Practical Applications of Artificial Intelligence in Clinical Microbiology

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October 14, 2021
Today’s Presenter: Dr. Daniel D. Rhoads, MD, D (ABMM), FCAP

- College of American Pathologists (CAP) Affiliations:
  - Vice Chair of College of American Pathologists Microbiology Committee
  - Fellow of College of American Pathologists (CAP)

- Section Head of Microbiology, Robert J. Tomsich Pathology & Laboratory Medicine Institute, Cleveland Clinic, United States

- Boards Certifications: Clinical Pathology and Medical Microbiology
Agenda

• Discuss machine learning
• Review examples using microbiological data
• Q&A
BLUF

The next decade is going to bring enormous changes to the practice of clinical microbiology because of the maturation of sequencing & digital imaging tools. Both of these applications require big data solutions, such as machine learning applications.
20th Century’s Data Model:

- Amount of data
- Human realization
21st Century’s Data Reality:
Objectives

• Give one definition of “machine learning.”
• Describe how one-way artificial intelligence can be used in clinical microbiology to improve efficiency.
• Describe how one-way artificial intelligence can be used in clinical microbiology to improve quality.
2011-2020

- MALDI for identification of cultured isolates
- Molecular multiplex syndromic panels
2021-2030

• Bigger data
• Better data analysis
“Data sets so large and complex that it becomes difficult to process using on-hand data management tools or traditional data processing applications.”

Big Data

• Image data (photos)
• MALDI data (mass spectra)
• Sequencing data (DNA reads)
Image Data (Photos)
“Machine learning is a current application of artificial intelligence based around the idea that we should really just be able to give machines access to data and let them learn for themselves.”

—Bernard Marr

Nugent Scored Gram Stains

FIG 2 Preprocessing for test sets B (a) and C (b). (c) Three typical edge expansion methods used for panel b, image ii.

FIG 3 The confusion matrix of the best points of the 1/4 NugentNet on the validation set.

Source: DOI: 10.1128/JCM.02236-20
### TABLE 3 Limit of detection data for the five runs

<table>
<thead>
<tr>
<th>Dilution</th>
<th>Technologist</th>
<th>Model</th>
</tr>
</thead>
</table>
| Neat     | *Giardia duodenalis,*  
1+ *Blastocystis sp.* | *Giardia duodenalis,*  
1+ *Blastocystis sp.* |
| 1:1      | *Giardia duodenalis,*  
1+ *Blastocystis sp.* | *Giardia duodenalis,*  
1+ *Blastocystis sp.* |
| 1:2      | *Giardia duodenalis,*  
1+ *Blastocystis sp.* | *Giardia duodenalis,*  
1+ *Blastocystis sp.* |
| 1:4      | *Giardia duodenalis,*  
1+ *Blastocystis sp.* | *Giardia duodenalis,*  
1+ *Blastocystis sp.* |
| 1:8      | *Giardia duodenalis,*  
1+ *Blastocystis sp.* | *Giardia duodenalis,*  
1+ *Blastocystis sp.* |
| 1:16     | Negative            | *Giardia duodenalis,*  
1+ *Blastocystis sp.* |
| 1:32     | Negative            | *Giardia duodenalis,*  
1+ *Blastocystis sp.* |
| 1:64     | Negative            | Negative<sup>a</sup> |
| 1:128    | Negative            | *Giardia duodenalis,*  
1+ *Blastocystis sp.* |
| 1:256    | Negative            | *Giardia duodenalis,*  
1+ *Blastocystis sp.* |

<sup>a</sup>Incomplete scan.

Source: DOI: 10.1128/JCM.02053-19
MALDI Data (Mass Spectra)
MALDI-TOF Mass Spectrometry
Machine Learning

“Machine learning is a current application of artificial intelligence based around the idea that we should really just be able to give machines access to data and let them learn for themselves.”

—Bernard Marr

MALDI-TOF MS

194 *Acinetobacter baumannii* isolates

- **Training Set N = 97**
  - Resistant N = 46
  - Susceptible N = 51
- **Test Set N = 97**

Hannah Wang, MD
Training Set Vote Fraction Distribution

The graph shows the vote fraction distribution for carbapenem resistance and susceptibility across different number of isolates. The x-axis represents the number of isolates ranging from 0 to 10, and the y-axis represents the vote fractions for carbapenem resistance and susceptibility. The orange bars indicate carbapenem-resistant isolates, while the blue bars indicate carbapenem-susceptible isolates. The distribution peaks for carbapenem-resistant isolates around 5 isolates, while carbapenem-susceptible isolates show a more uniform distribution across the range of isolates.
Training Set Vote Fraction Distribution

- **Carbapenem-Resistant**
- **Carbapenem-Susceptible**

Bar chart showing the distribution of vote fractions for carbapenem resistance across different numbers of isolates.
Training Set Vote Fraction Distribution

Vote Fractions for Carbapenem Resistance

- Carbapenem-Resistant
- Carbapenem-Susceptible

Number of Isolates

Susceptible
Training Set Vote Fraction Distribution

- **Carbapenem-Resistant**
- **Carbapenem-Susceptible**

Indeterminate
Training Set Vote Fraction Distribution

- Resistant
- Indeterminate
- Susceptible

The diagram shows the distribution of vote fractions for carbapenem resistance across different numbers of isolates.
MALDI-TOF MS

194 *Acinetobacter baumannii* isolates

Training Set $N = 97$
- Resistant $N = 46$
- Susceptible $N = 51$

Test Set $N = 97$
MALDI-TOF MS

Test Set
N=97

Prediction
Resistant (23)
Susceptible (19)
Indeterminate (55)

Accuracy
Correct (20)
Incorrect (3)
Correct (19)
Incorrect (0)
Resistant (29)
Susceptible (26)
Conclusion: The machine learning model was able to classify almost half of A. baumannii isolates as carbapenem susceptible or resistant with 93% accuracy and no very major errors using only mass spectral data.

Hannah Wang, MD
Sequencing Data (DNA Reads)
Whole Genome Sequencing

• Strain typing (clonality assessment)

https://www.cdc.gov/amd/how-it-works/detecting-outbreaks-wgs.html
Whole Genome Sequencing

• Strain typing (clonality assessment)
• Detection of mutations or acquired genes associated with resistance
• Machine learning to predict resistance…
Machine Learning

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—Bernard Marr

Using Machine Learning To Predict Antimicrobial MICs and Associated Genomic Features for Nontyphoidal *Salmonella*

Marcus Nguyen, S. Wesley Long, Patrick F. McDermott, Randall J. Olsen, Robert Olson, Rick L. Stevens, Gregory H. Tyson, Shaohua Zhao, James J. Davis

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*Department of Computer Science, University of Chicago, Chicago, Illinois, USA

Source: DOI: 10.1128/JCM.01260-18
“5,278 nontyphoidal *Salmonella* genomes, [...] was used to generate [...] machine learning models for predicting MICs for 15 antibiotics. The MIC prediction models had an overall average accuracy of 95% [...] The model predicted MICs with no *a priori* information about the underlying gene content or resistance phenotypes of the strains.”
2021-2030

- Bigger data
- Better data analysis

Today, we already have the data.
Tomorrow, we need to develop better analysis tools.
“History is a relentless master. It has no present, only the past rushing into the future. To try to hold fast is to be swept aside.”
Informatics Case-Based Education (ICBE/ICBE1)

- New for 2022
- Educates pathologists on common issues encountered in practice, including:
  - Software implementations
  - Test ordering issues
  - Regulatory compliance
  - Data security
- Appropriate for medical directors and/or staff pathologists
- Created by pathologists for pathologists
- 4 cases annually; each case offers 1 CME credit
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