COLLABORATIVE STAGE
DATA COLLECTION SYSTEM

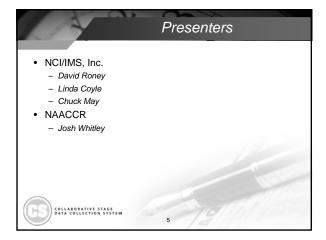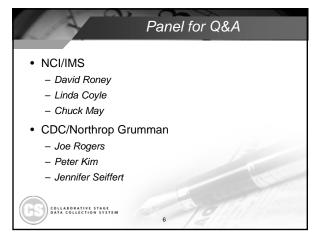### *CS Vendor Webinar*

*May 23, 2012*

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### *Questions*

- Please enter questions concerning todays presentation into the Q&A panel
  - Please include the name of the speaker you would like to address your question
  - All questions will be addressed after the last speaker
- If you experience technical difficulties, please contact us through the Chat panel or call us at 217 698 0800 x 111

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2

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### *Objectives of this Webinar*

1. Follow-up to the CS webinar conducted on April 11, 2012
2. Demonstrate two implementations of CS
3. Announce availability of CS comment/feedback web site

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3

## Agenda

- Introduction
- Demonstration of the SEER*Abs system in relation to CS
- Demonstration of the SEER API and Collaborative Stage
- Demonstration of the NAACCR Web site for Vendor/User Feedback on CSv2
- Questions & Answers

*COLLABORATIVE STAGE DATA COLLECTION SYSTEM*

4

## Presenters

- NCI/IMS, Inc.
  - *David Roney*
  - *Linda Coyle*
  - *Chuck May*
- NAACCR
  - *Josh Whitley*

*COLLABORATIVE STAGE DATA COLLECTION SYSTEM*

5

## Panel for Q&A

- NCI/IMS
  - *David Roney*
  - *Linda Coyle*
  - *Chuck May*
- CDC/Northrop Grumman
  - *Joe Rogers*
  - *Peter Kim*
  - *Jennifer Seiffert*

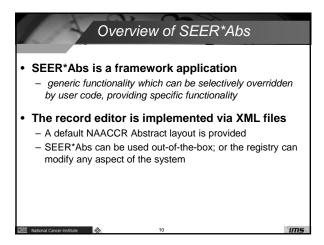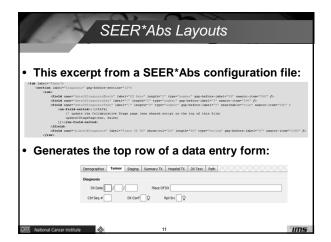*COLLABORATIVE STAGE DATA COLLECTION SYSTEM*

6

## Webinar #1
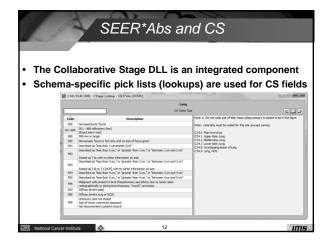
First webinar conducted on April 11, 2012

- Reviewed the full range of function calls and data structures within CS
- Reviewed and demonstrated the CDC Registry Plus and Abstract Plus systems
- Demonstrated the NCI CS Test site
- Announced plans for the CS Feedback web site
- Recording available at the NAACCR web site
  - http://www.naaccr.org/EducationandTraining/Webinars.aspx

**CS** COLLABORATIVE STAGE
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7

## Webinar #2

Second webinar will contain 3 demonstrations:

- NCI SEER*Abs and CS
- NCI SEER API and CS
- NAACCR CS Feedback web site

**CS** COLLABORATIVE STAGE
DATA COLLECTION SYSTEM

8

**CS** COLLABORATIVE STAGE
DATA COLLECTION SYSTEM

## SEER*Abs and CS

## Overview of SEER*Abs

- **SEER*Abs is a framework application**
  - *generic functionality which can be selectively overridden by user code, providing specific functionality*

- **The record editor is implemented via XML files**
  - A default NAACCR Abstract layout is provided
  - SEER*Abs can be used out-of-the-box; or the registry can modify any aspect of the system

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## SEER*Abs Layouts

- **This excerpt from a SEER*Abs configuration file:**



- **Generates the top row of a data entry form:**



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## SEER*Abs and CS

- **The Collaborative Stage DLL is an integrated component**
- **Schema-specific pick lists (lookups) are used for CS fields**



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## SEER*Abs and CS

- **Site-specific factors that are obsolete or not required are hidden, by default. Example: 2012 prostate case.**



13

## SEER*Abs and CS

- **The abstractor can click Show All Factors to see factors that are not required or not used for the schema (factors 18-25 are not show in this screen shot).**



14

## SEER*Abs and CS

- **Site-specific factors that are obsolete or not required are hidden, by default. Example: 2009 prostate case. Notice that SSF 4 is shown**



15

## CS Methods in SEER*Abs

- **Methods to get version information and verify schema**

| | |
|---|---|
| getCsVersion() | Returns the Collaborative Stage current version number. |
| checkCsDiscriminatorRequired(site, hist) | Returns true if the discriminator is required to determine a schema for the site and histology. |
| checkCsSchemaExists(site, hist) | Returns true if the site and histology corresponds to at least one valid Collaborative Stage schema. This method returns true whether or not a discriminator is required to determine the schema. |

- **Methods to display the general information about the schema**

| | |
|---|---|
| getCSSchemaName(site, hist, ssf25) | Returns the name of the requested Collaborative Stage schema. |
| getCsSchemaNumber(site, hist, ssf25) | Returns the number of the requested Collaborative Stage schema as string. |
| getCsSchemaSubtitle(site, hist, ssf25) | Returns the subtitle of the requested Collaborative Stage schema. |
| getCsSchemaTitle(site, hist, ssf25) | Returns the title of the requested Collaborative Stage schema. |

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## CS Methods in SEER*Abs

- **Methods to determine which factors to show for a schema**

| | |
|---|---|
| getCsAlreadyCollectedSiteSpecificFactors(site, hist, ssf25) | Returns the indexes of factors that are in the "Already collected in Csv01" category for the schema. |
| | Site-specific factors are organized into 6 categories in the CoC and SEER Combined Site Specific Factors List. The factors required in 2010+ fall into 3 of those categories: "Already coded in Csv01", "Needed for Staging", and "Additional clinically significant". There are five methods related to required factors: one for each of the 3 separate categories listed above, one for all factors required for 2010+ (getCsRequiredSiteSpecificFactors), and one method that returns a list of the factors for years of diagnosis prior to 2010 (this returns additional factor for prostate cancer). |
| getCsClinicallySignificantSiteSpecificFactors(site, hist, ssf25) | Returns the indexes of the factors that are in the "Additional clinically significant" category for the schema. |
| getCsNeededForStagingSiteSpecificFactors(site, hist, ssf25) | Returns a list of factors that are in the "Needed for staging" category for the schema. |
| getCsRequiredSiteSpecificFactors(site, hist, ssf25) | Returns a list of the site specific factors required in 2010 and later. Schema is defined by the parameters: site, hist, ssf25. The list returned by this method will include factors in 3 categories: "Already coded in Csv01", "Needed for Staging", and "Additional clinically significant". Separate methods are also available for those categories. These categories are based on the CoC and SEER Combined Site Specific Factors List that is available on the Csv2 website. |
| getCsRequiredSiteSpecificFactorsPre2010(site, hist, ssf25) | Returns a list of the site specific factors required prior to 2010. The list returned by this method will include factors in 4 of the color-coded categories in the CoC and SEER Combined Site Specific Factors List: "Already coded in Csv01", "Needed for Staging", "Additional clinically significant", and "SSF4 for prostate is required thru 2009 but is not required for 2010+". |
| getCsRelevantSiteSpecificFactors(site, hist, ssf25) | Returns the indexes of relevant site specific factors for the schema. This method excludes factors that are in the "Obsolete – not coded for CSv2" category on the CoC and SEER Combined Site Specific Factors List. The schema is defined by the parameters: site, histology, and ssf25. |

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## CS Methods in SEER*Abs

### Calling the CS methods in the layout XML

```
else if (newSchemaName != null && (newSchemaName != schemaName || entityOpening || dxYearChanged)) {
    env.utils.setLabelText('csSchemaName', newSchemaName)
    env.utils.setValue('csSchemaName', newSchemaName)

    def requiredList = env.utils.getCsRequiredSiteSpecificFactors(site, hist, ssf25)
    def requiredPre2010List = env.utils.getCsRequiredSiteSpecificFactorsPre2010(site, hist, ssf25)

    for (idx in 1..25) {
        def subtitle = env.utils.getCsTableSubtitle(site, hist, ssf25, "csSiteSpecFact${idx}")
        def obsolete = subtitle != null && subtitle.trim().startsWith('OBSOLETE')
        def required = requiredList.contains(idx)
        def requiredPre2010 = requiredPre2010List.contains(idx)
        if (subtitle != null && !obsolete && (required || (requiredPre2010 && dxYear < 2010))) {
            env.utils.showRow("cstageRow${idx}")
            if (!entityOpening && idx != 25)
                env.utils.setValue("csSiteSpecificFactor${idx}", null) // make sure to reset the values (not ssf25 because it is used as a discriminator)

            def style = 'plain'
            if (required) {
                subtitle = '[REQ] ' + subtitle
                style = 'bold'
            }
            else if (requiredPre2010) {
                subtitle = '[REQ PRE-2010] ' + subtitle
                style = 'bold'
            }
            env.utils.setLabel("csSiteSpecificFactor${idx}Lbl", subtitle, style, '128-0-0')
        }
```

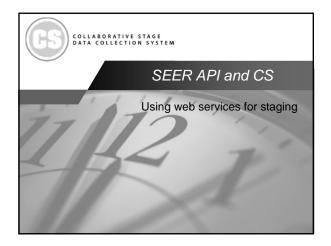National Cancer Institute — 18 — ims

## SEER*Abs and CS

- **The current version of SEER\*Abs:**
  - Uses the Collaborative Stage DLL to provide interactive data entry forms for collecting CS input fields
  - The DLL is not used to calculate values
  - Derived fields are not displayed
  - Utility methods could be added to display derived fields, if required by abstractors
  - SEER\*Abs automatically uses appropriate DLL (32 or 64 bit)

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## SEER*Abs and CS

- **SEER\*Abs is available on the SEER website:**
  - *seer.cancer.gov/seerabs*

- **For more information send an email to:**
  - *seerabs@imsweb.com*

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**CS** COLLABORATIVE STAGE
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## SEER*Abs Demonstration

## SEER API and CS

Using web services for staging

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## SEER API is…

- A RESTful web service that supports various SEER Program data sets and algorithms
- For developers who wish to incorporate SEER resources into their own systems
- Kept up-to-date with the latest SEER and NAACCR standards
- Free and easy to use
- Compatible with virtually all programming languages and operating systems
- NOT a tool for end-users
- An online resource which requires connectivity

National Cancer Institute                23                                   IMS
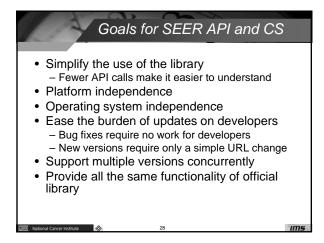
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## Supported APIs

- Collaborative Stage
  - Version 02.04.40
  - Will support multiple versions in the future
- Hematopoietic and Lymphoid Neoplasm Database
  - Supports both 2010 and 2012 versions
- SEER*Rx – Antineoplastic Drugs Database
- NAACCR documentation
  - Version 12.2
  - Will support multiple versions in the future
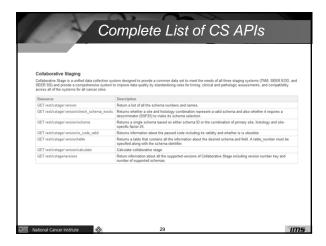- SEER Incidence Site Recode

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## Sites using SEER API

- Hematopoietic and Lymphoid Database
  - A tool to assist in screening for reportable cases and determining reportability requirements.
  - The database contains abstracting and coding information for all hematopoietic and lymphoid neoplasms (9590/3-9992/3).
  - http://seer.cancer.gov/seertools/hemelymph/
- SEER*Rx – Interactive Antineoplastic Drugs Database
  - A one-step lookup for coding oncology drug and regimen treatment categories in cancer registries.
  - http://seer.cancer.gov/seertools/seerrx/

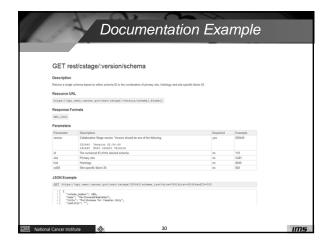National Cancer Institute                                    25                                    IMS

## Sites using SEER API

- SEER CS*Test
  - Derives Collaborative Stage and SEER Summary Stage values for individual cases.
  - You may enter cases, calculate values for CSv2 and SEER Summary Stage fields, and view the tables and logic used in the CSv2 algorithms.
  - Shown on the previous vendor webinar
  - *Web site going live in June*

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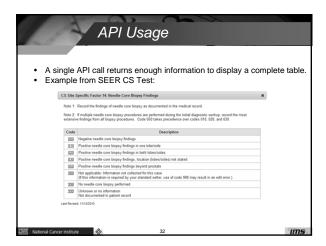
## How to use SEER API

- Sign up for a free account
- Find your API key in the "Account" page
- Build a request URL
  - All API calls are served over HTTPS.
  - API key must be supplied on the URL or as a header on the request.
  - Choose the type of data you want (either JSON or XML)
  - URL will look something like this:
    `https://api.seer.cancer.gov/rest/cstage/020440/table.json?id=112&table=3`
- Parse results
  - HTTP response code indicates success or failure
  - Parse JSON or XML to interpret results

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## Goals for SEER API and CS

- Simplify the use of the library
  - Fewer API calls make it easier to understand
- Platform independence
- Operating system independence
- Ease the burden of updates on developers
  - Bug fixes require no work for developers
  - New versions require only a simple URL change
- Support multiple versions concurrently
- Provide all the same functionality of official library

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## Complete List of CS APIs

**Collaborative Staging**

Collaborative Stage is a unified data collection system designed to provide a common data set to meet the needs of all three staging systems (TNM, SEE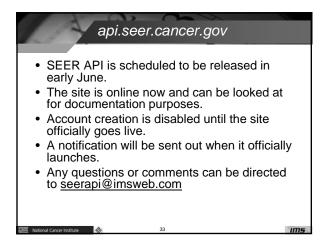R EOD, and SEER SS) and provide a comprehensive system to improve data quality by standardizing rules for timing, clinical and pathologic assessments, and compatibility across all of the systems for all cancer sites.

| Resource | Description |
|---|---|
| GET rest/cstage/:version | Return a list of all the schema numbers and names. |
| GET rest/cstage/:version/check_schema_exists | Returns whether a site and histology combination represent a valid schema and also whether it requires a descriminator (SSF25) to make its schema selection. |
| GET rest/cstage/:version/schema | Returns a single schema based on either schema ID or the combination of primary site, histology and site-specific factor 25. |
| GET rest/cstage/:version/is_code_valid | Returns information about the passed code including its validity and whether is is obsolete. |
| GET rest/cstage/:version/table | Returns a table that contains all the information about the desired schema and field. A table_number must be specified along with the schema identifier. |
| GET rest/cstage/:version/calculate | Calculate collaborative stage. |
| GET rest/cstage/versions | Return information about all the supported versions of Collaborative Stage including version number key and number of supported schemas. |

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## Documentation Example

GET rest/cstage/:version/schema

**Description**

Returns a single schema based on either schema ID or the combination of primary site, histology and site-specific factor 25.

**Resource URL**

https://api.seer.cancer.gov/rest/cstage/:version/schema[.format]

**Response Formats**

xml, json

**Parameters**

| Parameter | Description | Required | Example |
|---|---|---|---|
| version | Collaborative Stage version. Version should be one of the following. | yes | 020440 |
| | 020440  Version 02.04.40<br>latest  Most recent version. | | |
| id | The numerical ID of the desired schema. | no | 112 |
| site | Primary site | no | C481 |
| hist | Histology | no | 8240 |
| ssf25 | Site-specific factor 25 | no | 002 |

**JSON Example**

GET https://api.seer.cancer.gov/rest/cstage/020440/schema.json?site=C481&hist=8240&ssf25=002

```
1  {
2      "schema_number": 185,
3      "name": "PeritoneumFemaleGen",
4      "title": "Peritoneum for Females Only",
5      "subtitle": "",
```

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**API Demonstration**

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**API Usage**

- A single API call returns enough information to display a complete table.
- Example from SEER CS Test:

CS Site-Specific Factor 14: Needle Core Biopsy Findings

Note 1: Record the findings of needle core biopsy as documented in the medical record.

Note 2: If multiple needle core biopsy procedures are performed during the initial diagnostic workup, record the most extensive findings from all biopsy procedures. Code 050 takes precedence over codes 010, 020, and 030.

| Code | Description |
|---|---|
| 000 | Negative needle core biopsy findings |
| 010 | Positive needle core biopsy findings in one lobe/side |
| 020 | Positive needle core biopsy findings in both lobes/sides |
| 030 | Positive needle core biopsy findings, location (lobes/sides) not stated |
| 050 | Positive needle core biopsy findings beyond prostate |
| 988 | Not applicable: Information not collected for this case (If this information is required by your standard setter, use of code 988 may result in an edit error.) |
| 998 | No needle core biopsy performed |
| 999 | Unknown or no information Not documented in patient record |

Last Revised: 11/12/2010

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**api.seer.cancer.gov**

- SEER API is scheduled to be released in early June.
- The site is online now and can be looked at for documentation purposes.
- Account creation is disabled until the site officially goes live.
- A notification will be sent out when it officially launches.
- Any questions or comments can be directed to seerapi@imsweb.com

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*Feedback Mechanism for CS*

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# CSv2 Improvement Suggestion Form

NAACCR

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## The Form

- Allows for the anonymous submission of suggestions to the CSv2 development team.
- Spam deterrence using ReCAPTCHA

CSv2 Improvement Ticket Submission Form

This form is intaded to allow the submission of suggestions for improving CSv2 or software interfaces with CSv2.

*Subject:

*Description:

Type the two words:

Submit Issue

36

NAACCR

## The Management System

**CSv2** ▾   NAACCR, Inc.
**Home**   New Issue   Search ▾   Statistics ▾   Timeline   Wiki   Admin ▾
4 Members      3 Total Issues      3 Unresolved Issues      0 Unresolved Issues Assigned to Me

This is a project to manage additions, bugs, or improvements for CSv2.

- Utilizes SquishList by IMS, Inc.
- Directly interfaces with The Form through an API.
- Allows for assignment and routing of submitted suggestions/questions.

37

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## The Demo

38

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*Questions & Answers*

### Acknowledgment

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  - Its contents are solely the responsibility of the authors and do not necessarily represent the official views of the NCI, NIH, or DHHS.

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40