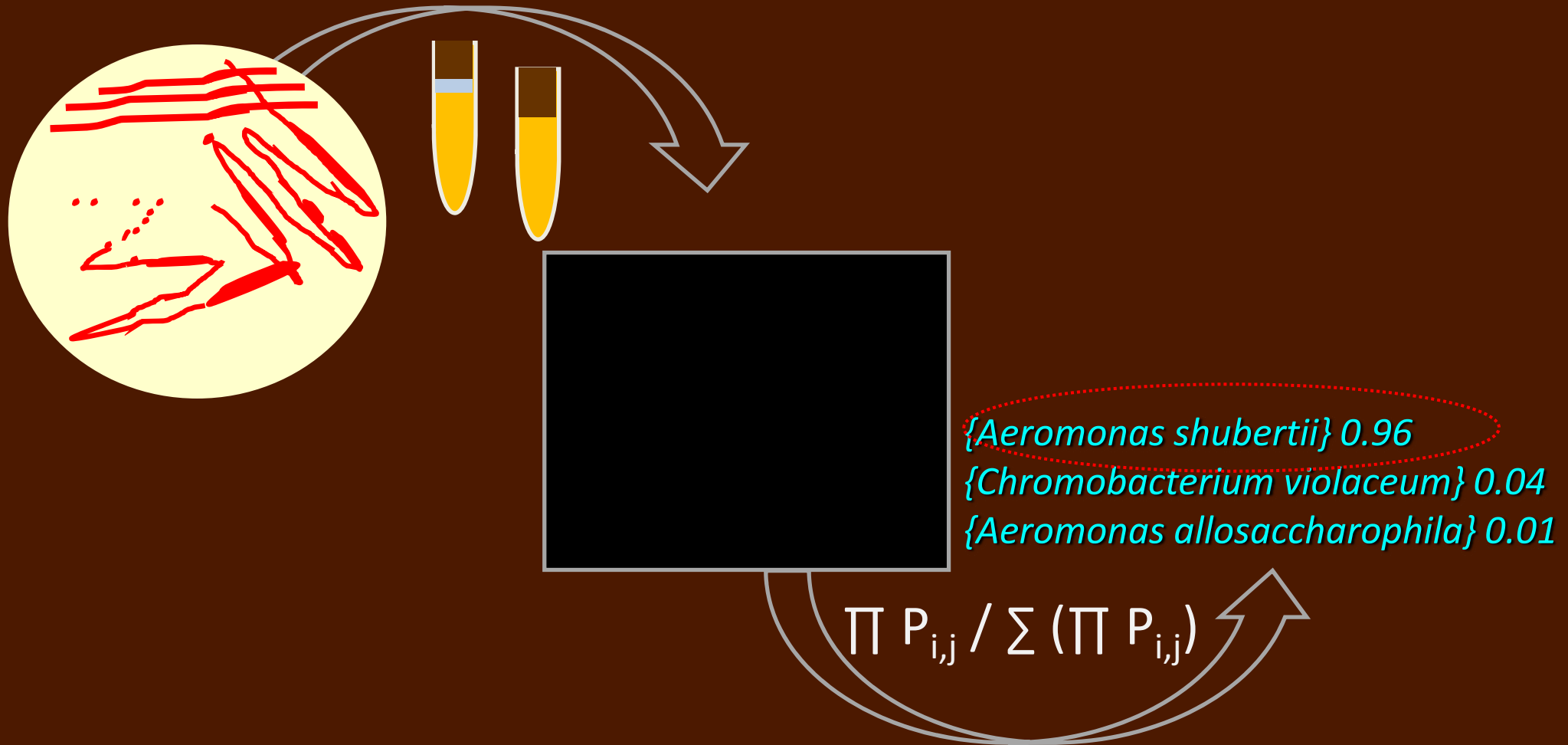


Bacteria Lot Identification Matrix Program

Jeff Bardwell, Diane Hartman



Bacteria Identification Steps:

1) Collect sample

2) Culture sample on agar

3) Isolate individual bacteria colonies

4a) Describe colony morphotype

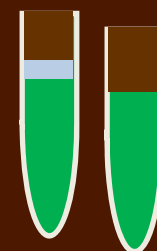
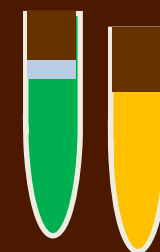
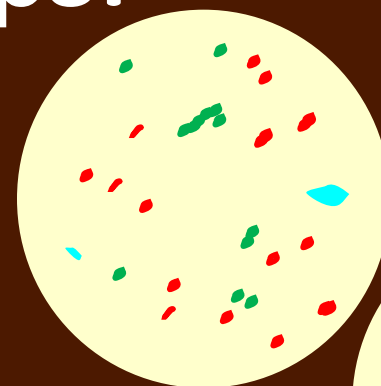
4b) Describe colony genotype

4c) Describe colony phenotype

5a) Construct flowchart







5b) Construct matrix

6) Compare unknown colony



	Trait 1	Trait 2	Trait 3	Trait 4
Taxon A				
Taxon B				
Taxon C				

Bacteria Identification Steps:

- 1) Collect sample 
- 2) Culture sample on agar 
- 3) Isolate individual bacteria colonies 
- 4a) Describe colony morphotype *Useful after identification*
- 4b) Describe colony genotype *16s RNA technology: \$\$\$??? []*
- 4c) Describe colony phenotype 
- 5a) Construct flowchart *Can't analyze or quantify test results*
- 5b) Construct matrix 
- 6) Compare unknown colony to prior data 

Bacteria Identification Steps:

- 1) Collect sample
- 2) Culture and isolate colonies on agar
- 3) Run phenotype tests on isolates
- 4) Use matrix to analyze phenotype trait results

	Trait 1	Trait 2	Trait 3	Trait 4
Taxon A	0.99	0.01	0.01	0.99
Taxon B	0.99	0.99	0.01	0.99
Taxon C	0.50	0.99	0.01	0.01

Probability Taxon X will score a positive test result for Trait x

	Trait 1	Trait 2	Trait 3	Trait 4
Results	+	+	-	+

Taxon B provides best match

Matrix Probability Analyses:

1) Additive probability

$$P = (x_1) (x_1) (x_3)$$

	Trait 1	Trait 2	Trait 3	Trait 4
Results	+	+	-	+

+ : x = probability

- : x = 1 - probability

	Trait 1	Trait 2	Trait 3	Trait 4
Taxon A	0.99	0.01	0.01	0.99
Taxon B	0.99	0.99	0.01	0.99
Taxon C	0.50	0.99	0.01	0.01

$$(0.99) (0.01) (1 - 0.01) (0.99) = 0.01$$

$$(0.99) (0.99) (1 - 0.01) (0.99) = 0.96$$

$$(0.50) (0.99) (1 - 0.01) (0.01) = 0.00$$

Matrix Probability Analyses:

1) Additive probability

2) Geometric mean

$$\Pi = [(x_1) (x_1) (x_3)]^{(1/n)}$$

	Trait 1	Trait 2	Trait 3	Trait 4
Results	+	+	-	+

+ : x = probability

- : x = 1 - probability

	Trait 1	Trait 2	Trait 3	Trait 4
Taxon A	0.99	0.01	0.01	0.99
Taxon B	0.99	0.99	0.01	0.99
Taxon C	0.50	0.99	0.01	0.01

$$[(0.99) (0.01) (1 - 0.01) (0.99)]^{(1/3)} = 0.22$$

$$[(0.99) (0.99) (1 - 0.01) (0.99)]^{(1/3)} = 0.99$$

$$[(0.50) (0.99) (1 - 0.01) (0.01)]^{(1/3)} = 0.10$$

Matrix Probability Analyses:

1) Additive probability

2) Geometric mean

3) Bayes theorem / Likelihood

$$P(\text{taxon}_i | \text{trait}) = P(\text{trait} | \text{taxon}_i) P(\text{taxon}_i) / \sum P(\text{trait} | \text{taxon}_i) P(\text{taxon}_i)$$

$$P(\text{taxon}_i) = \prod P_{i,j} / \sum (\prod P_{i,j})$$

	Trait 1	Trait 2	Trait 3	Trait 4
Results	+	+	-	+

+ : x = probability

- : x = 1 - probability

	Trait 1	Trait 2	Trait 3	Trait 4
Taxon A	0.99	0.01	0.01	0.99
Taxon B	0.99	0.99	0.01	0.99
Taxon C	0.50	0.99	0.01	0.01

$$(0.99) (0.01) (1 - 0.01) (0.99) = 0.01 \quad 0.01/0.97 = 0.01$$

$$(0.99) (0.99) (1 - 0.01) (0.99) = 0.96 \quad 0.96/0.97 = 0.99$$

$$(0.50) (0.99) (1 - 0.01) (0.01) = 0.00 \quad 0.00/0.97 = 0.00$$

$$\Sigma = 0.97$$

$$\Sigma = 1.00$$

Lapage 1974, Wilcox 1980

BACTERIA GROUP







- ☒ Gram Negative Facultative Anaerobe Bacillus
- ☐ Gram Negative Aerobe Bacillus
- ☐ Gram Negative Aerobe Coccus
- ☐ Gram Positive Facultative Anaerobe Bacillus
- ☐ Gram Positive Aerobe Bacillus
- ☐ Gram Positive Facultative Anaerobe Coccus
- ☐ Gram Positive Aerobe Coccus
- ☐ Spore Forming Bacillus and Coccus

GROWTH FACTORS

- ☒ None
- ☐ Blood
- ☐ Salt
- ☐ Yeast

SAMPLE ANALYSIS

- ☐ Geometric Mean
- ☒ Bayes Theorem

Marine	Vegetation
1.00	1.00
	
Freshwater	Clinical
1.00	1.00
	
Soil	Fecal
1.00	1.00
	

IDENTIFICATION SCORE

Matrix Selection:

B. L. I. M. P.

Bacteria Lot Identification Matrix Program

Instructions
Database
Procedure
Analysis

GRAM STAIN:

SHAPE:

METABOLISM:

ENDOSPORE:

CATALASE:

OXIDASE:

SALINITY RANGE:

TEMP RANGE:

MOTILITY:

HYDROGEN SULFIDE:

INDOLE:

CITRATE:

NO3->NO2:

NO3->NO2->N2:

GLUCOSE FERM:

GLUCOSE GAS:

L-ARABINOSE FERM:

DULCITOL FERM:

GLYCEROL FERM:

MYO-INOSITOL FERM:

LACTOSE FERM:

MALTOS FERM:

D-MANNITOL FERM:

D-MANNOSE FERM:

MELIBIOSE FERM:

RAFFINOSE FERM:

L-RHAMNOSE FERM:

SALICIN FERM:

D-SORBITOL FERM:

SUCROSE FERM:

TREHALOSE FERM:

D-XYLOSE FERM:

ARGININE DIHYDROLASE:

LYSINE DECARBOXYLASE:

ORNITHINE DECARBOXYLASE:

PHENYLALANINE DEAMINASE:

ESCULIN HYDROLYSIS:

GELATIN HYDROLYSIS:

UREA HYDROLYSIS:

ONPG:

VOGES-PROSKAUER:

BACTERIA GROUP

☒ Gram Negative Facultative Anaerobe Bacillus
☐ Gram Negative Aerobe Bacillus
☐ Gram Negative Aerobe Coccus
☐ Gram Positive Facultative Anaerobe Bacillus
☐ Gram Positive Aerobe Bacillus
☐ Gram Positive Facultative Anaerobe Coccus
☐ Gram Positive Aerobe Coccus
☐ Spore Forming Bacillus and Coccus

GROWTH FACTORS

☒ None
☐ Blood
☐ Salt
☐ Yeast

Submit

SAMPLE ANALYSIS

☐ Geometric Mean
☒ Bayes Theorem

Marine	Vegetation
1.00	1.00
Freshwater	Clinical
1.00	1.00
Soil	Fecal
1.00	1.00

IDENTIFICATION SCORE

Identify
Reset

NEGFACBAC:

nonfastidious cat – oxi – endo – glu + (22)

Xenorhabdus 22

nonfastidious cat + oxi – endo – nit1 – glu + (33)

Brennaria 4, Erwinia 9, Klebsiella 6, Pantoea 2,
Photorhabdus 1, Yersinia 11, Vibrio 1

nonfastidious cat + oxi – endo – nit1 + glu + (117)

Budvicia 1, Buttiauxella 1, Cedecea 5, Citrobacter 11,
Edwardsiella 3, Enterobacter 13, Erwinia 1, Escheria 6,
Ewingella 1, Hafnia 1, Klebsiella 6, Kluyvera 2, Lecleria 1,
Leminorella 2, Moellerella 1, Morganella 1, Pantoea 3,
Pectobacterium 7, Pragia 1, Proteus 5, Providencia 5,
Rahnella 1, Raoultella 3, Salmonella 7, Serratia 11, Shigella
4, Tatumella 1, Trabulsiella 1, Yersinia 11, Yokenella 1

nonfastidious cat + oxi + endo – nit1+ glu + (27)

Aeromonas 18, Chromobacterium 2, Plesiomonas 1, Vibrio 6

salt cat + oxi + endo – nit1+ glu + (103)

Colwellia 5, Listonella 3, Photobacterium 12, Shewanella 9,
Vibrio 74

yeast cat + oxi – endo – glu + (3)

Obesumbacterium 2, Zymomonas 1

blood cat – oxi – endo – glu +

Gardnerella, Streptobacillus

blood cat – oxi + endo – nit1 + glu – (1)

Eikenella 1

blood cat – oxi + endo – nit1 – glu + (1)

Cardiobacterium 1

blood cat + oxi + endo – nit1+ glu +

Actinobacillus, Aggregatibacter,
Haemophilus, Mannheimia, Pasteurella

B. L. I. M. P.

Bacteria Lot Identification Matrix Program

Instructions

Database

Procedure

Analysis

GRAM STAIN:

+

--

?

SHAPE:

bacillus

coccus

spirillus

?

METABOLISM:

aerobe

fac anaerobe

?

ENDOSPORE:

+

--

?

CATALASE:

+

--

?

OXIDASE:

+

--

?

SALINITY RANGE:

<6%

>6%

?

TEMP RANGE:

25C

35C

45C

?

MOTILITY:

+

--

?

HYDROGEN SULFIDE:

+

--

?

INDOLE:

+

--

?

CITRATE:

+

--

?

NO3->NO2:

+

--

?

NO3->NO2->N2:

+

--

?

GLUCOSE FERM:

+

--

?

GLUCOSE GAS:

+

--

?

L-ARABINOSE FERM:

+

--

?

DULCITOL FERM:

+

--

?

GLYCEROL FERM:

+

--

?

MYO-INOSITOL FERM:

+

--

?

LACTOSE FERM:

+

--

?

MALTOSE FERM:

+

--

?

D-MANNITOL FERM:

+

--

?

D-MANNOSE FERM:

+

--

?

MELIBIOSE FERM:

+

--

?

RAFFINOSE FERM:

+

--

?

L-RHAMNOSE FERM:

+

--

?

SALICIN FERM:

+

--

?

D-SORBITOL FERM:

+

--

?

SUCROSE FERM:

+

--

?

TREHALOSE FERM:

+

--

?

D-XYLOSE FERM:

+

--

?

ARGININE DIHYDROLASE:

+

--

?

LYSINE DECARBOXYLASE:

+

--

?

ORNITHINE DECARBOXYLASE:

+

--

?

PHENYLALANINE DEAMINASE:

+

--

?

ESCULIN HYDROLYSIS:

+

--

?

GELATIN HYDROLYSIS:

+

--

?

UREA HYDROLYSIS:

+

--

?

ONPG:

+

--

?

VOGES-PROSKAUER:

+

--

?

Identify

Reset

BACTERIA GROUP

☒ Gram Negative Facultative Anaerobe Bacillus

☐ Gram Negative Aerobe Bacillus

☐ Gram Negative Aerobe Coccus

☐ Gram Positive Facultative Anaerobe Bacillus

☐ Gram Positive Aerobe Bacillus

☐ Gram Positive Facultative Anaerobe Coccus

☐ Gram Positive Aerobe Coccus

☐ Spore Forming Bacillus and Coccus

GROWTH FACTORS

☒ None

☐ Blood

☐ Salt

☐ Yeast

Submit

SAMPLE ANALYSIS

☐ Geometric Mean

☒ Bayes Theorem

Marine	Vegetation
1.00	1.00
Freshwater	Clinical
1.00	1.00
Soil	Fecal
1.00	1.00

Search

IDENTIFICATION SCORE

{Citrobacter youngae} 0.45

{Citrobacter freundii} 0.33

{Citrobacter gillenii} 0.17

NEGFACEBAC

nonfastidious cat + oxi – endo – nit1 + glu + (117)

Budvicia 1, Buttiauxella 1, Cedecea 5, Citrobacter 11, Edwardsiella 3, Enterobacter 13, Escheria 6, Ewingella 1, Hafnia 1, Klebsiella 6, Kluyvera 2, Lecleria 1, Leminorella 2, Moellerella 1, Morganella 1, Pantoea 3, Pectobacterium 7, Pragia 1, Proteus 5, Providencia 5, Rahnella 1, Raoultella 3, Salmonella 7, Serratia 11, Shigella 4, Tatumella 1, Trabulsiella 1, Yersinia 11, Yokenella 1

B. L. I. M. P.

Bacteria Lot Identification Matrix Program

Instructions
Database
Procedure
Analysis

GRAM STAIN: + -- ?
SHAPE: bacillus coccus spirillus ?
METABOLISM: aerobe fac anaerobe ?
ENDOSPORE: + -- ?
CATALASE: + -- ?
OXIDASE: + -- ?
SALINITY RANGE: <6% >6% ?
TEMP RANGE: 25C 35C 45C ?
MOTILITY: + -- ?
HYDROGEN SULFIDE: + -- ?
INDOLE: + -- ?
CITRATE: + -- ?
NO3->NO2: + -- ?
NO3->NO2->N2: + -- ?
GLUCOSE FERM: + -- ?
GLUCOSE GAS: + -- ?

L-ARABINOSE FERM: + -- ?
DULCITOL FERM: + -- ?
GLYCEROL FERM: + -- ?
MYO-INOSITOL FERM: + -- ?
LACTOSE FERM: + -- ?
MALTOSE FERM: + -- ?
D-MANNITOL FERM: + -- ?
D-MANNOSE FERM: + -- ?
MELIBIOSE FERM: + -- ?
RAFFINOSE FERM: + -- ?
L-RHAMNOSE FERM: + -- ?
SALICIN FERM: + -- ?
D-SORBITOL FERM: + -- ?
SUCROSE FERM: + -- ?
TREHALOSE FERM: + -- ?
D-XYLOSE FERM: + -- ?

ARGININE DIHYDROLASE: + -- ?
LYSINE DECARBOXYLASE: + -- ?
ORNITHINE DECARBOXYLASE: + -- ?
PHENYLALANINE DEAMINASE: + -- ?
ESCULIN HYDROLYSIS: + -- ?
GELATIN HYDROLYSIS: + -- ?
UREA HYDROLYSIS: + -- ?
ONPG: + -- ?
VOGES-PROSKAUER: + -- ?

BACTERIA GROUP

☒ Gram Negative Facultative Anaerobe Bacillus
☐ Gram Negative Aerobe Bacillus
☐ Gram Negative Aerobe Coccus
☐ Gram Positive Facultative Anaerobe Bacillus
☐ Gram Positive Aerobe Bacillus
☐ Gram Positive Facultative Anaerobe Coccus
☐ Gram Positive Aerobe Coccus
☐ Spore Forming Bacillus and Coccus

GROWTH FACTORS

☒ None
☐ Blood
☐ Salt
☐ Yeast

Submit

SAMPLE ANALYSIS

☐ Geometric Mean
☒ Bayes Theorem

Marine	Vegetation
1.00	1.00
Freshwater	Clinical
1.00	1.00
Soil	Fecal
1.00	1.00

IDENTIFICATION SCORE

{Citrobacter freundii} 0.97
{Citrobacter gillenii} 0.02

Identify

Reset

NEGFACEBAC

nonfastidious cat + oxi – endo – nit1 + glu + (117)

Budvicia 1, Buttiauxella 1, Cedecea 5, Citrobacter 11, Edwardsiella 3, Enterobacter 13, Escheria 6, Ewingella 1, Hafnia 1, Klebsiella 6, Kluyvera 2, Lecleria 1, Leminorella 2, Moellerella 1, Morganella 1, Pantoea 3, Pectobacterium 7, Pragia 1, Proteus 5, Providencia 5, Rahnella 1, Raoultella 3, Salmonella 7, Serratia 11, Shigella 4, Tatumella 1, Trabulsiella 1, Yersinia 11, Yokenella 1

Search Engine:

B. L. I. M. P.

Bacteria Lot Identification Matrix Program

[Instructions](#)
[Database](#)
[Procedure](#)
[Analysis](#)

GRAM STAIN: ☐+ ☐- ☐?

SHAPE: ☐bacillus ☐coccus ☐spirillus ☐?

METABOLISM: ☐aerobe ☐fac anaerobe ☐?

ENDOSPORE: ☐+ ☐- ☐?

CATALASE: ☐+ ☐- ☐?

OXIDASE: ☐+ ☐- ☐?

SALINITY RANGE: ☐<6% ☐ >6% ☐?

TEMP RANGE: ☐25C ☐35C ☐45C ☐?

MOTILITY: ☐+ ☐- ☐?

HYDROGEN SULFIDE: ☐+ ☐- ☐?

INDOLE: ☐+ ☐- ☐?

CITRATE: ☐+ ☐- ☐?

NO3->NO2: ☐+ ☐- ☐?

NO3->NO2->N2: ☐+ ☐- ☐?

GLUCOSE FERM: ☐+ ☐- ☐?

GLUCOSE GAS: ☐+ ☐- ☐?

L-ARABINOSE FERM: ☐+ ☐- ☐?

DULCITOL FERM: ☐+ ☐- ☐?

GLYCEROL FERM: ☐+ ☐- ☐?

MYO-INOSITOL FERM: ☐+ ☐- ☐?

LACTOSE FERM: ☐+ ☐- ☐?

MALTOSE FERM: ☐+ ☐- ☐?

D-MANNITOL FERM: ☐+ ☐- ☐?

D-MANNOSE FERM: ☐+ ☐- ☐?

MELIBIOSE FERM: ☐+ ☐- ☐?

RAFFINOSE FERM: ☐+ ☐- ☐?

L-RHAMNOSE FERM: ☐+ ☐- ☐?

SALICIN FERM: ☐+ ☐- ☐?

D-SORBITOL FERM: ☐+ ☐- ☐?

SUCROSE FERM: ☐+ ☐- ☐?

TREHALOSE FERM: ☐+ ☐- ☐?

D-XYLOSE FERM: ☐+ ☐- ☐?

ARGININE DIHYDROLASE: ☐+ ☐- ☐?

LYSINE DECARBOXYLASE: ☐+ ☐- ☐?

ORNITHINE DECARBOXYLASE: ☐+ ☐- ☐?

PHENYLALANINE DEAMINASE: ☐+ ☐- ☐?

ESCULIN HYDROLYSIS: ☐+ ☐- ☐?

GELATIN HYDROLYSIS: ☐+ ☐- ☐?

UREA HYDROLYSIS: ☐+ ☐- ☐?

ONPG: ☐+ ☐- ☐?

VOGES-PROSKAUER: ☐+ ☐- ☐?

BACTERIA GROUP

☒ Gram Negative Facultative Anaerobe Bacillus

☐ Gram Negative Aerobe Bacillus

☐ Gram Negative Aerobe Coccus

☐ Gram Positive Facultative Anaerobe Bacillus

☐ Gram Positive Aerobe Bacillus

☐ Gram Positive Facultative Anaerobe Coccus

☐ Gram Positive Aerobe Coccus

☐ Spore Forming Bacillus and Coccus

GROWTH FACTORS

☒ None

☐ Blood

☐ Salt

☐ Yeast

Submit

SAMPLE ANALYSIS

☐ Geometric Mean

☒ Bayes Theorem

Marine	1.00	Vegetation	1.00
Freshwater	1.00	Clinical	1.00
Soil	1.00	Fecal	1.00

Aeromonas schubertii

Search

IDENTIFICATION SCORE

Identify

Reset

Sample Bias:

B. L. I. M. P. Bacteria Lot Identification Matrix Program

Instructions Database Procedure Analysis

GRAM STAIN:
 SHAPE:
 METABOLISM:
 ENDOSPORE:
 CATALASE:
 OXIDASE:
 SALINITY RANGE:
 TEMP RANGE:
 MOTILITY:
 HYDROGEN SULFIDE:
 INDOLE:
 CITRATE:
 NO3->NO2:
 NO3->NO2->N2:
 GLUCOSE FERM:
 GLUCOSE GAS:
 L-ARABINOSE FERM:
 DULCITOL FERM:
 GLYCEROL FERM:
 MYO-INOSITOL FERM:
 LACTOSE FERM:
 MALTOS FERM:
 D-MANNITOL FERM:
 D-MANNOSE FERM:
 MELIBIOSE FERM:
 RAFFINOSE FERM:
 L-RHAMNOSE FERM:
 SALICIN FERM:
 D-SORBITOL FERM:
 SUCROSE FERM:
 TREHALOSE FERM:
 D-XYLOSE FERM:
 ARGININE DIHYDROLASE:
 LYSINE DECARBOXYLASE:
 ORNITHINE DECARBOXYLASE:
 PHENYLALANINE DEAMINASE:
 ESCULIN HYDROLYSIS:
 GELATIN HYDROLYSIS:
 UREA HYDROLYSIS:
 ONPG:
 VOGES-PROSKAUER:

BACTERIA GROUP

☒ Gram Negative Facultative Anaerobe Bacillus
☐ Gram Negative Aerobe Bacillus
☐ Gram Negative Aerobe Coccus
☐ Gram Positive Facultative Anaerobe Bacillus
☐ Gram Positive Aerobe Bacillus
☐ Gram Positive Facultative Anaerobe Coccus
☐ Gram Positive Aerobe Coccus
☐ Spore Forming Bacillus and Coccus

GROWTH FACTORS

☒ None ☐ Blood ☐ Salt ☐ Yeast

SAMPLE ANALYSIS

☐ Geometric Mean ☒ Bayes Theorem

	Marine	Vegetation
	1.00	1.00
Freshwater	1.00	1.00
Soil	1.00	1.00

IDENTIFICATION SCORE

{Erwinia ananas} 0.50
 {Photorhabdus (Xenorhabdus) luminescens} 0.22
 {Vibrio metschnikovii} 0.04

NEGFACBAC

nonfastidious cat + oxi – endo – nit1 – glu + (33)

Brennaria 4, Erwinia 9, Klebsiella 6, Pantoea 2, Photorhabdus 1, Yersinia 11, Vibrio 1

Sample Bias:

B. L. I. M. P. Bacteria Lot Identification Matrix Program

Instructions Database Procedure Analysis

GRAM STAIN: **SHAPE:** **METABOLISM:** **ENDOSPORE:** **CATALASE:** **OXIDASE:** **SALINITY RANGE:** **TEMP RANGE:** **MOTILITY:** **HYDROGEN SULFIDE:** **INDOLE:** **CITRATE:** **NO3->NO2:** **NO3->NO2->N2:** **GLUCOSE FERM:** **GLUCOSE GAS:** **L-ARABINOSE FERM:** **DULCITOL FERM:** **GLYCEROL FERM:** **MYO-INOSITOL FERM:** **LACTOSE FERM:** **MALTOSE FERM:** **D-MANNITOL FERM:** **D-MANNOSE FERM:** **MELIBIOSE FERM:** **RAFFINOSE FERM:** **L-RHAMNOSE FERM:** **SALICIN FERM:** **D-SORBITOL FERM:** **SUCROSE FERM:** **TREHALOSE FERM:** **D-XYLOSE FERM:** **ARGININE DIHYDROLASE:** **LYSINE DECARBOXYLASE:** **ORNITHINE DECARBOXYLASE:** **PHENYLALANINE DEAMINASE:** **ESCULIN HYDROLYSIS:** **GELATIN HYDROLYSIS:** **UREA HYDROLYSIS:** **ONPG:** **VOGES-PROSKAUER:** **BACTERIA GROUP** ☒ Gram Negative Facultative Anaerobe Bacillus ☐ Gram Negative Aerobe Bacillus ☐ Gram Negative Aerobe Coccus ☐ Gram Positive Facultative Anaerobe Bacillus ☐ Gram Positive Aerobe Bacillus ☐ Gram Positive Facultative Anaerobe Coccus ☐ Gram Positive Aerobe Coccus ☐ Spore Forming Bacillus and Coccus **GROWTH FACTORS** ☒ None ☐ Blood ☐ Salt ☐ Yeast **Submit** **SAMPLE ANALYSIS** ☐ Geometric Mean ☒ Bayes Theorem

Marine	Vegetation
1.00	0.01
Freshwater	Clinical
0.01	0.01
Soil	Fecal
0.01	0.01

Search **IDENTIFICATION SCORE** {Vibrio metschnikovii} 0.04 {Erwinia ananas} 0.01 {Brennaria (Erwinia) nigrifluens} 0.00 **Identify** **Reset**

NEGFACBAC













nonfastidious cat + oxi – endo – nit1 – glu + (33)

Brennaria 4, Erwinia 9, Klebsiella 6, Pantoea 2, Photorhabdus 1, Yersinia 11, Vibrio 1

BACTERIA GROUP

GROWTH FACTORS

SAMPLE ANALYSIS

Marine	1.00	Vegetation	1.00
			
Freshwater	1.00	Clinical	1.00
			
Soil	1.00	Fecal	1.00
			

IDENTIFICATION SCORE

Issues:

- 1) Built to accommodate, but does not yet include, obligate anaerobes, thermophiles, psychrophiles
- 2) Lot Identification Matrix anomalies
- 3) Does not account for multiple or esoteric growth factor requirements
- 4) Does not account for test result strength
- 5) Sample analyses can be expanded
- 6) Taxonomic shifts occur frequently
- 7) Taxonomic resolution: sp, subsp, biovar, strain

Acknowledgements:

Baylor University Department of Biology

Baylor University Research Committee

Vice Provost for Research at Baylor University

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Questions and Comments?

