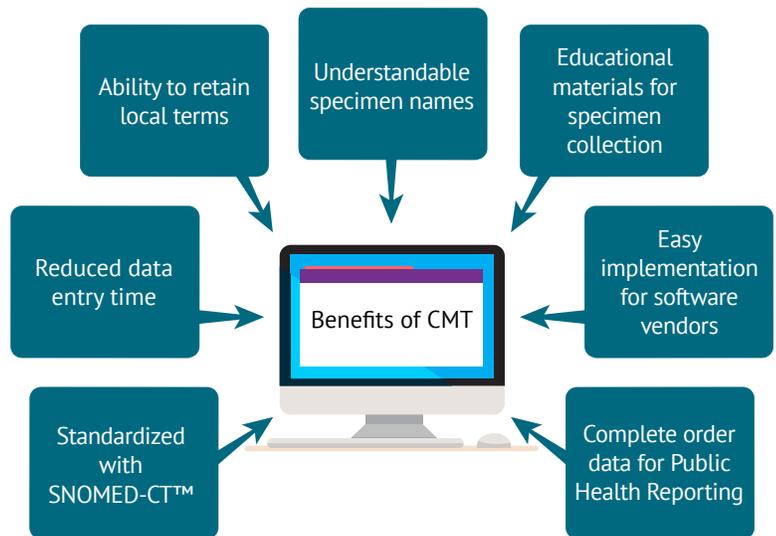


# A Standardized Approach to Getting Complete Specimen Details

Get the specimen details right every time!

The Specimen Cross Mapping Table (CMT), developed by the Centers for Disease Control and Prevention (CDC) and the Association of Public Health Laboratories (APHL), is intended to improve the standardization, completeness, and understanding of specimen details for healthcare providers and clinical laboratory professionals.

Timely testing of patient specimens and accurate interpretation of test results depend on both the quality of the specimens sent to the laboratory and the adequacy of accompanying information such as patient demographics, clinical diagnosis, date and time of collection, specimen type, and the anatomic site of collection. Without comprehensive specimen information, it may be difficult or impossible to initiate appropriate laboratory testing, resulting in delayed results and challenges in providing appropriate test interpretation, which can lead to patient harm.



*The Specimen Cross Mapping Table offers adaptable solutions with usability in mind for clinicians, software vendors, laboratory professionals, and public health agencies.*

## How can we make specimen information easier for clinical laboratory professionals to obtain?

▶ We use community driven solutions. The **Laboratory Community of Practice (LabCoP)**, a voluntary group of public health and clinical laboratory professionals, have identified two issues at the root of the problem.

### Challenges

The names used to describe the same specimen vary widely among different providers. Also, different Electronic Health Records (EHRs) use their own local codes to define specimens, making data harmonization across different systems difficult.

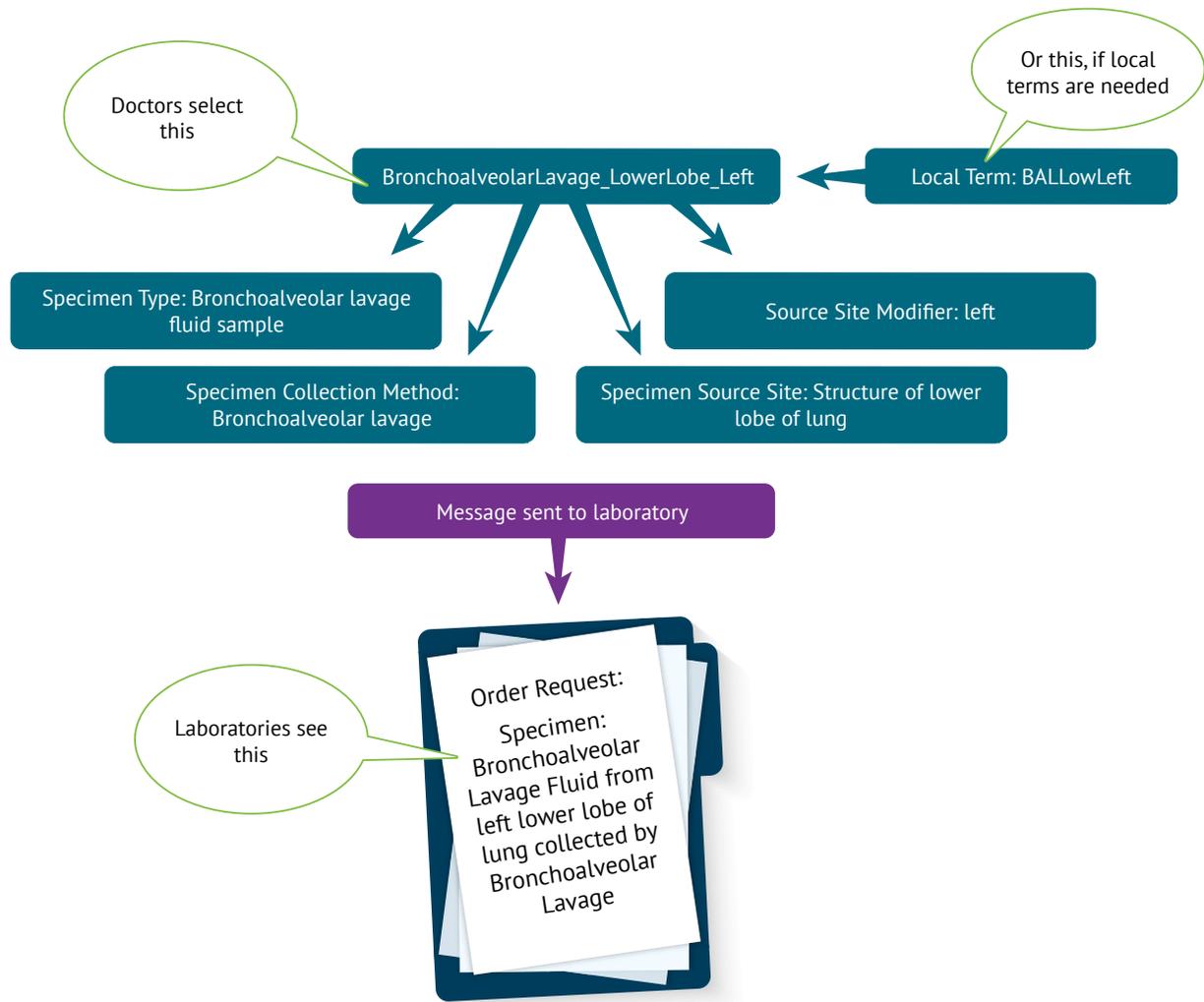
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Clinicians make test requests through EHRs, which electronically send those requests to laboratories. The standard electronic message from EHRs to the laboratories contain fields for all specimen details. Yet, most EHRs have limited input boxes to capture specimen details. Adding multiple input boxes for each specimen detail could lead to increased burden to the ordering clinician.

The challenge is to fill all the electronic message fields with all applicable information for a specimen without increasing physician burden.

### Opportunities

A preferred specimen name agreed upon by the subject matter experts will reduce the confusion among specimen names. These preferred names can be coded to accepted nomenclature standards.

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With the Specimen CMT programmed into EHRs, mapping a preferred specimen term to all related message fields could potentially solve this problem. Then, when the provider selects the specimen term, the mapping results in those fields being populated with details by the EHR.



*Example use of an adaptable specimen cross map.*

## Implementing Solutions

### Standardized and Complete Specimen Details

LabCoP created the Specimen CMT as a possible solution consisting of a knowledge base that starts with a preferred specimen term mapped to all details, coded in SNOMED-CT™\* for each specimen.

APHL is in the process of putting the Specimen CMT through a thorough review process with organizations such as the American Society of Microbiology (ASM), the College of American Pathologists (CAP), the Association for Molecular Pathology (AMP), the American Clinical Laboratory Association (ACLA) and the American Association for Clinical Chemistry (AACC).

Once the Specimen CMT is completed, it will be available as a database for implementation by software developers of medical information systems.

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**For more Information**  
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