Use of Electronic Data for the Surveillance
Of
Antimicrobial Resistance

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Functional Area: Informatics in Action & IT Solutions   Category: Applications and Services

ABSTRACT

Monitoring trends in emerging antimicrobial resistance is critical to military and public health. Empirical therapy guided by validated resistance data can lead to improved patient outcomes and a reduction in the emergence of resistance. Health Level 7 (HL7) microbiology data are restructured for analysis in Structured Query Language (SQL) for import into WHONET© to produce detailed reports characterizing antibiotic resistance in Military Health System (MHS) beneficiaries. Validated results will be disseminated to their respective Military Treatment Facilities (MTFs) for use by infection control practitioners and clinicians.

The efficiency and scope of DOD level electronic surveillance improves upon institutional surveillance techniques. DOD-wide implementation of this first methodology to provide timely analysis of antibiotic resistance in the military population will lead to improvements in medical readiness, health outcomes and healthcare costs.

BACKGROUND

The EpiData Center (EDC) Division at the Navy and Marine Corps Pubic Health Center (NMCPHC) receives HL7 microbiology data from Executive Information Decision Support (EIDS). The HL7 messages which are sent via the MHS Composite Health Care System (CHCS) to EIDS are restructured and sent to the EDC through a secured daily feed. The database administrator (DBA) transfers the large volume of compressed data to a storage area on a secured server. The compressed raw data are backed up to disk for disaster recovery efforts. Before the data are uploaded to the database, they are validated for anomalies, such as missing or skewed data.

Incoming MHS HL7 data present challenges due to the inclusion of non-standard laboratory test names and results, inconsistent date formats and field lengths, null values and duplicate records. These data require extensive processing in SQL or Statistical Analysis Software (SAS) to restructure them for analysis with standard tools. Methodology has been developed by EDC programmers and epidemiologists to utilize these data for infectious disease surveillance and case finding.

METHODS

EIDS supplied HL7 Microbiology data, containing certified laboratory results for MHS beneficiaries seen in MTFs, are restructured using SQL methods developed with SAS. Restructuring rules developed in SAS were recreated in SQL for efficiency and automation purposes.

Rows are identified as records of bacterial isolation or antibiotic testing based upon classification of the test name field. Record sets containing isolate identifications for each unique specimen and associated antibiotic tests are grouped, and the final set is selected according to result status and result certification date/time. Variables containing test order, specimen site, specimen type and clinical comment data are utilized in the creation of standard patient and specimen groups.

The restructured data are output to a pipe delimited file and converted using BACLINK©. Conversion of BACLINK© requires definition of organism, antibiotic and specimen source codes, and description of the output file structure and data fields. The converted files are then imported into WHONET©, a standard World Health Organization (WHO) developed tool, that rapidly generates detailed antibiogram reports.

CONCLUSION

This is the first methodology to provide a timely analysis of antibiotic resistance in the military population. Utility of the MHS HL7 microbiology data for public health surveillance purposes depends on proper infrastructure and resources, storage and retrieval of data.

Restructured data can be utilized for the generation of detailed reports to support clinical and public health decisions.

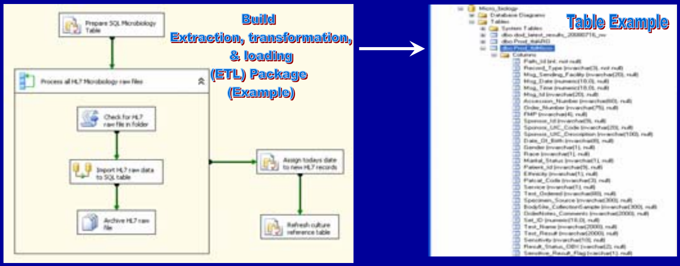
DATA TRANSFORMATION

STEP 1. RECEIVE HL7 2.5.1 MESSAGE (Raw Data Example)

```
MSH|\&|^2.16.840.1.114222.4.3.2^ISO|^2.16.840.1.114222.4.3.2^ISO|^2.16.840.1.114222.4.3.2^ISO|^2.16.840.1.114222.4.3.2^ISO|200602171830||ORU^R01^ORU_R01|
          99999999999|P^T|2.5|||||USA||||LR-V1.4^^2.16.840.1.114222.4.3.2^ISO<CR>
PID|||9510110000^^^&2.16.840.1.114222.4.3.2&ISO^MR~111-11-
          1111^^^&2.16.840.1.113883.4.1&ISO^SS||LASTNAME^FIRSTNAME^MI^^MS^^L||19981004|F||20543^Black^2.16.840.1.113883.6.238 |807 LAKE ST.^APT
          A^SUFFOLK^OH^21412^USA^H^^13121||^PRN^PH^^^614^9998888||eng^ENGLISH^2.16.840.1.113883.6.100|S^Single^2.16.840.1.113883.12.2||||| |2186-5^Non-
          Hispanic^2.16.840.1.113883.6.238||||USA^UNITED STATES^2.16.840.1.113883.5.28||USA^UNITED STATES^2.16.840.1.113883.5.28||N|Y||200602171830<CR>
```

Delimiters: | ^ <CR> &

STEP 2. RESTRUCTURE HL7 TO RELATIONAL DATABASE



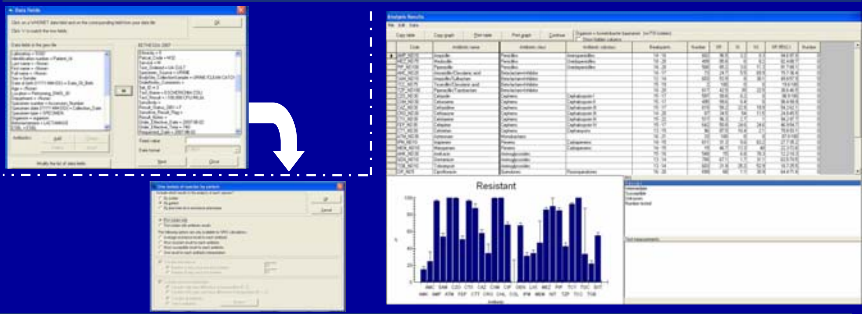
Development of coding has been initiated to prepare the raw data for importation into a relational database for querying.

STEP 3. RESTRUCTURE FOR WHONET © (SQL CODE SAMPLE)

```sql
--Insert microbiology records from HL7 into a temporary work table.
INSERT #work_table
SELECT DISTINCT mb.Msg_Id, mb.Accession_Number, mb.Order_Number, b.FMP, mb.Sponsor_Id, mb.Specimen_Source, mb.BodySite_CollectionSample,
RTRIM(mb.OrderNotes_Comments) AS OrderNotes_Comments, mb.Set_ID, mb.Test_Name, RTRIM(mb.Test_Result)) AS Test_Result, mb.Sensitivity, mb.Result_Status_OBX,
RTRIM(mb.Sensitive_Result_Flag) AS Sensitive_Result_Flag, RTRIM(mb.Result_Notes) as Result_Notes, CAST(CAST(CASE IsDate(mb.Collection_Date) WHEN 1 THEN
mb.Collection_Date ELSE '18000101' END AS VARCHAR(18)) AS DATETIME) AS Collection_Date, mb.Collection_Time, CAST(CAST(CASE IsDate(mb.Certify_Date) WHEN 1 THEN
mb.Certify_Date ELSE '18000101' END AS VARCHAR(18)) AS DATETIME) AS Certify_Date, mb.Certify_Time, RTRIM(mb.Requesting_DMIS_ID) AS Requesting_DMIS_ID,
RTRIM(mb.Requesting_DMIS_Facility_Name) AS Requesting_DMIS_Facility_Name, RTRIM(mb.Clinical_Comments) AS Clinical_Comments,
RTRIM(mb.Performing_DMIS_ID) AS Performing_DMIS_ID,  RTRIM(mb.Performing_DMIS_Facility_Name) AS Performing_DMIS_Facility_Name, mb.Meprs_Code,  COALESCE
(c.culture_id,88) AS culture, SUBSTRING(mb.Meprs_code,1,1) AS pt_type, SUBSTRING(mb.Meprs_code,2,LEN(mb.Meprs_code)-1) AS clinic, CASE
RTRIM(LTRIM(mb.Result_Status_OBX)) WHEN 'P' THEN 1 WHEN 'F' THEN 2 WHEN 'C' THEN 3 ELSE 0  END AS status
FROM Micro_biology.dbo.prod_tblMicro mb LEFT OUTER JOIN Micro_biology.dbo.tblCulture_data c  ON rtrim(mb.test_name) = c.test_name ORDER BY
mb.sponsor_id,mb.fmp,mb.Order_Number,mb.Msg_Id,mb.set_id
```

STEP 4. CONVERT IN BACLINK©

STEP 5. ANALYZE IN WHONET©



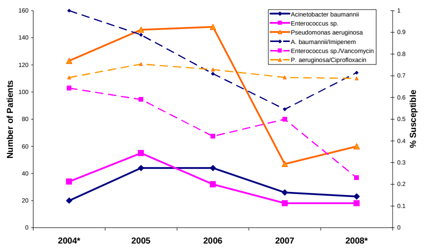
STEP 6. PRODUCE RESULTS

Approximately 1.5M bacterial isolates were identified in the HL7 microbiology data for the period of May 2004 through June 2008. 851,016 of these were the first isolates per patient and 30,170 were isolates from blood or cerebrospinal fluid.

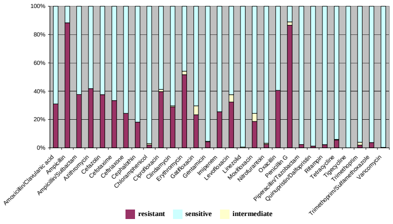
Top 10 Organisms

Rank	Organism	% Total
1	Escherichia coli	27
2	Staphylococcus aureus ss. aureus	13
3	Streptococcus, beta-haem. Group A	9
4	Streptococcus, beta-haem. Group B	6
5	Streptococcus, beta-haemolytic	5
6	Staphylococcus, coagulase negative	4
7	Streptococcus agalactiae	3
8	Streptococcus pyogenes	3
9	Klebsiella pneumoniae ss pneumoniae	3
10	Lactobacillus sp.	2

Select Organisms, Blood and CSF Isolates



Staphylococcus aureus Antibiogram
Blood or CSF Specimens, May 2004 to June 2008, N=2,382



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