

# SEERaBomb Overview

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## Introduction

**SEERaBomb** is for SEER and Japanese A-bomb survivor data analysts. It contributes speed to SEER analyses by reducing file sizes to contain only items of interest. This document assumes that the data has been downloaded into folders off of the root called `/data/SEER` and `/data/abomb`. To obtain the data please visit the links in [gettingData.pdf](#). Use cases are given in R scripts in the `courses` and `papers` directories.

## SEER Data R Binaries

The incidence directory of the SEER dataset contains a SAS file that defines the field names, their starting positions, and their fixed widths. This file can be used to read the SEER data into SAS, but it is used here to: 1) present the field choices (see `fieldNames.html` and the output of `getFields()`); and 2) given user choices, automatically determine the sequence of widths needed to extract the data of interest using the speedy R package `LaF`. `getFields()` has one parameter, `seerHome="/data/SEER"`, which should be overridden if the SEER data lives elsewhere. Its `data.frame` output and the SEER file `seerdic.pdf` in the SEER incidence directory must be thoroughly examined to determine which fields will be useful. Once this is determined, the output and list of field choices, the default of which is

```
picks=c("casenum","reg","race","sex","agedx","yrbrth",  
        "seqnum","yrdx","histo2","histo3","radiatn","agerec",  
        "ICD9","histrec","numprims","COD","surv"),
```

must then be inputted into `pickFields()`.

The output of `pickFields()` contains not only pulled rows from the input, but also inserted rows with widths computed to fill the gaps of no interest. Knowing these gap sizes enables fast file reading by `LaF` in `mkSEER()`. This function produces R Data binaries in SEER dataset subdirectories of `seerHome` such as `/data/SEER/00` for SEER18 data (which was collected since 2000).

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```

> library(SEERaBomb)
> df=getFields()
> (df=pickFields(df))

```

	start	width	names	desc	type
casenum	1	8	casenum	Patient ID number	integer
reg	9	10	reg	Registry ID	integer
3	19	1			string
race	20	2	race	Race/Ethnicity	integer
5	22	2			string
sex	24	1	sex	Sex	integer
agedx	25	3	agedx	Age at diagnosis	integer
yrbrth	28	4	yrbrth	Year of birth	integer
9	32	3			string
seqnum	35	2	seqnum	Sequence Number--Central	integer
11	37	2			string
yrdx	39	4	yrdx	Year of diagnosis	integer
13	43	5			string
histo2	48	4	histo2	Histology (92-00) ICD-0-2	integer
15	52	1			string
histo3	53	4	histo3	Histologic Type ICD-0-3	integer
17	57	110			string
radiatn	167	1	radiatn	RX Summ--Radiation	integer
19	168	24			string
agerec	192	2	agerec	Age Recode <1 Year olds	integer
21	194	10			string
ICD9	204	4	ICD9	Recode ICD-0-2 to 9	integer
23	208	18			string
histrec	226	2	histrec	Histology Recode--Broad Groupings	integer
25	228	15			string
numprims	243	2	numprims	Number of primaries	integer
27	245	10			string
COD	255	5	COD	Cause of death to SEER site recode	integer
29	260	41			string
surv	301	4	surv	Survival months	integer
31	305	27			string

```

> #mkSEER(df,dataset="92") #places 1992-2010 binaries in /data/SEER/92

```