

# Rediscretizing Tracks

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**These analyses only consider the first two releases, intended as Phase 1 (phase 2 = survival study)**

However, there were 221 additional fish released in phases 3 - 5 that could be incorporated. They were released at higher flows, which would add interesting complexity, and additional analysis needs.

## Rediscretization of Tracks

- Using primary and secondary filtered data to rediscretize tracks for further analysis
- Tracks with gaps > 150 m have been removed entirely from the analysis. =/- this threshold can be altered in “Final\_Filtering.Rmd” if desired
- Before redistributing, remove bursts with < 10 positions (too few to rediscretize in adehabitatLT)
- After, recalculated migration speed between positions

```
load("Maestros/AllFish_FiltSec5Gaps.RData") # single object, named red9  
  
dim(red9) # 76269 detections
```

```
## [1] 76269    15
```

```
length(unique(red9$id)) # 374 unique fish
```

```
## [1] 374
```

```
length(unique(red9$burst)) # 374 unique bursts
```

```
## [1] 374
```

```
ndetects.fish = summarize(group_by(red9, id), ndet = n())  
mean(ndetects.fish$ndet) # 203.9 per fish
```

```
## [1] 203.9278
```

```
range(ndetects.fish$ndet) # ranges from 22 - 578
```

```
## [1] 22 578
```

```
# bursts.rem = data.frame(ndetects.burst[ndetects.burst$ndet<10,])  
#   nrow(bursts.rem) # 104 bursts removed  
#   sum(bursts.rem$ndet) # 535 positions removed + 166 removed when cut the bursts (<4 pos remaining  
#   red.br = red9[(red9$burst %in% bursts.rem$burst),]
```

```

#
#   river3 = fortify(river3)
#   ggplot(data = red.br, aes(x=east, y=north)) + geom_point() +
#   geom_path(data = river3, aes(long, lat), col="gold", size=1.2 ) +
#   ggtitle(label = "Positions Removed within Short Bursts") +
#   theme_bw() + coord_fixed()

red8 = red9#[!(red9$burst %in% bursts.rem$burst),]

# prep object for redisltraj()
red8.ltraj = as.ltraj(xy=red8[,c("east", "north")], date=red8$date,
                     id=factor(red8$id), burst = factor(red8$burst),
                     infolocs=red8[,c("Hpes", "east", "north")])

# discretize in space
redlt.ssrz = (redisltraj(red8.ltraj, u=21, type="space", nnew=5))
# u=21 is the smallest distance where the code will work.

# convert back to dataframe
red8.ssrz = ld(redlt.ssrz)
red8.ssrz=red8.ssrz[order(red8.ssrz$id, red8.ssrz$date),]

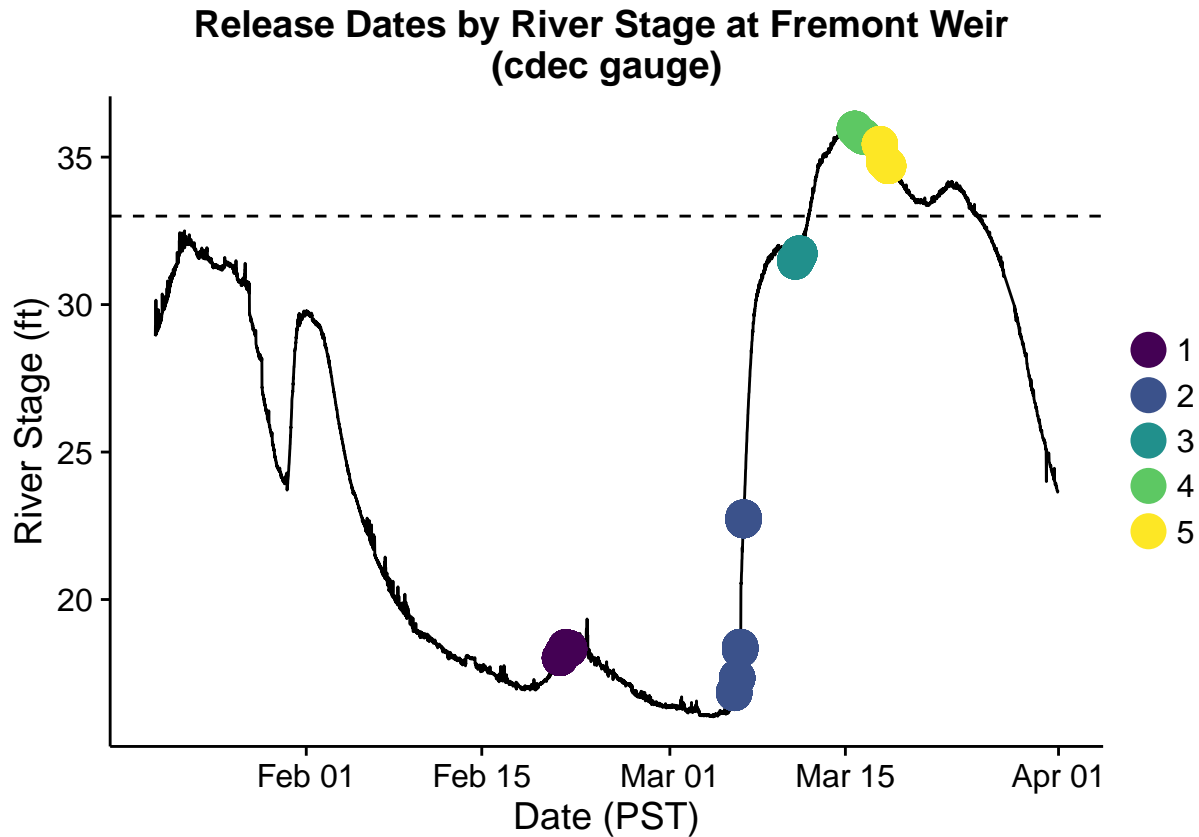
# recalculate migration speed
red8.ssrz$spd_mps = red8.ssrz$dist / red8.ssrz$dt

```

Add covariates (release event, river stage) back into dataframe to possibly use later

\*Compared un-QAQced data on river stage from CDEC station (no discharge available) with USGS measured values

Save the discretized object to RData



And finally, output the general metrics about the remaining dataset

```
dim(red8.ssrdez) # 11540 detections after discretization
```

```
## [1] 11540    31
```

```
length(unique(red8.ssrdez$id)) # 374
```

```
## [1] 374
```

```
ndetects.discr = summarize(group_by(red8.ssrdez, id), ndet = n())
mean(ndetects.discr$ndet) # 30.9 per fish
```

```
## [1] 30.85561
```

```
range(ndetects.discr$ndet) # ranges from 14-40
```

```
## [1] 14 40
```

```
max(red8.ssrdez$spd_mps, na.rm=T) # 12.0 mps
```

```
## [1] 12.03344
```