

SEER 2021 SUBMISSION REQUIREMENTS AND GUIDELINES

Please complete for each submission and email to:

SEERSUBM-L@list.nih.gov

	Standard Case Transmission File	NCCR Case Transmission File	Linkage Data File
Due Date	11/1/2021	11/1/2021	11/1/2021
Cohort	All resident cases thru 12/31/2020; 2020 used for in-house research only	All tumors for resident cases diagnosed with a tumor at age 0-39 between 1995 and 2019	Pharmacy claims 2013 thru 2nd quarter of 2021 for all patients in the Standard Case Transmission File Decipher and Castle variables linked to patients in the Standard Case Transmission File. See Attachment E for additional information.
Cases Edited	Cases diagnosed thru 12/31/2019 must pass all SEER edits. Cases with later years of diagnosis must pass inter-record edits, but do not need to pass other SEER edits.	Cases diagnosed thru 12/31/2019 must pass all SEER edits.	None
SEER*Edits Version	Version 6.20	Version 6.20	Not applicable
Upload	Upload data files and Attachment A to November 2021 folder on portal https://seer.cancer.gov/subreports/teamspace Link to Attachment A https://seer.cancer.gov/tools/2021Submission_Attachments-nov.docx		
File Format	NAACCR V21 XML User dictionary https://seer.cancer.gov/tools/seer-submission-dictionary-210-nov2021.xml	NAACCR V21 XML User dictionary https://seer.cancer.gov/tools/nccr-dictionary-2021.xml	NAACCR XML with extensions See Appendix E for technical information
File Naming Convention	RR.nov21.seer.xml.gz (where RR is the two-character registry abbreviation) Use Gzip to compress your XML file	RR.nov21.nccr.xml.gz (where RR is the two-character registry abbreviation) Use Gzip to compress your XML file	RR.nov21.linkage.xml.gz (where RR is the two-character abbreviation) Use Gzip to compress your XML file
Required Items	http://seer.cancer.gov/tools/seer.nov21.dataitems.pdf	http://seer.cancer.gov/tools/nccr.2021.dataitems.pdf	See Attachment E for required items
Sort Order	(NAACCR Item #40), Patient ID Number (NAACCR Item #20), and Record Number Recode (NAACCR Item #1775).		Patient ID Number (NAACCR Item #20)
Follow-Up	Submission should meet your registry's contract standards and goals for follow-up. See Attachment B.		Not applicable

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IHS indicator (NAACCR Item #192) and Record Linkage	<p>All SEER registries, with the exceptions of the Alaska Native Tumor Registry and the Cherokee Nation Cancer Registry, need to submit a file to IHS. Please submit the current value that you have from the November 2019 IHS linkage. We will update your file with the new IHS linkage information prior to the December submission to NAACCR. The IHS indicator should have:</p> <ul style="list-style-type: none"> • 0 if sent for linkage and no match • 1 if sent for linkage and matched <p>blank if case not sent for linkage See Attachment C for additional instructions</p>		<p>Not applicable</p>
NHAPIIA	<p>Use the NHAPIIA algorithms to update the API indicator (NAPIIA, NAACCR Item #193) and the Hispanic indicator (NHIA, NAACCR Item #191). These fields may be calculated by the registry's data management system or in a post-processing step. The algorithms are available in File*Pro. Every registry must run the algorithm.</p> <p>Indicate Option in Attachment A</p>		<p>Not applicable</p>
Collaborative Staging	<p>Please run your 2004+ data through the CS algorithm before submission. CS Version Derived [NAACCR item # 2936] must be CS version 02.05.</p>		<p>Not applicable</p>
Survival Time Fields Based on Complete Dates	<p>All registries must submit the calculated Survival Time date fields.</p> <p>File*Pro or SEER*DMS can be used to calculate the Survival Time fields.</p> <p>See Attachment D for instructions and more information</p>		<p>Not applicable</p>

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Attachment A

Submission to NCI

Please complete for each submission and email to:

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	Standard Case Transmission File	NCCR Case Transmission File	Data Linkage File
Registry Name			
Registry ID Number			
File Transfer Date			
File Name			
Years Submitted			
# Records Submitted			
NDI Linkage Date			Not applicable

Technical Contact

Name:

Telephone number:

e-mail address:

Registry Manager Contact

Name:

Telephone number:

e-mail address:

SEER 2021 SUBMISSION REQUIREMENTS AND GUIDELINES

Attachment A

Submission to NCI

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STANDARD CASE TRANSMISSION FILE QUESTIONS

NHAPIIA Options: Registries may select one of the options listed below when executing the NHIA algorithm. The option setting affects counties in which less than 5% of the population is of Hispanic/Latino ethnicity or to include all records.

Which option did you use when running NHAPIIA?

1. Option 1 – Only run the surname portion of the algorithm only on cases reported as Spanish surname only or as unknown whether Spanish (item 190 codes 7 or 9). In this choice, the surname portion will not be run on cases coded as 0, non-Hispanic.
2. Option 2 - Run the surname portion of the algorithm only on cases with a code of 7 on data element 190 (to verify that the surname is on the list of allowable Hispanic surnames) AND convert all cases with a code of 9 (unknown if Hispanic) to a code of 0 (Not Hispanic).
3. All Records – Apply all NHIA algorithms to all records. Note: this is listed as NHAPIIA option 0 in the SEER*DMS header information.

SEER*DMS Registries: The NHAPIIA option is documented with the version information. Click the SEER*DMS version on the home page.

NAACCR Call for Data Dec 2021:

Do you want SEER to submit your data to NAACCR? YES or NO

If YES:

For DMS registries: please submit the NAACCR file created using EXT-02 at the time of submission.

For Non-DMS registries: Include the extra year of data? YES or NO

NAACCR has requested certain items that are not required by SEER. Unless directed otherwise, we will send all NAACCR required data items, <https://www.naacr.org/call-for-data/>. **Please indicate if there are any items you do not wish to include.**

Known Data Problems including reasons:

SEER 2021 SUBMISSION REQUIREMENTS AND GUIDELINES

Attachment A

Submission to NCI

Please complete for each submission and email to:

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NCCR CASE TRANSMISSION FILE

Known Data Problems including reasons:

DATA LINKAGE FILE

Known Data Problems including reasons:

ADDITIONAL COMMENTS:

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Attachment B

SEER Patient Follow-up Calculations

The last reporting year for this submission is **2019**. The percent of patients diagnosed through 2019 who have current follow-up is defined as

$$P = 100(D + A)/T$$

Where....

- A patient is counted by selecting one record per person where sequence is 00 or 01.
- D is the number of patients who have died.
- A is the number of alive patients with follow-up dates on or after January 1, 2020
- T is the total number of patients. This includes A + D + the number of patients who were last known to be alive with follow-up dates prior to January 1, 2020.

P can be calculated for individual years of diagnosis up through 2019 and for all years combined.

November Submission Requirements

Reportable cases followed into 2020	Contractual Standard	Minimum Acceptable
All invasive (includes bladder in situ)	>=95%	>=90%
Age < 20 (invasive)	>=90%	>=80%
Ages 20-64 (invasive)	>=90%	>=80%
Ages 65+ (invasive)	>=95%	>=90%
All In situ (excluding cervix in situ)	>=90%	>=80%
Benign and borderline CNS	Follow-up is expected but no contractual standards are set at this time	

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Attachment C

IHS linkage instructions

Record selection criterion:

1. SEER-reportable cases;
2. Diagnosed between 01/01/1988 and 12/31/2019 (inclusive);
3. For diagnosis years 1988-2009 (or SEER start year to 2019), the cases in this file should be the same as those that will be submitted in the November 2021 file (i.e., no more, no less).

File structure:

1. ASCII format
2. File must be submitted in the condensed file structure described in Table 1 (below)
3. Encrypted/password protected file (password to be sent separately via e-mail or direct telephone contact).

File can be delivered in one of the following 3 methods:

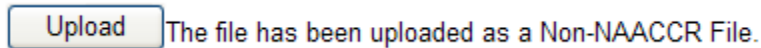
1. Submit your files electronically via the New Mexico Tumor Registry's sFTP web-site according to the following steps:
 - a. Send an e-mail message to the following address: NMTRHelpDesk@salud.unm.edu
 - b. Specify that you are requesting a folder on our secure sFTP web-site for the SEER-IHS linkage. Be sure to let NMTR Help Desk know which registry you are representing.
 - c. NMTR Help Desk will receive an e-mail message that contains your assigned user-name.
 - d. Respond to the NMTR Help Desk e-mail message; they will send you a password via a separate e-mail message. This second message will include instructions for accessing our sFTP site.
 - e. Please feel free to contact Chuck Wiggins at (505) 272-3127 (direct) if you have questions.

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Attachment C

IHS linkage instructions

2. IHS WebPlus – please contact Melissa Jim to set up a WebPlus account.
 - a. Zip the extract file that will be used for the IHS Linkage.
 - b. Open Internet Explorer and type in the following web address: <http://webplus.ihs.gov/logonen.aspx>
 - c. Press Enter.
 - d. Type in the User ID and password that was emailed to you.
 - e. Click Log in.
 - f. Click on the File Upload link.
 - g. Click on the New Upload button on the menu bar.
 - h. The Upload Abstract Bundle page will appear.
 - i. Select non-NAACCR File button.
 - ii. Click on Browse to select the zip file to upload.
 - iii. Type in any comments.
 - iv. Click on the Upload button.
 - v. Once the file is uploaded you should be able to see this message:



- i. Click on Log out on the menu bar.
 - j. Close Internet Browser.
3. Ship encrypted/strong-password-protected “hard copies” of the file via express courier service to:
Charles Wiggins, PhD
Director, New Mexico Tumor Registry
2325 Camino de Salud NE, Building 229, Room G-63
Albuquerque, NM 87131-0001

Follow up:

1. Results from the IHS linkage will be returned to each registry and to the NCI (only case identification number and linkage results will be provided to NCI; patient-identifying information such as name and social security number will be sent only to the IHS for linkage and will not be sent to NCI).
2. NCI will be responsible for updating the November submission files from the registries with the new IHS linkage results and will also supply the linkage results to NAACCR for those registries for which NCI has performed this submission in the past.
3. Registries that submit their own data to NAACCR must update their files with the IHS linkage results since the IHS Link variable [NAACCR #192] is included as part of the NAACCR call for data.

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Attachment C

IHS linkage instructions

Item #	Length	Condensed layout Column #	Name
10	1	1-1	Record Type
20	8	2-9	Patient ID Number
50	3	10-12	NAACCR Record Version
40	10	13-22	Registry ID
70	50	23-72	Addr at DX--City
80	2	73-74	Addr at DX--State
100	9	75-83	Addr at DX--Postal Code
90	3	84-86	County at DX
160	2	87-88	Race 1
161	2	89-90	Race 2
162	2	91-92	Race 3
163	2	93-94	Race 4
164	2	95-96	Race 5
190	1	97-97	Spanish/Hispanic Origin
220	1	98-98	Sex
230	3	99-101	Age at Diagnosis
240	8	102-109	Date of Birth
241	2	110-111	Date of Birth Flag
192	1	112-112	IHS Link
380	2	113-114	Sequence Number--Cntrl
390	8	115-122	Date of Diagnosis
391	2	123-124	Date of Diagnosis Flag
1750	8	125-132	Date of Last Contact
1751	2	133-134	Date of Last Contact Flag
1760	1	135-135	Vital Status
1810	50	136-185	Addr Current--City
1820	2	186-187	Addr Current--State
1830	9	188-196	Addr Curr--Postal Code
1840	3	197-199	County—Current

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Attachment C

IHS linkage instructions

Item #	Length	Condensed layout Column #	Name
2230	40	200-239	Name--Last
2240	40	240-279	Name--First
2250	40	280-319	Name--Middle
2280	40	320-359	Name--Alias
2390	40	360-399	Name--Maiden
2290	60	400-459	Name--Spouse/Parent
2320	9	460-468	Social Security Number
2330	60	469-528	Addr at DX--No & Street
2335	60	529-588	Addr at DX--Supplement
2350	60	589-648	Addr Curr--No & Street
2355	60	649-708	Addr Curr--Supplement

Contacts:

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Director, New Mexico Tumor Registry
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cwiggins@salud.unm.edu

SEER 2021 SUBMISSION REQUIREMENTS AND GUIDELINES

Attachment D

Survival Calculation Methods

SEER program requires all registries to submit the Survival Time calculated fields prior to submission. Additional information is available at: <http://seer.cancer.gov/survivaltime/>. Please submit questions and report software issues to SEERSUBM-L@list.nih.gov.

Instructions:

- Use File*Pro or SEER*DMS to calculate these survival fields. File*Pro and SEER*DMS use complete Date of Diagnosis and Date of Last Contact, including day, and creates seven fields.
- The input file for File*Pro must include the day of diagnosis and day of last contact. Those fields and the calculated fields must have day removed prior to submission.

Additional considerations:

- Please do not attempt to recode any missing date fields for Date of Diagnosis or Date of Last Contact. One purpose of the algorithm is to standardize specification of missing month and day fields.
- These data items will not affect the Data Quality Profiles.

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Attachment E

Linkage Data File Format

The linkage file needs to use the NAACCR XML Data Exchange format; specifications for that format can be found on the NAACCR website.

The linkage data needs to be transmitted as an “extension” of that format. Extensions are an advanced feature of the NAACCR XML Data Exchange format that allows customized XML tags to be inserted within the standard XML syntax.

The extensions require to be defined in their own XML namespace to avoid any conflict with the standard XML tags defined by NAACCR. This is accomplished by adding the following root attribute:

```
xmlns:seer="https://seer.cancer.gov/naaccrxml/linkage"
```

In addition to that namespace, the root attributes also need to specify the data linkage version, this is accomplished by adding the following root attribute:

```
seer:linkageDataVersion="1.0"
```

The linkage file should contain only two NAACCR standard items: the Patient ID Number and the Tumor Record Number (when applicable). If a Patient doesn't have any linkage data, it should not appear in the linkage file. A given Patient ID Number can only appear once in the linkage file. The Patient entries should be sorted by their Patient ID Number in the file. Tumors need to be added to the file if they contain some linkage data; the Tumor Record Number is then required for each Tumor. The Tumors should be provided in the same order as the main data file.

The following extension tags must be used:

- <seer:PatientLinkageData>: under the standard <Patient> tag, optional, must appear after the Patient ID Number item. Wrapper for all patient-level linkage data.
- < seer:PharmacyData>: under < seer:PatientLinkageData>, optional, if provided, can only appear once. Wrapper for all Pharmacy data.
- < seer:PharmacyMedication>: under < seer:PharmacyData>, can appear once or more.
- < seer:MedicalDispenserIdentifier>: under < seer:PharmacyMedication>, required. Canonical identifier of a medication dispensing event. Will be calculated as follow: events will be order by dispense date (request date if dispense date is not available), and a sequence number will be assigned to the sorted event. The sequence is reset to 1 for each new Patient. Identifiers are expected to change from one submission to another. Values should not be zero-padded (use 1, 2, etc...).
- < seer:MedicationRequestAuthoredOn>: under < seer:PharmacyMedication>, optional. Date medication was requested. Use the "yyyymmdd" format (8 digits); use the "yyyymm" format (6 digits) if only year and month are known, use the "yyyy" format (4 digits) if only year is known. Don't transmit the date if all parts are unknown.
- < seer:MedicationDispenseAuthoredOn>: under < seer:PharmacyMedication>, optional. Date medication was dispensed. Use the "yyyymmdd" format (8 digits); use the "yyyymm" format (6 digits) if only year and month are known, use the "yyyy" format (4 digits) if only year is known. Don't transmit the date if all parts are unknown.

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Linkage Data File Format

- `< seer:MedicationRequestNdc>`: under `< seer:PharmacyMedication>`, optional. Identifies medication being requested by National Drug Code 11-digit. National Drug Code Directory; format 5-4-2; 50242-0040-62. Dashes should not be included. NDC should not be transmitted if unknown.
- `< seer:MedicationDispenseQuantity>`: under `< seer:PharmacyMedication>`, optional. The amount of medication that has been dispensed. FHIR 2.24.0.6 Quantity. Do not transmit if unknown.
- `< seer:MedicationDispenseDuration>`: under `< seer:PharmacyMedication>`, optional. Identifies the period time over which the supplied product is expected to be used, or the length of time the dispense is expected to last. Number of days. Do not transmit if unknown.
- `<seer:TumorLinkageData>`: under the standard `<Tumor>` tag, optional, must appear after the Tumor Record Number item. Wrapper for all tumor-level linkage data.
 - `<seer:DecipherData>`: under `<seer:TumorLinkageData>`, optional, if provided, can only appear once. Wrapper for all Decipher data.
 - `<seer:DecipherResult>`: under `<seer:DecipherData>`, can appear once or more.
 - `<seer:DecipherOrderIdentifier>`: under `<seer:DecipherResult>`, required. Unique order identifier. The same identifier can appear more than once for the same Patient if the result is linked to more than one Tumor.
 - `<seer:DecipherTestType>`: under `<seer:DecipherResult>`, optional. The type Decipher test which was ordered: Decipher Biopsy, Decipher Post-Op, Decipher Bladder, etc...
 - `<seer:DecipherSequenceAvail>`: under `<seer:DecipherResult>`, optional. Availability of genomic data: 0=Indicates genomic data is not available for analysis; 1=Indicates genomic data is available for analysis.
 - `<seer:DecipherReportStatus>`: under `<seer:DecipherResult>`, optional. Status of Decipher Report: 0=Indicates Decipher Report was not provided to ordering physician; 1=Indicates Decipher Report was provided to ordering physician.
 - `<seer:DecipherClassifierScore>`: under `<seer:DecipherResult>`, optional. Genomic Classifier score calculated using the sample .CEL file to determine the probability of metastatic disease progression.
 - `<seer:DecipherClassifierCategory>`: under `<seer:DecipherResult>`, optional. Decipher Risk Category determined by the "Decipher Score": Lower <0.45 ; Average $[0.45-0.60]$; Higher >0.60
 - `<seer:DecipherInitiationDate>`: under `<seer:DecipherResult>`, optional. Date of Decipher order initiation. Use the "yyyymmdd" format (8 digits); use the "yyyymm" format (6 digits) if only year and month are known, use the "yyyy" format (4 digits) if only year is known. Don't transmit the date if all parts are unknown.
- `<seer:DecisionDxData>`: under `<seer:TumorLinkageData>`, optional, if provided, can only appear once. Wrapper for all Decision-DX data.
- `<seer:DecisionDxResult>`: under `<seer:DecisionDxData>`, can appear once or more.

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Attachment E

Linkage Data File Format

- <seer:DecisionDxOrderIdentifier>: under <seer:DecisionDxResult>, required. Order ID from Castle. The same identifier can appear more than once for the same Patient if the result is linked to more than one Tumor.
- <seer:DecisionDxReportDate>: under <seer:DecisionDxResult>, optional. Date of report are provided for DecisionDx. Use the "yyyymmdd" format (8 digits); use the "yyyymm" format (6 digits) if only year and month are known, use the "yyyy" format (4 digits) if only year is known. Don't transmit the date if all parts are unknown.
- <seer:DecisionDxUmGep>: under <seer:DecisionDxResult>, optional. UM SEER Cases Decode: UM Castle GEP Class Score (DecisionDx-UM) 10 Class 1A (includes normal and reduced classification) 20 Class 1B (includes normal and reduced classification) 30 Class 2 (includes normal and reduced classification) 99 No score available/unknown.
- <seer:DecisionDxUmPrame>: under <seer:DecisionDxResult >, optional. UM Castle reported PRAME; 01 PRAME negative; 02 PRAME positive; 99 PRAME unknown.
- <seer:DecisionDxCmGepMainClass>: under <seer:DecisionDxResult >, optional. Genomic Classifier score calculated using the sample .CEL file to determine the probability of metastatic disease progression.
- <seer:DecisionDxCmGepSubClass>: under <seer:DecisionDxResult >, optional. CM Castle GEP Main Class Score: 10 Class 1 (includes 1A, 1B); 20 Class 2 (includes 2A, 2B, 2 reduced); 99 No score available/unknown.

A full example of a linkage file for a single Patient with two Tumors can be found here: <https://seer.cancer.gov/tools/submission.html>