

# Retrieve standard data from Seatrack

*Jens Åström*

*4/20/2018*

## Connect

```
require(seatrackR)

## Loading required package: seatrackR
connectSeatrack("testreader", "testreader")
```

## Get basic data

As of now, 4 functions exist to retrieve data from the database through prebuilt queries. Apart from that, users are free to use their own queries through the functions in DBI and `dplyr`, using the connection named `con` made by the `connectSeatrack()`-function.

```
require(DBI)

## Loading required package: DBI
myQuery <- "SELECT * from loggers.logger_info
           WHERE producer = 'Biotrack'"

biotrackLoggers <- dbGetQuery(con, myQuery)
head(biotrackLoggers)
```

##	id	logger_id	logger_serial_no
## 1	dcfbe79c-3bd7-11e8-adeb-005056b165f3	1	V1416004
## 2	dcfd32b4-3bd7-11e8-adeb-005056b165f3	2	V1416049
## 3	dcfd87dc-3bd7-11e8-adeb-005056b165f3	3	V1416065
## 4	dcfd87dc-3bd7-11e8-adeb-005056b165f3	4	V2012314
## 5	dcfe30d8-3bd7-11e8-adeb-005056b165f3	5	V1416001
## 6	dcfe81a0-3bd7-11e8-adeb-005056b165f3	6	V1416002

  

##	logger_model	producer	production_year	project
## 1	mk3006	Biotrack	2014	SEATRACK
## 2	mk3006	Biotrack	2014	SEATRACK
## 3	mk3006	Biotrack	2014	SEATRACK
## 4	mk3006	Biotrack	2014	SEATRACK
## 5	mk3006	Biotrack	2014	SEATRACK
## 6	mk3006	Biotrack	2014	SEATRACK

## The getFileArchive function

```
eynhallowFiles <- getFileArchive(selectColony = "Eynhallow")
eynhallowFiles
```

```
## # A tibble: 353 x 9
##   file_id session_id colony    ring_number euring_code year_tracked
##   <int>    <int> <chr>    <chr>      <chr>      <chr>
## 1      1      1      5 Eynhallow FP96304    GBT      2014_15
## 2      2      2      5 Eynhallow FP96304    GBT      2014_15
## 3      3      3      5 Eynhallow FP96304    GBT      2014_15
## 4      4      4      5 Eynhallow FP96304    GBT      2014_15
## 5      5      5      5 Eynhallow FP96304    GBT      2014_15
## 6      6      6      6 Eynhallow FS68841    GBT      2014_15
## 7      7      7      6 Eynhallow FS68841    GBT      2014_15
## 8      8      8      6 Eynhallow FS68841    GBT      2014_15
## 9      9      9      6 Eynhallow FS68841    GBT      2014_15
## 10     10     10      6 Eynhallow FS68841    GBT      2014_15
## # ... with 343 more rows, and 3 more variables: logger_serial_no <chr>,
## #   logger_model <chr>, filename <chr>
```

## The getIndividInfo function

We can also select the year interval the bird where tracked.

```
eynhallowIndivids <- getIndividInfo(selectColony = "Eynhallow", selectYear = "2014_15")
eynhallowIndivids
```

```
## # A tibble: 82 x 29
##   session_id colony    year_tracked ring_number euring_code color_ring.x
##   <int> <chr>    <chr>      <chr>      <chr>      <chr>
## 1      50 Eynhallow 2014_15    FC28999    GBT      N/O/R
## 2      50 Eynhallow 2014_15    FC28999    GBT      N/O/R
## 3      50 Eynhallow 2014_15    FC28999    GBT      N/O/R
## 4      50 Eynhallow 2014_15    FC28999    GBT      N/O/R
## 5      46 Eynhallow 2014_15    FH89008    GBT      BL/Y/N
## 6      46 Eynhallow 2014_15    FH89008    GBT      BL/Y/N
## 7      20 Eynhallow 2014_15    FH89013    GBT      O/R/W
## 8      20 Eynhallow 2014_15    FH89013    GBT      O/R/W
## 9      20 Eynhallow 2014_15    FH89013    GBT      O/R/W
## 10     20 Eynhallow 2014_15    FH89013    GBT      O/R/W
## # ... with 72 more rows, and 23 more variables: species <chr>,
## #   subspecies <chr>, morph <chr>, age <chr>, sex <chr>,
## #   sexing_method <chr>, status_date <date>, weight <dbl>, scull <dbl>,
## #   tarsus <dbl>, wing <dbl>, breeding_stage <chr>, eggs <int>,
## #   chicks <int>, hatching_success <lgl>, breeding_success <lgl>,
## #   breeding_success_criterion <chr>, data_responsible <chr>,
## #   back_on_nest <lgl>, comment <chr>, status_sex <chr>,
## #   status_sexing_method <chr>, status_age <chr>
```

!Note the weird duplicate records here!

```
eynhallowIndivids %>% print(width = Inf)
```

```
## # A tibble: 82 x 29
##   session_id colony    year_tracked ring_number euring_code color_ring.x
##   <int> <chr>    <chr>      <chr>      <chr>      <chr>
## 1      50 Eynhallow 2014_15    FC28999    GBT      N/O/R
## 2      50 Eynhallow 2014_15    FC28999    GBT      N/O/R
## 3      50 Eynhallow 2014_15    FC28999    GBT      N/O/R
```

##	4	50 Eynhallow	2014_15	FC28999	GBT	N/O/R		
##	5	46 Eynhallow	2014_15	FH89008	GBT	BL/Y/N		
##	6	46 Eynhallow	2014_15	FH89008	GBT	BL/Y/N		
##	7	20 Eynhallow	2014_15	FH89013	GBT	O/R/W		
##	8	20 Eynhallow	2014_15	FH89013	GBT	O/R/W		
##	9	20 Eynhallow	2014_15	FH89013	GBT	O/R/W		
##	10	20 Eynhallow	2014_15	FH89013	GBT	O/R/W		
##		species	subspecies	morph	age	sex	sexing_method	
##		<chr>	<chr>	<chr>	<chr>	<chr>	<chr>	
##	1	Northern fulmar	<NA>	LL	23	male	dna	
##	2	Northern fulmar	<NA>	LL	23	male	dna	
##	3	Northern fulmar	<NA>	LL	23	male	dna	
##	4	Northern fulmar	<NA>	LL	23	male	dna	
##	5	Northern fulmar	<NA>	LL	adult_unknown	female	morphology	
##	6	Northern fulmar	<NA>	LL	adult_unknown	female	morphology	
##	7	Northern fulmar	<NA>	LL	adult_unknown	male	morphology	
##	8	Northern fulmar	<NA>	LL	adult_unknown	male	morphology	
##	9	Northern fulmar	<NA>	LL	adult_unknown	male	morphology	
##	10	Northern fulmar	<NA>	LL	adult_unknown	male	morphology	
##		status_date	weight	scull	tarsus	wing	breeding_stage	eggs
##		<date>	<dbl>	<dbl>	<dbl>	<dbl>	<chr>	<int>
##	1	2016-07-11	1557	NA	NA	NA	rearing chicks	1
##	2	2015-06-03	NA	NA	57.0	NA	nonbreeding/failed_breeder	NA
##	3	2015-06-03	NA	NA	57.0	NA	nonbreeding/failed_breeder	NA
##	4	2014-07-12	NA	NA	NA	NA	rearing chicks	NA
##	5	2015-06-01	NA	NA	54.4	NA	incubating	1
##	6	2014-07-15	NA	NA	NA	NA	rearing chicks	NA
##	7	2017-07-08	1949	840	NA	58.3	failed breeder	1
##	8	2016-07-11	1949	NA	NA	NA	rearing chicks	1
##	9	2017-07-08	1949	840	NA	58.3	failed breeder	1
##	10	2015-06-04	NA	NA	57.6	NA	nonbreeding/failed_breeder	NA
##		chicks	hatching_success	breeding_success	breeding_success_criterion			
##		<int>	<lgl>		<lgl>		<chr>	
##	1	1	T		T		30d	
##	2	NA	NA		NA		<NA>	
##	3	NA	NA		NA		<NA>	
##	4	NA	NA		NA		<NA>	
##	5	NA	F		F		30d	
##	6	NA	NA		NA		<NA>	
##	7	0	F		F		<NA>	
##	8	1	T		T		30d	
##	9	0	F		F		<NA>	
##	10	NA	NA		NA		<NA>	
##		data_responsible	back_on_nest	comment			status_sex	
##		<chr>	<lgl>	<chr>			<chr>	
##	1	Paul Thompson	T	<NA>			<NA>	
##	2	Paul Thompson	NA	<NA>			male	
##	3	Paul Thompson	NA	<NA>			male	
##	4	Paul Thompson	NA	Feathers for SI			male	
##	5	Paul Thompson	T	<NA>			female	
##	6	Paul Thompson	NA	Feathers for Sex & SI			unknown	
##	7	Paul Thompson	T	5 feathers for ARCTOX			male	
##	8	Paul Thompson	T	<NA>			<NA>	
##	9	Paul Thompson	T	5 feathers for ARCTOX			male	

```
## 10 Paul Thompson      NA          <NA>          male
##   status_sexing_method status_age
##   <chr>                <chr>
## 1 <NA>                <NA>
## 2 dna                  23
## 3 dna                  23
## 4 dna                  22
## 5 morphology           adult_unknown
## 6 dna                  adult_unknown
## 7 morphology           adult_unknown
## 8 <NA>                 <NA>
## 9 morphology           adult_unknown
## 10 morphology          adult_unknown
## # ... with 72 more rows
```

The getPosdata function

```
eynhallowPositions <- getPosdata(selectColony = "Eynhallow")
eynhallowPositions
```

```
## Simple feature collection with 1000 features and 42 fields
## geometry type:  POINT
## dimension:      XY
## bbox:           xmin: -50.10751 ymin: 46.85275 xmax: 43.68781 ymax: 76.62713
## epsg (SRID):    4326
## proj4string:     +proj=longlat +datum=WGS84 +no_defs
## # A tibble: 1,000 x 43
##   id      date_time      logger logger_id logger_model year_tracked
##   <chr>   <dtm>         <chr>  <chr>    <chr>        <chr>
## 1 419e8d0~ 2015-11-22 02:10:30 V1416~ V1416051 mk3006      2015_16
## 2 8af4074~ 2015-11-22 14:07:00 V1416~ V1416051 mk3006      2015_16
## 3 e4c8879~ 2015-11-23 01:55:30 V1416~ V1416051 mk3006      2015_16
## 4 04f9d0d~ 2015-11-23 13:42:00 V1416~ V1416051 mk3006      2015_16
## 5 29f9ad3~ 2015-11-24 01:26:30 V1416~ V1416051 mk3006      2015_16
## 6 c6f99be~ 2015-11-24 13:11:30 V1416~ V1416051 mk3006      2015_16
## 7 8c1c5e5~ 2015-11-25 00:49:00 V1416~ V1416051 mk3006      2015_16
## 8 d486c60~ 2015-11-25 12:06:30 V1416~ V1416051 mk3006      2015_16
## 9 01487c4~ 2015-11-26 00:05:30 V1416~ V1416051 mk3006      2015_16
## 10 7334c8f~ 2015-11-27 12:06:00 V1416~ V1416051 mk3006      2015_16
## # ... with 990 more rows, and 37 more variables: session_id <int>,
## #   year_deployed <int>, year_retrieved <int>, ring_number <chr>,
## #   euring_code <chr>, species <chr>, colony <chr>, lon_raw <dbl>,
## #   lat_raw <dbl>, lon_smooth1 <dbl>, lat_smooth1 <dbl>,
## #   disttocol_s2 <dbl>, eqfilter1 <int>, eqfilter2 <int>, eqfilter3 <int>,
## #   lat_smooth2_eqfilt3 <dbl>, sex <chr>, morph <chr>, subspecies <chr>,
## #   age <chr>, col_lon <dbl>, col_lat <dbl>, tfirst <dtm>,
## #   tsecond <dtm>, twl_type <int>, conf <int>, sun <dbl>, software <chr>,
## #   light_threshold <int>, analyzer <chr>, data_responsible <chr>,
## #   logger_yeartracked <chr>, posdata_file <chr>, import_date <date>,
## #   data_version <int>, database_version <int>, geometry <S3: sfc_POINT>
```