

# 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 see the links in `dataLinks.docx`. Use cases are given in the `blood2012` functions available from `help` and in the R scripts in the `papers` directory.

## 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 over-ridden 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 that can be found in SEER dataset subdirectories of `seerHome`, e.g. in directories 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
```