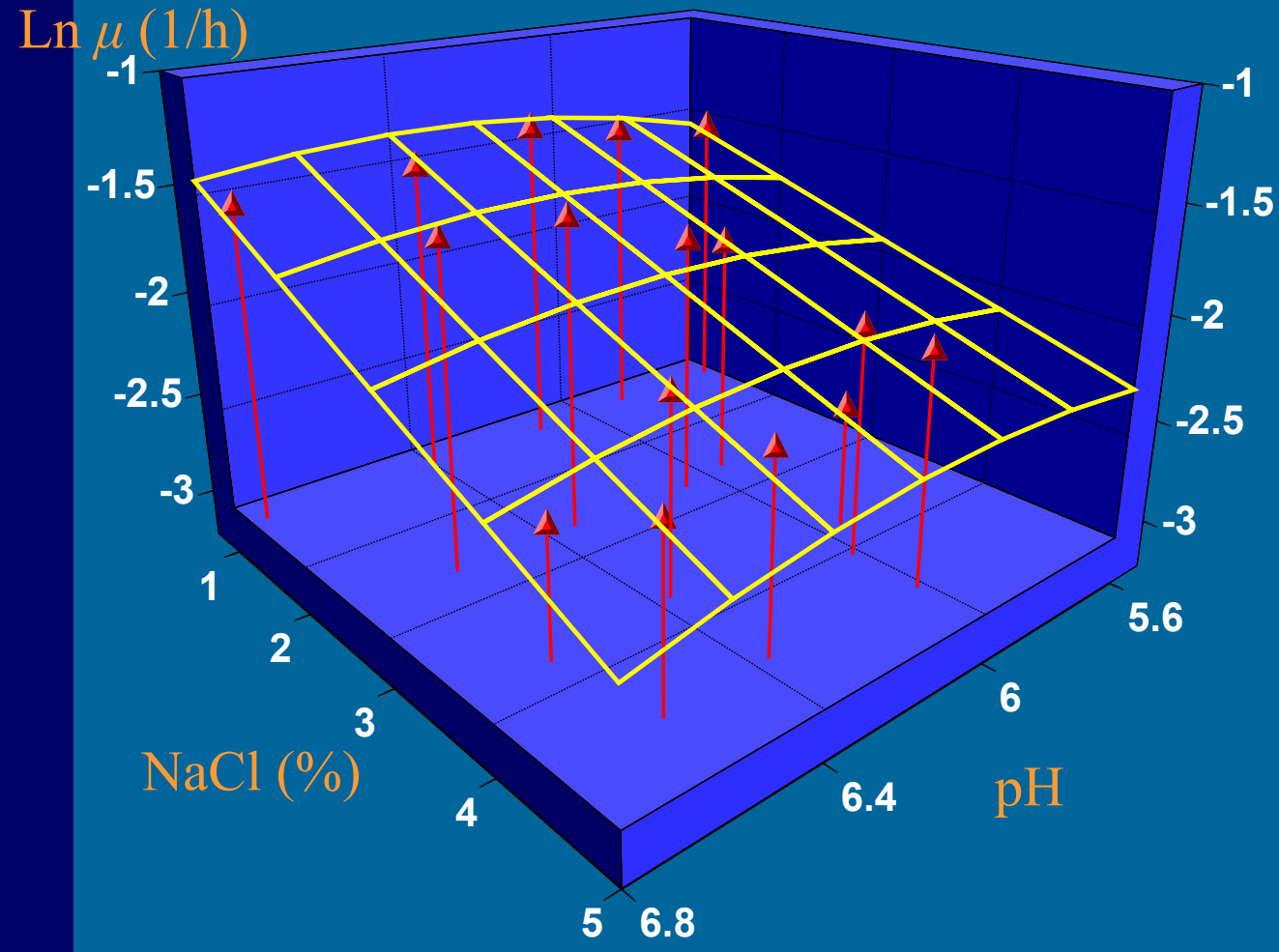


“Classical” Predictive Models II.



Growth model analogous to the linear death model.

Response surface fitted to the logarithm of observed growth rates



Fitting a quadratic multivariate polynomial.

Data: *Salmonellae* at 15°C (Gibson *et al*, 1988)

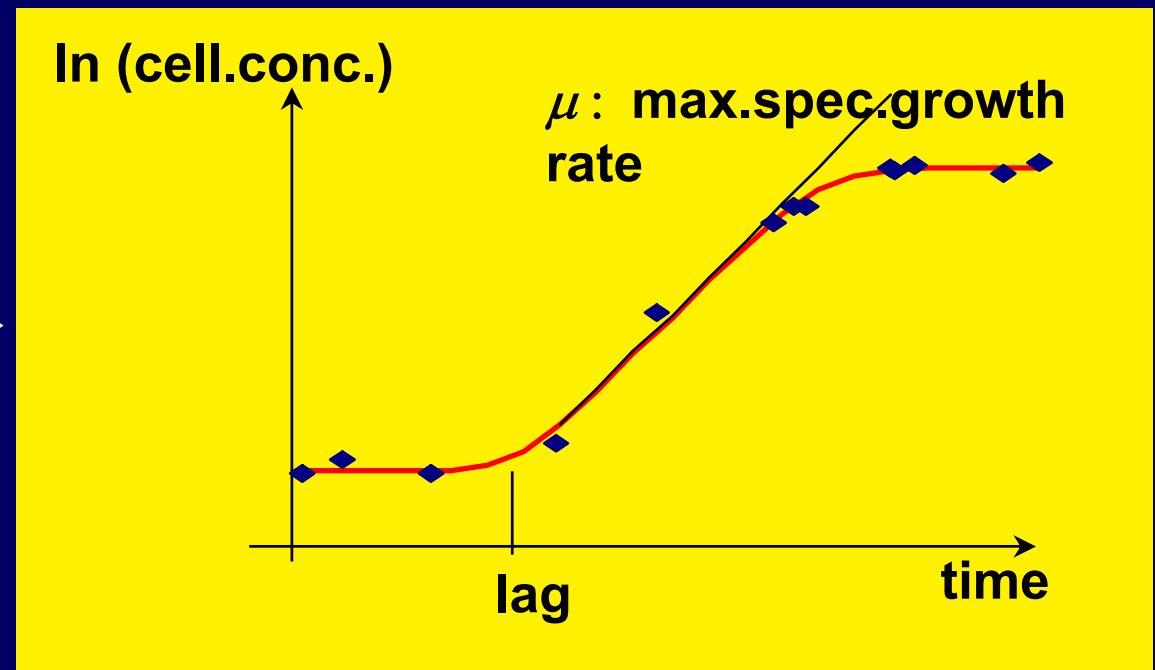
Predictive microbiology: Quantitative Microbial Ecology of Food

Environment

Temperature
pH
water availability
atmosphere
preservatives
competition
food structure
etc .



Microbial kinetics (Response)



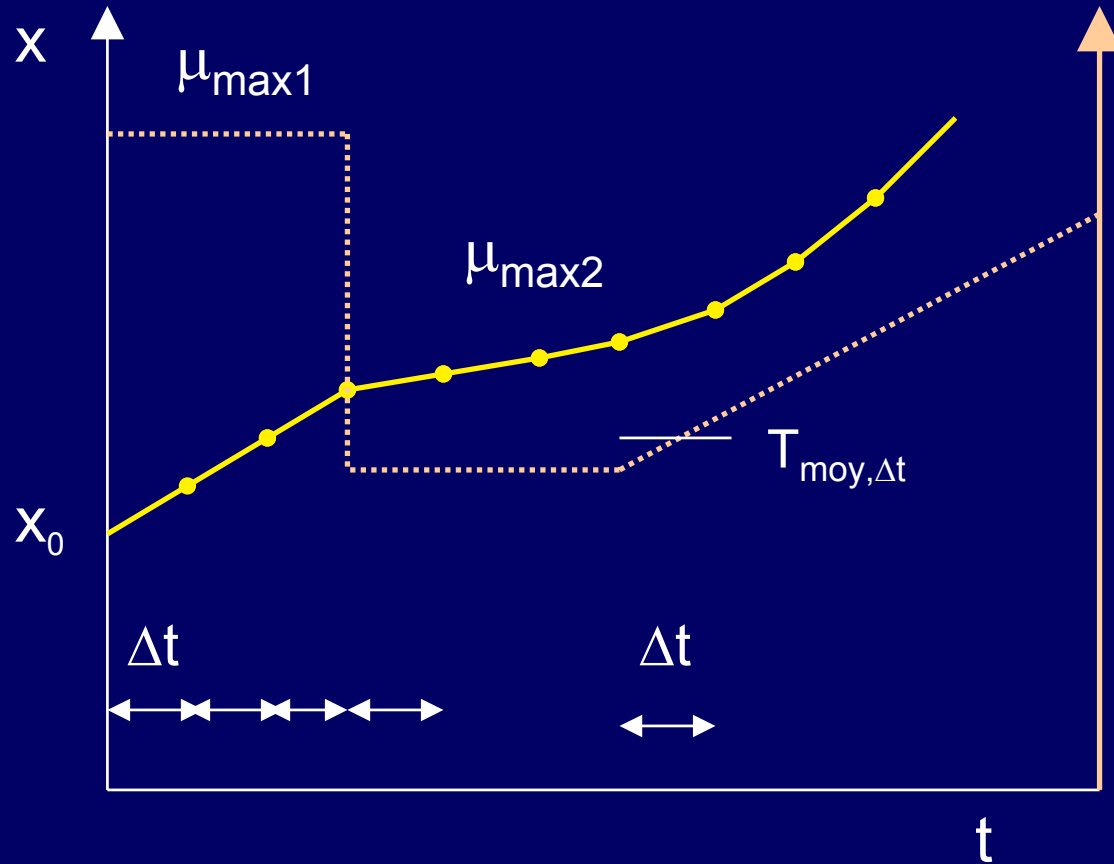
Bacterial curve with the main parameters

Dynamic conditions

$$\frac{dy}{dt} = \mu_{\max}(T(t))$$

$$\mu_{\max} = b(T(t) - T_{\min})^2$$

$$\Delta y = b(T(t) - T_{\min})^2 \Delta t$$



ComBase Consortium, 2003



FSA, UK



**US Department of
Agriculture,
Agricultural
Research Service**



**Eastern Regional Research Center
Wyndmoor, PA, USA**



**Institute of Food
Research, Norwich, UK**



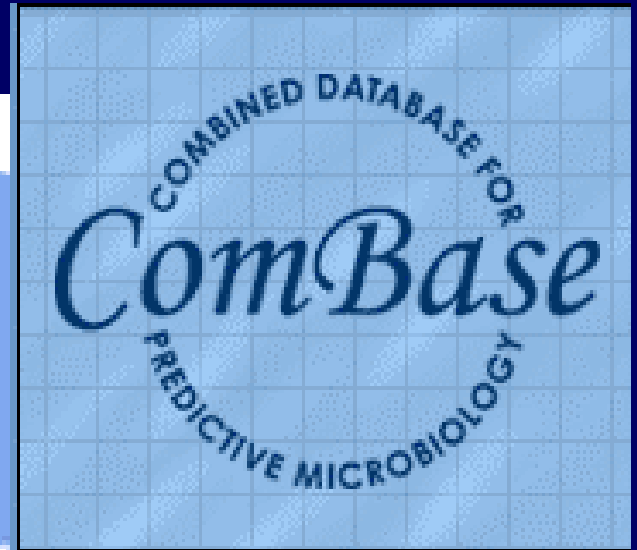
**e-ComBase: 2yrs Accompanying Measures project to
populate ComBase by data from Supporting Partners**

EC Quality of Life and Management of Living Resources (QoL)
Key Action 1 - Food, Nutrition and Health

e-COMBASE SUPPORTING INSTITUTES
contributing to ca 20% of ComBase

SUPPORT. One record = one response (generally logcount curve) to one combination of conditions

Dept. Food Micro.; Univ. Cordoba, Spain	Listeria in vegetables; ca 500 rec.
Dept of Ind. Microbiol., Univ. Complutense	OD-derived rates of spoilage organisms; ca 1000 rec.
Budapest University, Hungary.	Listeria growth in presence of LAB; ca 50 rec.
<u>Dpt Nutr. y Brom. III. Univ. Complutense, Spain</u>	Pathogens, spoilage; mainly in MA; viable count curves and doubling times measured by OD; ca 2000 rec.
Danish Institute of Fisheries Research	Spoilage organisms in broth and seafood; ca 200 rec.
INRA, Avignon. France	Growth and survival of various pathogens; ca 400 rec.
<u>Agricultural University of Athens. Greece</u>	Spoilage organisms, mainly in olives; ca 2000 rec.
Technical University of Bratislava, Slovakia	Pathogens and spoilage, in broth and milk ca 50 rec.
Public Health Laboratory Services - UK	Pathogens at low water activity; ca 100 rec.
Metropolitan University. London UK	Spoilage organisms in broth and food; ca 500 rec.
University of Reading. UK	Pathogens in broth, inactivation and survival; ca 100 rec.
Unilever Research Sharnbrook. UK	Pathogens in food; ca 200 rec.
Campden and Chorlywood FRA. UK	Spoilage organisms; ca 500 rec.
TNO, Holland	Lactic acid bacteria in broth and food; ca 500 rec.
Veterinary University of Vienna, Austria	Spoilage organisms in broth and food; ca 200 rec.
<u>Instituto Zooprofilattico Sperimentale Brescia, Italy</u>	In cheese and salami; ca 1500 rec.



The screenshot shows the ComBase website with a blue header and a light blue main content area. A navigation menu is on the left, and a world map with partner logos is at the bottom. The browser's address bar and status bar are visible at the very bottom.

ComBase HOME Contact us

A COMBINED DATABASE FOR PREDICTIVE MICROBIOLOGY

HOME

WELCOME TO COMBASE

ComBase is a free web-based database of food microbiology data. The dataset consists of thousands of microbial growth and survival curves that are the basis for numerous microbial models used by industry, academia and government regulatory agencies.

The *ComBase* database is a major international initiative to coordinate the collection and dissemination of food microbiology data. It is maintained by the ComBase Consortium, established in London on the 5th of May, 2003, as a collaboration between the **Food Standards Agency** and the **Institute of Food Research**, UK, and the **USDA Agricultural Research Service** and its **Eastern Regional Research Center**, USA.

USDA **ARS** **FOOD STANDARDS AGENCY**
US DEPARTMENT OF AGRICULTURE AGRICULTURAL RESEARCH SERVICE

ERRC **ifir** **INSTITUTE OF FOOD RESEARCH**
EASTERN REGIONAL RESEARCH CENTER

Done Internet

Search criteria and results from the ComBase Internet browser

File Number 1 of 28 files returned

Record ID Information

Organism: Environment:

Maximum Rate ($\log_{10}(\text{CFU/h})$): Temperature: °C pH:

a_{w} :

Doubling time(growth) or D-value(survival) (h):

Source:

Conditions:

Further specifications:

ComBase ID = EcBook16_136_1an

Time (h)	logc
0.00	3.090
24.00	3.000
48.00	4.520
72.00	5.350
96.00	6.900
99.00	6.980
103.00	7.370
168.00	9.260
174.00	9.420
192.00	9.100

Details:

Search Criteria

Organism: Temperature °C from to

Environment: pH from to

Conditions: Water activity from to

Source:

Growth Predictor: successor of Food MicroModel

(<http://www.ifr.ac.uk/Safety/GrowthPredictor>)

Growth Predictor

Environment
 Temperature (C)
 pH
 NaCl(%) Aw
 Factor4: CO2(%)
 Initial logc. Phys. state
 Obs.time (h)
 For default values, leave these boxes empty

Escherichia coli with CO2(%) In broth

time(h)	conc.(log cells/g)
0.00	3.00
3.53	3.07
7.07	3.31
10.60	3.78
14.13	4.39
17.67	5.05
21.20	5.71
24.73	6.38
28.27	7.03
31.80	7.63

Prediction

Max.rate (log conc/h)
0.1897

Doubling time (h)
1.59

Model region CO2(%) max 100

	Temp (C)	pH	Aw
min	10	4.5	0.961
max	30	7	1

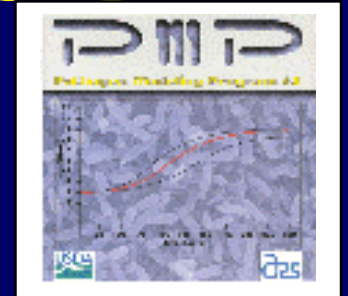
Predict **Exit** **Zoom In** **Help**

Growth model: Baranyi, J. and Roberts, T. A. (1994): A dynamic approach to predicting bacterial growth in food. International Journal

Currently available predictors

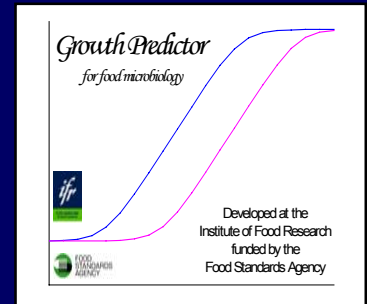
Pathogen Modeling Program (USDA-ARS ERRC, US)

<http://www.arserrc.gov/mfs/pathogen.htm>



Growth Predictor (FSA-IFR, UK), the successor of Food MicroModel

<http://www.ifr.ac.uk/Safety/GrowthPredictor>



Forecast (Campden and Chorleywood, UK):

+44 (0)1386 842071 (Buro service, not software).

Seafood Spoilage Predictor (Institute of Fisheries Research, Denmark):

www.dfu.min.dk/micro/ssp

Food Spoilage Predictor (University of Tasmania, Australia):

www.hdl.com.au/html/body_fsp.htm



File Number 1 of 28 files returned

Record ID EcBook16_136 Information

Organism: Escherichia coli Environment: culture medium

Temperature 12 °C pH 7
 a_w 0.989

rate (log conc/h): 0.045

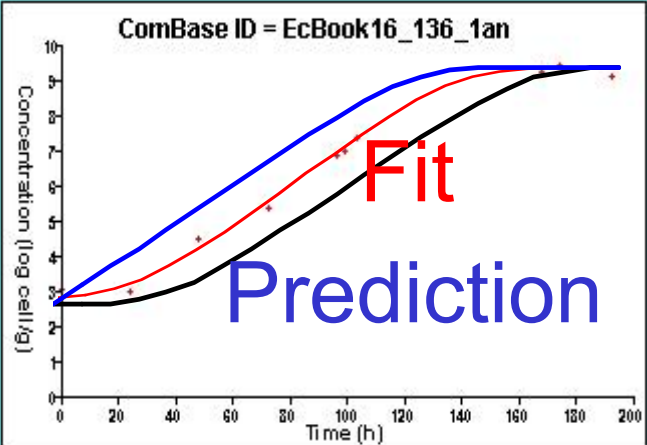
lag (h) : 15

Source: Buchanan(et al.), 1994: Expansion of response surface models for the growth of Escherichia coli O157:H7 to

Conditions: Shaken. Anaerobic. N_2. NaCl(%):2.

Further specifications: In: BHI, Strain(s): 933 A9218-C1 45753-35, Serotype(s): O157:H7. Mixed culture of strains produced the response. Measurement by colony counts.

Details: Strains: Escherichia coli O157:H7 strains: 933, 45753-35, and A9218-C1. Inoculum: Stock cultures were maintained in BHI broth stored at 4C and transferred monthly. Starter cultures were prepared by adding 0.1 ml of stock cultures to 50 ml of BHI broth and incubating on a rotary shaker (150 rpm) for 18-20 h at 37C. A 1.0-ml portion of each starter culture was transferred to a tube containing 7.0 ml of peptone water. Additional dilutions were made to



Time (h)	logc
0.00	3.090
24.00	3.000
48.00	4.520
72.00	5.350
96.00	6.900
99.00	6.980
103.00	7.370
168.00	9.260
174.00	9.420
192.00	9.100

Search Criteria

Organism: Escherichia coli Temperature °C from 8 to 15

Environment: (In broth or any food) pH from 6 to 7

Conditions: anaerobic Water activity from 0.01 to 1

Source: All

Lag:

Depends on the “work to be done” during lag (uncertainty).

Typical lag is predicted via typical “work to be done”