

Mark-recapture distance sampling (MRDS) in the `mrds` R package

- Data requirements
- MRDS analyses

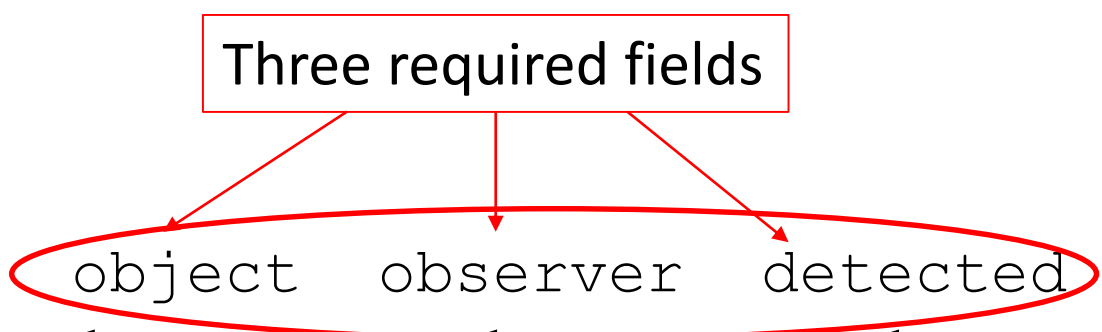
Data requirements

Detection data must have:

- 2 rows per object – one for Observer 1 and one for Observer 2
- Fields for:
 - **object** (unique object ID)
 - **observer** (1 or 2)
 - **detected** (1=yes, 0=no)
 - distance (perpendicular distance)
 - size (cluster size, if required)
- Additional covariate data can be included
- Tables for region and samples (see later)

Example: golf tee survey data – ‘detections’

Three required fields



| | object | observer | detected | distance | size | sex | exposure |
|---|--------|----------|----------|----------|------|-----|----------|
| 1 | 1 | 1 | 1 | 2.68 | 2 | 1 | 1 |
| 1 | 1 | 2 | 0 | 2.68 | 2 | 1 | 1 |
| 2 | 1 | 1 | 1 | 3.33 | 2 | 1 | 0 |
| 2 | 1 | 2 | 0 | 3.33 | 2 | 1 | 0 |
| 3 | 1 | 1 | 1 | 0.34 | 1 | 0 | 0 |
| 3 | 1 | 2 | 0 | 0.34 | 1 | 0 | 0 |

MRDS analysis

```
library(mrds)
```

```
ddf (data, method, mrmmodel, dsmodel, meta.data)
```

Depends on method

E.g. Truncation

Observer configuration and point/full independence

```
E.g. ddf (data=detections, method="trial",  
          mrmmodel=~glm(link='logit', formula=~distance),  
          dsmodel=~cbs(key='hn'),  
          meta.data=list(width=4))
```

When is DS model required?

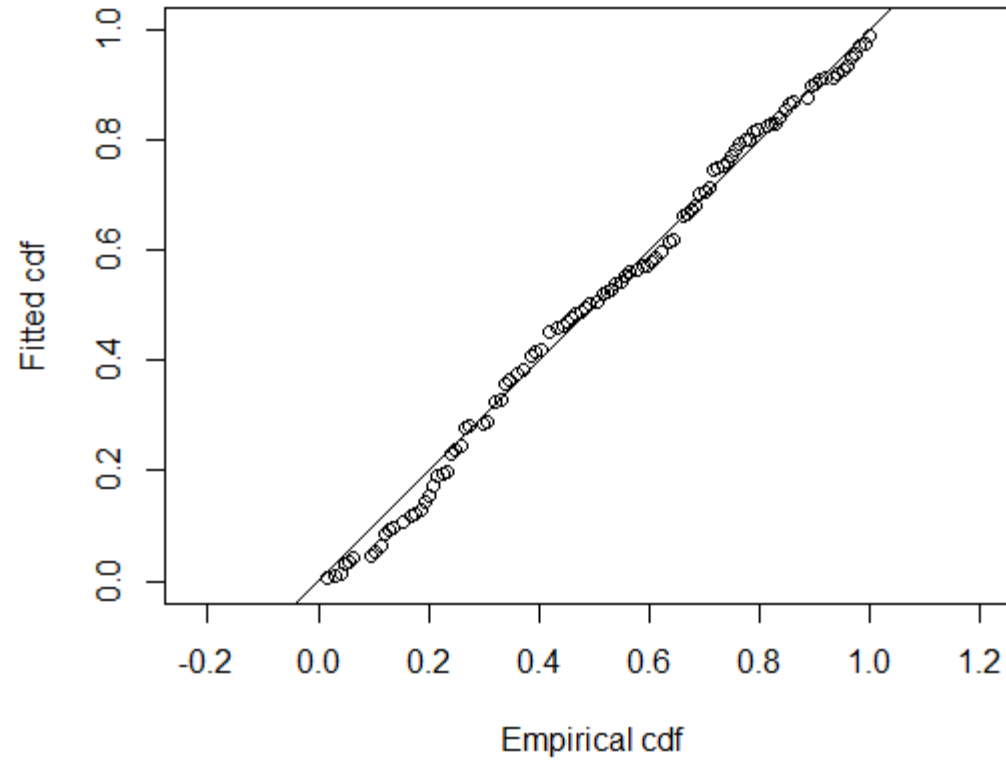
| Observer configuration | Point/Full independence | Method | MR model | DS model |
|------------------------|-------------------------|-----------------------|----------|----------|
| Trial | Point | <code>trial</code> | Yes | Yes |
| Trial | Full | <code>trial.fi</code> | Yes | No |
| IO | Point | <code>io</code> | Yes | Yes |
| IO | Full | <code>io.fi</code> | Yes | No |

Additional covariates

```
fit.mrds <- ddf(data=detections, method="trial",  
  mrmmodel=~glm(link='logit', formula=~distance+sex),  
  dsmodel=~mcids(key='hn', formula=~size),  
  meta.data=list(width=4))
```

Results: goodness of fit tests, qq plots

```
ddf.gof(fit.ddf)
```

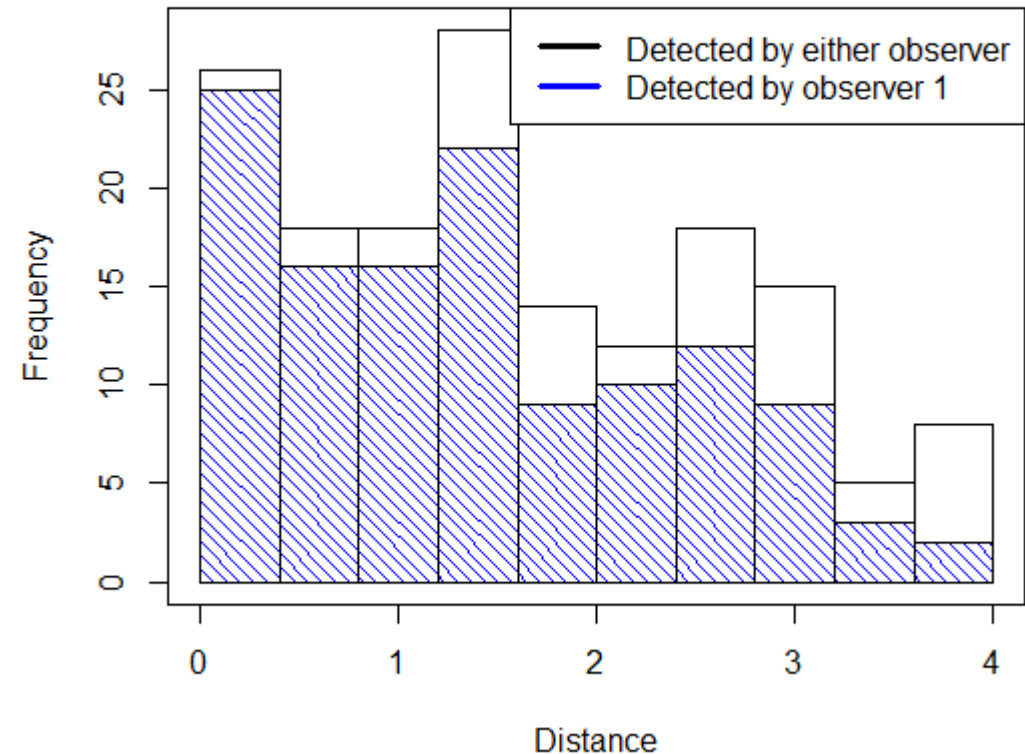


Results: summary tables and plots

```
det.tables(fit.trial.pi)    plot(det.tables(fit.trial.pi))
```

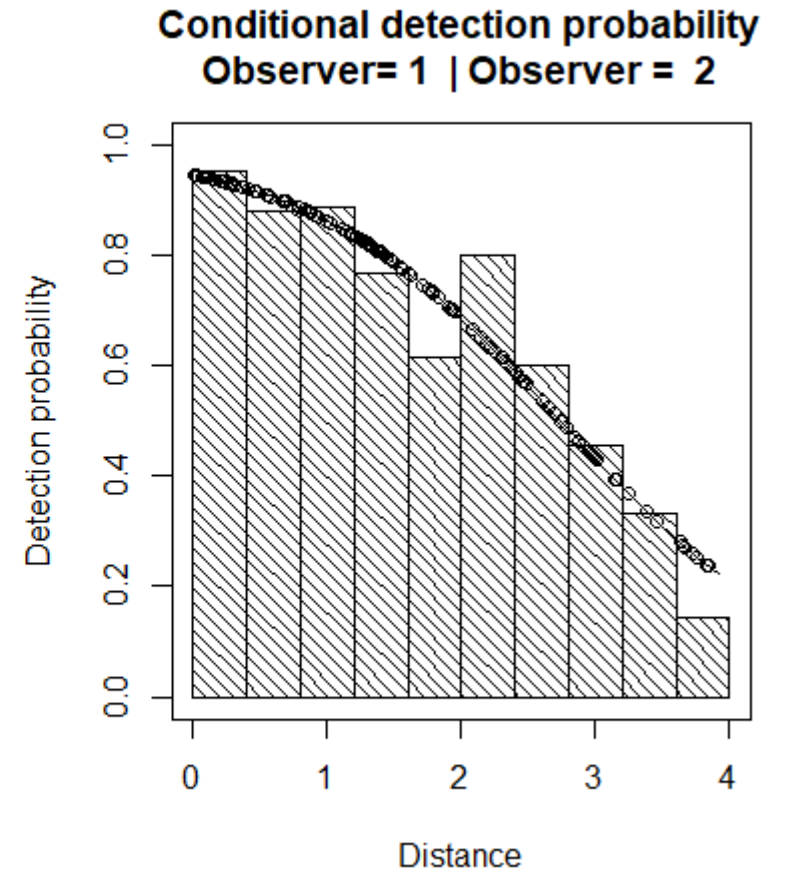
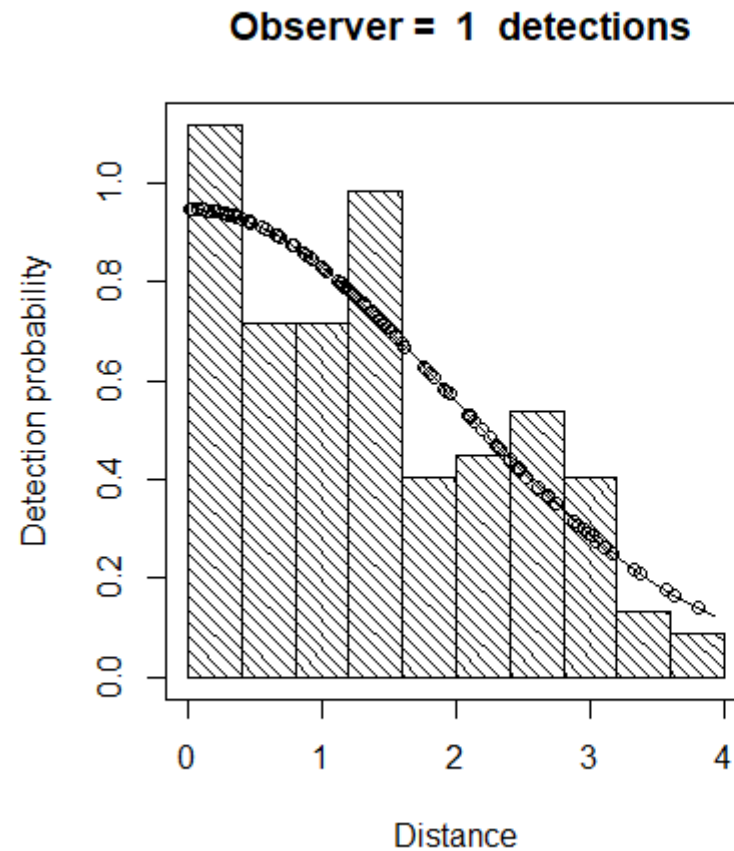
Observer 1 detections

| | Detected | Missed | Detected |
|------------|----------|--------|----------|
| [0, 0.4] | 1 | | 25 |
| (0.4, 0.8] | 2 | | 16 |
| (0.8, 1.2] | 2 | | 16 |
| (1.2, 1.6] | 6 | | 22 |
| (1.6, 2] | 5 | | 9 |
| (2, 2.4] | 2 | | 10 |
| (2.4, 2.8] | 6 | | 12 |
| (2.8, 3.2] | 6 | | 9 |
| (3.2, 3.6] | 2 | | 3 |
| (3.6, 4] | 6 | | 2 |

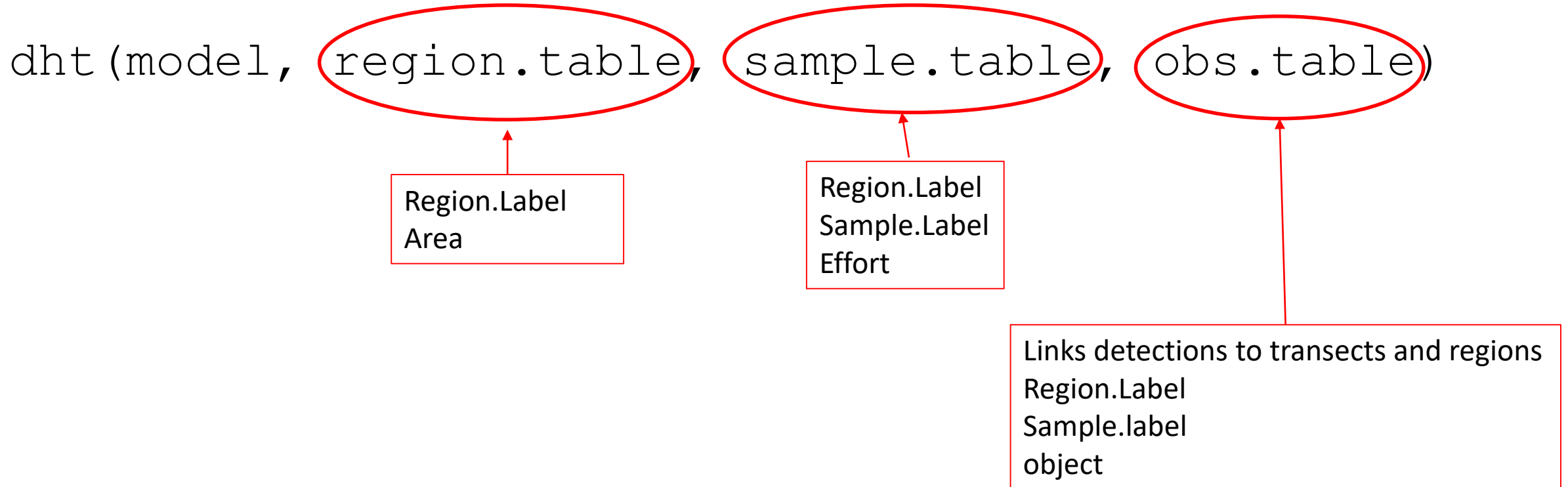


Results: detection function plots

```
plot(fit.trial.pi)
```



Estimating abundance: dht



Note, can convert a flatfile format to hierarchical structure using
`Distance:::checkdata(flatfile)`