SEER*DMS Change Control Advisory Board (CCAB) Users Group
Teleconference
April 28, 2025
12:30 p.m. to 2:00 p.m. EDT

Representatives from NCI, IMS, the Scientific Consulting Group, Inc. (SCG), and 27 cancer registries participated in the SEER*DMS Users Group conference call on April 28, 2025. Participants included:

REGISTRIES:

Alaska
Arkansas
California Cancer Registry
Cherokee Nation
Connecticut
Detroit
Georgia
Greater Bay Area
Greater California
Hawaii
Idaho
Illinois
Indiana
Iowa
Kentucky
Los Angeles
Louisiana
Massachusetts
Michigan
Minnesota
New Jersey
New Mexico
New York
Seattle
Texas
Utah

NCI: Marina Matatova, Steve Friedman, Valentina Petkov

IMS: Suzanne Adams, Linda Coyle, Chuck May, Nikki Schussler, Katherine Kurby, David Angelaszek

SCG: Lily Neff, rapporteur

Action Items

- IMS will query registries to determine their interest and scope of reducing reports for the same patient and specimen.
- Registries should consider if a batch based on a specific query is always being set to non-reportable or receiving worklist flags, which can be automated by IMS.
- Linda will create a Squish ticket for registries to provide feedback on their respective needs for the proposed path screening updates.
- Marina will reach out to CMS to determine if updated CLIA is available.

Overview of Meeting **Linda Coyle, Marina Matatova**

The primary goal of this meeting was to discuss efforts to update path screening. Mock-ups and screenshots of the developed workflows were provided.

Linda noted that over the past several months, IMS has met with NCI and individual registries to gather feedback that provided the foundation for these updates. She provided an overview of the manual path screening updates, addressed questions, and highlighted use in the registries.

Path Processing Improvement Project Updates **Linda Coyle, Marina Matatova**

Path processing in SEER*DMS continues to increase because of new registries implementing SEER*DMS for path processing; new path feeds are being developed between registries, labs, and regional path processing vendors; and unfiltered path report data are being added by several registries. NCI and IMS are working on multiple path projects to promote automation where possible and ensure a user-friendly experience for tasks. New SEER*DMS automated processes include evaluation of path reports to minimize duplicates, and keyword algorithms, in addition to Reportability API, to reduce screening of non-reportable reports.

New manual processes of SEER*DMS include streamlining the user experience from home page to screening tasks, a "multi-report" task that processes reports for the same patient in one task, and a feature that allows managers and senior staff to review and process batches of path reports using registry-defined search criteria.

Linda emphasized that these are screen prototypes, so they are not currently functional. The improvements to manual tasks and workflows will be released in phases. Phase 1 is scheduled to be released in August 2025. Currently from the SEER*DMS landing page, users can access the "All Tasks" worklist or move to the "Path Screening Tasks" to access the "Path Task with a Single Record." On the landing page, the new proposed features will be a "Path Batch Updates." The path screening task will have two options, single or multiple, with the links taking users to a new Path Screening Worklist Page.

A comparison of the current and proposed full worklist was provided. The first tab on the worklist will indicate the task filter (e.g., All Tasks vs. Path Tasks). A summary of the filters chosen by the user will be displayed on the top of the main page and will have an option for easily removing the filter(s). When users choose filters, they will be automatically applied. (The current worklist requires users to choose their filters, and then click apply. The "apply" and "reset" buttons will be removed.)

A comparison of the current and proposed path screen worklist was provided. Over the years, registries have requested new filters be incorporated, resulting in an extensive filter list. The filters will be refined based on task type to optimize visualization and selection by users. As proposed for the full worklist, a summary of the filters chosen will be displayed at the top. Automatic sorting by patient identifiers and same specimen reports being grouped into the path screen multiple records task will be available. This new task type allows users to identify that several reports are within the task and enables managers to control task assignments to users. A new feature for users with permission (e.g., managers, senior staff) will be a tab to update batches. These updates make the workflow more dynamic and are strategic modifications with the intent to help users navigate and optimize workflow steps.

Phase 2 plans were briefly discussed. The Multiple Report task will include reports for different specimens originating from one patient. Reports for the same patient and specimen will be reduced (e.g., multiple copies of the same report with the differing time stamps, an algorithm to auto delete a duplicate report if all pertinent information is available in one of the reports). An example was shown that Report A

and Report B were created on the same day, differing by 20 minutes. Report B included all information from Report A (e.g., patient identifiers, path number, date specimen collected) and contained an additional message on interpretation. Based on the redundancy, Report A could be deleted. Another example displayed two reports provided by the lab to the registry on the same day. Both reports included the same information, and Report A had an attached supplemental addendum field. In this example, Report B could be removed because all text is available in Report A.

In response to concerns about functionality and usability, the Multiple Report task now has a unique interface. Reports will be shown in consecutive columns, and they can be managed in groups (e.g., specific disease codes for all reports in the group). Additional options include removing a report from the group and changing the status of a report to non-reportable. Another new feature is updating path reports in batches, if a registry uses data searches to identify and complete bulk changes on non-reportable reports. This new feature uses a combination of text queries and API Results to search for a registry-defined batch of reports, which can be modified with worklist flags or to non-reportable, if appropriate. A batch that needs manual path screening can be removed from the result list by selecting "Set Review Completed.".

Linda provided a prototype demonstration of the worklist and task improvements in the development systems in Phase 1 and 2. She emphasized that approximately 10–20% of current manual path screening tasks have two or more reports for the same specimen. Implementing the automation algorithms would help registries reduce the number of duplicate reports. Columns, based on task type, will be reduced where possible to ensure practicality.

Discussion

April Austin from the New York registry inquired about the edit option. In response, Linda noted that in the proposed Multiple Reports task, users will be able to open a full record in editor. April asked about the linkage feature for multiple pathology reports. Linda responded that all features in the standard path screening task will be available in the multiple path screening task. She noted that linking to a CTC is based on registry preferences and user permission, but the proposed change would allow a user to link multiple records to the same CTC in one step.

Mona Highsmith from the Minnesota registry noted when staff make changes on the review or consultation slides, changes often need to be made to fields in the full record as well. Certain registries may want to review the path report to code cytology behavior while other registries may want to make field changes in the full report that are not shown in the path screening report.

Valerie Yoder from the Utah registry asked if batch screening will support a saved data search where reports will be changed to non-reportable based on two different text fields (e.g., nature of specimen – pap test, final diagnosis – no malignancy found). This request will be added to the backlog and reviewed for incorporation.

Marina asked the Georgia and New York registries if the workflows in the prototype demonstration address the areas discussed in previous meetings; these registries agreed that these updates accomplished the previous requests.

Robin emphasized that the highlighted differences between reports on the multi-record view are valuable. Marina noted that highlighting can be for all differences or limited to cancer terms with a different UI component used for other differences. Registry members discussed different options—including a different highlighter color, a toggling option for report differences versus cancer terms, a red line next to altered text, red font, bold font, or italic font—to display text variations between reports. Using

highlighter color variations for these separate features is not recommended because the same method should not be used for two unique action needs. For a seamless user experience, the current highlighting association with cancer terms should not be altered. These suggestions will be internally reviewed and compared to the current user experience guidelines to determine the best option to employ for variations between reports that are not related to cancer terms.

Marina expressed gratitude to the Connecticut, Georgia, New York, and Texas registries for meeting with NCI and IMS in several sessions to discuss how registries utilize their workflows for manually processing pathologies. From these meetings, areas for improvement were identified and registries provided suggestions (e.g., batch updates, multiple record comparisons). Marina emphasized that strategic system refinements will continue and additional meetings with registries will be held to ensure that updates streamline and expedite path processing.

April requested that auditable—a flag that notes the registry wishes to follow up with the facility or physician about a sample without creating a tumor outcome—be retained in the batch report with reportable and non-reportable. Marina responded that this would be reviewed for potential incorporation in phase 1. Linda commented that a Squish has been developed for a similar request flagged by the Iowa registry, and the two requests can be combined.

Jovanka Harrison from the New York registry requested a flag for genomic report results. The Texas registry previously requested the option to flag staging or treatment in path reports. Linda requested registries mention which flags are of interest and to elaborate on their use. Robin commented that genomic reports are not diagnostic, and if these reports could be flagged as supplementals and have SSDI information. In response to a question from Marina about the use of these genomic reports, Robin responded that it is dependent on whether genomic information will be used to co-site specific data items. Marina proposed that genomic reports could be set as a separate task which would allow registries to view the genomic information. April requested the option of a batch feature to identify genomic reports and this data not be carried through the same workflow. Mona noted that genomic reports would be kept with cancer data but marked as non-reportable. There are facilities that only provide genomic reports (e.g., Neogenomics). After further discussion, a combination of facility plus keyword to identify reports would be beneficial to isolate genetic tests (e.g., cytogenetic). A pilot phase for this feature would be implemented to ensure facility plus keyword is accurately identifying genomic reports. This will be a separate effort with unique phases.

Reports that lack active cancer will not be considered reportable by eMarc Lite. Robin recommended IMS review the number of facilities that begin utilizing eMarc Lite because surgical reports that are negative for residual disease will not be included in the registry workflow and will rely on facilities reporting them.

Robin queried the group about reports being picked as reportable or auditable. An example genomic report stated the reason for referral was the absence of AML remission, the final diagnosis was AML, and a diagnosis date was unavailable. Jennifer Hafterson from the Seattle registry responded that these types of reports would be considered potentially reportable. April commented that it depends on the genetic test, but the example provided would be considered non-reportable. She continued that for a reportable pathology report, the registry would receive other pathology results (e.g., bone marrow, flow cytometry, biopsy), and the registry has too many reports to screen through all of them. In response to a question from Marina about the example provided being used to build a new case or incorporated into an existing case as supplementary information, Jennifer replied a patient set with an unknown diagnosis is created. It would not be SEER reportable but would be processed in a manner that would allow staff to follow up with physicians. Robin commented that patients could be diagnosed over 10 years ago, and the missing information makes it difficult to build a case; this could be classified as auditable. Jennifer noted a Squish has been submitted for the first facility involved with the Seattle registry to be incorporated into

SEER*DMS with past screening data. Based on how this affects processing, auditable could be reviewed as a flag. She continued that registry size and data volume may lead to differences between registries as well.

Valeria noted that the HL7 definition includes a genomic report standard, but lab implementation of this standard varies. Jovanka continued that LOINC codes, facility CLIA, and keywords can be used. Marina will inquire about CLIA updates.

Marina requested registries provide feedback on their respective needs for this pilot, and a Squish ticket will be created. After phase 1 implementation, a qualitative analysis and user feedback assessment will be completed to determine the impact. Marina requested that interested registries develop protocols of current path processing and note estimated workflow times to complete a comparison when the new functionalities are active.

Next Steps **CCAB**

The next regular CCAB meeting is scheduled for May 19, 2025.