Methods

Study design and population
For this simulation study (3 cohort study), two networks of ICUs were simulated, with numbers of ICUs and patient-days comparable to Table 1:
1. Québec provincial network (SPIN-BACTOT, 2009-10 data)

Indicators of AM use previously compared (15 indicators of use of different AM classes were studied, combining 5 numerators and 3 denominators).

Numerators (prescribed AMs)
1. Defined daily doses (DDD)
2. Recommended daily doses (RDD), accounting for weight of pediatric patients
3. Agent-days
4. Course-days
5. Courses

Denominators
1. Patient-days
2. Admissions
3. Patients present

Generation of datasets
In a previous cohort study, predictive accuracy of these indicators was compared, using MAEs, where absolute error = |observed prevalence or incidence – predicted prevalence or incidence|.

Scenarios investigated are in Tables 2 and 3. For each one:
• 200 simulations (generated datasets) were performed
• Absolute errors in prediction of resistance (prevalence and incidence rates) were generated for three indicators (the most, 2nd most and least accurate), per 4-week period and per simulated ICU, over 4 years of surveillance
• Absolute errors were randomly generated, based on MAEs observed in the previous cohort study for the most accurate AMs varied according to ICU type, absolute errors were generated stratifying per ICU type.

Conclusion: The two most accurate indicators of AM use would often offer similar predictions of resistance, even in large networks. The least accurate indicators could frequently be distinguished, but not always, especially in the Quebec network, which is smaller.

Statistical analyses
The p-value was computed, as an average proportion; simulated MAEs were then compared for each scenario, with a p-value < 0.05 was then computed, as an estimate of statistical power.

Results

The two most accurate indicators of AM use would usually offer similar predictions of resistance, even in large networks (2 / 20 scenarios for prevalence and 8 / 20 scenarios for incidence). The most accurate indicators could frequently be distinguished, but not always.

Table 3. Scenarios studied for the prediction of resistance incidence rates (incident resistant strains per patient-days) and their proportion of simulations with a p-value < 0.05.

Contact information
Caroline Quach, MD MSc FRCP Infectious Diseases Division and Medical Microbiology Department McGill University Health Centre
Phone: 1-514-833-3877
email: caroline.quach@mcgill.ca

Elise Fortin, PhD(c) Epidemiology, Biostatistics and Occupational Health McGill University Health Centre Phone: 1-418-666-7000 #115

# 160

A Simulation Study to Assess Indicators of Antimicrobial Use as Predictors of Resistance

Elise Fortin, PhD(c)1,2, Caroline Quach, MD MSc1,2,3, Patricia Fontela, MD PhD4, David L. Buckeridge, MD PhD1 and Robert W. Platt, PhD1
1) Epidemiology, Biostatistics, and Occupational Health, McGill University, Canada; 2) Institut National De Santé Publique Du Québec, Canada; 3) Division of Infectious Disease, Department of Pediatrics, The Montreal Children’s Hospital, Canada; 4) Pediatric Intensive Care, The Montreal Children’s Hospital, Canada.

Contact information
Élise Fortin, PhD(c)1,2, Caroline Quach, MD MSc1,2,3, Patricia Fontela, MD PhD4, David L. Buckeridge, MD PhD1 and Robert W. Platt, PhD1
1) Epidemiology, Biostatistics, and Occupational Health, McGill University, Canada; 2) Institut National De Santé Publique Du Québec, Canada; 3) Division of Infectious Disease, Department of Pediatrics, The Montreal Children’s Hospital, Canada; 4) Pediatric Intensive Care, The Montreal Children’s Hospital, Canada.

Statistical analyses
For each scenario, a t-test comparing the most accurate indicator to each of the other indicators was calculated. P-values were stored. For each scenario, the proportion of simulations with a p-value < 0.05 was then computed, as an estimate of statistical power.

Results

The two most accurate indicators of AM use would usually offer similar predictions of resistance, even in large networks (2 / 20 scenarios for prevalence and 8 / 20 scenarios for incidence). The two most accurate indicators could frequently be distinguished, but not always.

Bigger networks were more powerful to detect differences between indicators. With these networks, a difference was always found between the least and most accurate indicators (20 / 20 scenarios, for both prevalence and incidence). However, an 80% power to distinguish the most and least accurate indicators was reached for less than half of scenarios (9 / 20). Differences were also detected more often in prediction of resistance incidence rates (27 / 40, versus 15 / 40 for prevalence).

Conclusion

• Large networks of ICUs would be necessary to identify the most accurate indicator for the prediction of resistance prevalence and incidence.
• This indicator could differ between resistance / AM use combinations
• In smaller networks, the choice of an indicator for an eventual surveillance system could rely on criteria other than predictive accuracy (feasibility, external comparisons).

Table 1. Description of the SPIN-BACTOT and NHSN networks.

Table 2. Scenarios studied for the prediction of resistance rate incidents (resistant strains per patient-days) and their proportion of simulations with a p-value < 0.05.

Note: See Table 1 for more detail.

Table 3. Scenarios studied for the prediction of resistance incidence rates (incident resistant strains per patient-days) and their proportion of simulations with a p-value < 0.05.

Note: See Table 1 for more detail.

Table 4. Compared indicators: Simulations with a p-value < 0.05 (%)

Note: See Table 1 for more detail.

Table 5. Compared indicators: Simulations with a p-value < 0.05 (%)

Note: See Table 1 for more detail.

Table 6. Compared indicators: Simulations with a p-value < 0.05 (%)

Note: See Table 1 for more detail.

Table 7. Compared indicators: Simulations with a p-value < 0.05 (%)

Note: See Table 1 for more detail.

Table 8. Compared indicators: Simulations with a p-value < 0.05 (%)

Note: See Table 1 for more detail.

Table 9. Compared indicators: Simulations with a p-value < 0.05 (%)

Note: See Table 1 for more detail.

Table 10. Compared indicators: Simulations with a p-value < 0.05 (%)

Note: See Table 1 for more detail.

Table 11. Compared indicators: Simulations with a p-value < 0.05 (%)

Note: See Table 1 for more detail.

Table 12. Compared indicators: Simulations with a p-value < 0.05 (%)

Note: See Table 1 for more detail.

Table 13. Compared indicators: Simulations with a p-value < 0.05 (%)

Note: See Table 1 for more detail.

Table 14. Compared indicators: Simulations with a p-value < 0.05 (%)

Note: See Table 1 for more detail.

Table 15. Compared indicators: Simulations with a p-value < 0.05 (%)

Note: See Table 1 for more detail.

Table 16. Compared indicators: Simulations with a p-value < 0.05 (%)

Note: See Table 1 for more detail.

Table 17. Compared indicators: Simulations with a p-value < 0.05 (%)

Note: See Table 1 for more detail.

Table 18. Compared indicators: Simulations with a p-value < 0.05 (%)

Note: See Table 1 for more detail.

Table 19. Compared indicators: Simulations with a p-value < 0.05 (%)

Note: See Table 1 for more detail.