Introduction of artificial intelligence for high throughput culture-based MRSA screening

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Background

- Automating routine procedures in medical laboratories has become a key feature of modern diagnostics in part due to the potential increase in precision and traceability.
- In medical microbiology, automation has – in addition to ID/AST testing – so far largely focused on inoculation.
- In the laboratory, AI-based systems that aid in the plate-reading process may increase the overall sample throughput, and can also improve the workflow and the overall quality by reducing subjectivity and increasing precision of reads.
- The APAS® Independence (APAS ®, Clever Culture Systems, Figure 1) in combination with MRSA Analysis Module was developed and evaluated using over 17,000 routine specimens over a 6 month period. MRSA screening was performed using chromID® MRSA (bioMerieux). Samples were processed using the AutoPlak® (Beckman Coulter), Previ Isola, and evaluated after 24 and 48 hours of incubation. Results of APAS ® AI-based classification were compared to conventional plate reading by experienced medical technicians and microbiologists to determine sensitivity and specificity.

Materials and Methods

- The development of the classifiers is an interactive and iterative process incorporating microbiologist feedback into software development (Figure 2).
- For this study, the MRSA algorithm (classifier) was developed for chromID® MRSA. Samples were processed using the AutoPlak®, Previ Isola, and manual streaking and also imaged by APAS® after 24 and 48 hours.
- Plates inoculated from liquid based microbiology swaps (LBMS, Copan) and from enrichment broth (Thioglycollate, bioMerieux) were used. All samples in this part of the study were read after 18-24 hours, and at 36-48 hours total incubation time by conventional methods (Labtech and microbiologist, plate in hand) and the APAS® system. Results of whether growth was suspicious of MRSA were independently recorded and compared. Discordant results were reviewed by another experienced microbiologist. The study included over 200 unique MRSA strains to challenge the system.
- An average of 400 samples per day were processed in order to determine whether this new automated system could cope with a larger number of samples.

Results

- Improvement of the classifier through the development process is displayed in Figure 3. APAS® AI-based classification results were compared to the microbiologist to estimate sensitivity and specificity.
- Figures 4 shows the analysis of sensitivity and specificity of the APAS system in comparison with conventional plate reading by experienced technicians and microbiologists during routine testing.
- Analysis of discrepant samples resolved all of the initial APAS® false negatives, achieving a sensitivity of 100%.
- A low number of false positives occurred predominantly due to confusion with organisms that were pigmented.
- For known MRSA positive strains, the sensitivity and specificity of MRSA detection using APAS® is 100%.

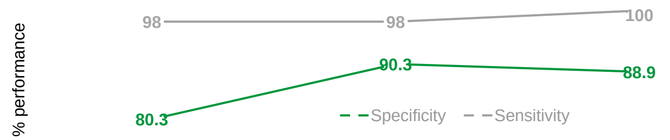

Figure 3: Improvement of the sensitivity of the classifier during the development phase

Figure 1: APAS® Independence

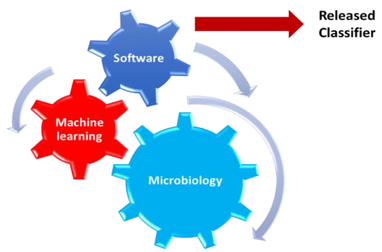

Figure 2: Schematic of machine learning iterations

Conclusions

- ✓ AI-based APAS® was at least comparable to conventional reading, maintaining an average read rate of 200 plates / hour.
- ✓ APAS® reliably screens for MRSA and would significantly reduce time to report and would reprioritize technician/microbiologist time.
- ✓ AI-based systems may provide a great addition to current practices in cultural microbiology.

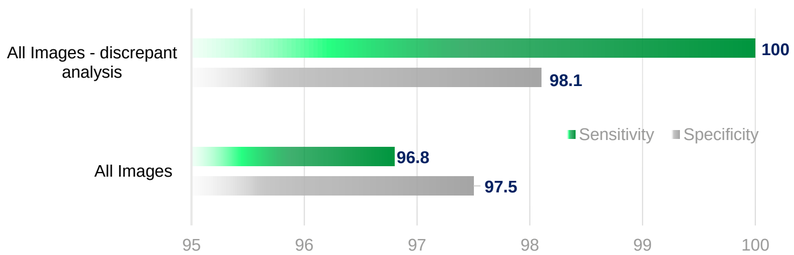

Figure 4: Performance of MRSA classification using APAS ® Independence

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