Links between each patient’s microbiological identification and microbiological cure episodes, can provide significant clinical insights into disease diagnoses, presentation, progression, treatment, and prognosis.

**Title:** Hierarchical clustering of microbial resistance profiles and ventilation protocols using the oncology extension

**Rationale:**
- Ventilator associated pneumonia (VAP), often caused by multi-drug resistant bacteria, is a frequent complication of mechanically-ventilated ICU patients.
- Failing to distinguish between location of infection is challenging and leads to unnecessary use of broad-spectrum antibiotics which produces antimicrobial resistance (AMR).
- Eccard Base, a Horizon Europe project, funded by EHEDN to work with edenhealth to transform participant-level data captured using CDASH to OMOP CDM to facilitate reuse of participant-level data from collected from a European network of VAP-related perpetual observational studies (POSIs).

The dataset in OMOP CDM format will facilitate:
- Timely reuse of the data through participation in international federated studies on prevention, diagnosis and treatment of VAP and hospital-associated pneumonia (HAP).
- Efforts to improve AMR surveillance and Antimicrobial Stewardship (AMS).

**Discussion and Future Directions:**
- Clustering approach facilitates accurate analyses of complex patient presentations through relation-based covariates like quantity and type of child AMR for parent bacterial species, and context-based covariates like combinations of fungi and bacteria present in sputum sample.
- Clusters defined by patient and date; enabling multiple clusters within patients related to different ICU admissions.
- Nuanced approach to describing relationships used here may be reused in other domains with complex hierarchical structures like pregnancy.
- Limited in that: (1) oncology extension not designed for capturing VAP or AMR-related data, and (2) events are restricted to one parent in hierarchical tree.
- Created nested episodes for each type of cluster.
- Linked nested episodes to all events in tree using EPISODE and EPISODE_EVENT tables.
- Linked events using patient and date information.
- Transferred data into OMOP relational tables.

**Approach:**
- Reused oncology OMOP CDM 5.4 extension.
- Created hierarchical clusters for (1) samples collected and measurements performed related to antimicrobial resistance and (2) Clinical criteria-based protocols implemented for invasive mechanical ventilation.
- Linked events in each cluster unidirectionally from child to great-grandparent.
- Created nested episodes for each type of cluster.
- Linked nested episodes to all events in tree using EPISODE and EPISODE_EVENT tables.
- Linked events using patient and date information.
- Transferred data into OMOP relational tables.

**Challenges:**
- OS-VAP data must appropriately record hierarchical, cross-domain, inter-event dependencies, a challenge within the current OMOP CDM specifications.
- VAP events must be understood through the quality and direction of their linkages to other events.
- Microbiological identification, microbiological cure episodes, VAP onset, and clinical cure episodes must be linked to adately describe disease diagnoses, presentation, progression, treatment, and prognosis.

**Figure 1:** Hierarchical structure and linking of events related to microorganisms and their various attributes and antibiotic resistance profiles. Note that each block may represent more than one event per hierarchical tree, and that a patient may have multiple episodes on a given day if multiple samples were drawn.

**Figure 2:** Hierarchical structure and linking of events related to VAP onset and relevant clinical criteria deduced through chest imaging. Note that each block may represent more than one event per hierarchical tree.

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**Table 1:** Sample Quality and Microbial Identification

<table>
<thead>
<tr>
<th>Sample Type</th>
<th>Observation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Specimen</td>
<td>Sample Analysis - Microorganism Identification</td>
</tr>
<tr>
<td></td>
<td>Fungus</td>
</tr>
<tr>
<td></td>
<td>Bacteria</td>
</tr>
<tr>
<td></td>
<td>Virus</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Organism Identification</th>
<th>Observation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fungus Name or Genus</td>
<td>CPE Name</td>
</tr>
<tr>
<td></td>
<td>Measurement</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Microbial Culture Value</th>
<th>Observation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Qual. Microbial Culture Value</td>
<td>Microbial Culture Value</td>
</tr>
</tbody>
</table>