Rediscretizing Tracks

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August 16, 2016

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 have been split into bursts where successive positions were seperated by > 50m
- this threshold can be altered in "Final_Filtering.Rmd" if desired
- Before redistretizing, remove bursts with < 10 positions (too few to rediscretize in adehabitatLT)
- After, recalculated migration speed between positions

```
load("Maestros/AllFish_FiltSec4Bursts.RData")  # single object, named red7

dim(red7) # 102633 detections
```

```
## [1] 102633      16
```

```
    length(unique(red7$id))   # 430 unique fish
```

```
## [1] 430
```

```
    length(unique(red7$burst))   # 588 unique bursts
```

```
## [1] 588
```

```
    ndetects.fish = summarize(group_by(red7, id), ndet = n())
      mean(ndetects.fish$ndet) # 238.9 per fish
```

```
## [1] 238.6814
```

```
      range(ndetects.fish$ndet) # ranges from 28 - 660
```

```
## [1]  28 660
```

```
    ndetects.burst = summarize(group_by(red7, burst), ndet = n())
      mean(ndetects.burst$ndet) # 174.5 per fish
```

```
## [1] 174.5459
```

```
    range(ndetects.burst$ndet) # ranges from 3 - 660
```

[1]   3 660

```
    max(red7$spd_mps, na.rm=T)   # 86.6 mps
```

[1] 86.61481

```
  bursts.rem = data.frame(ndetects.burst[ndetects.burst$ndet<10,])
    nrow(bursts.rem) # 74 bursts removed
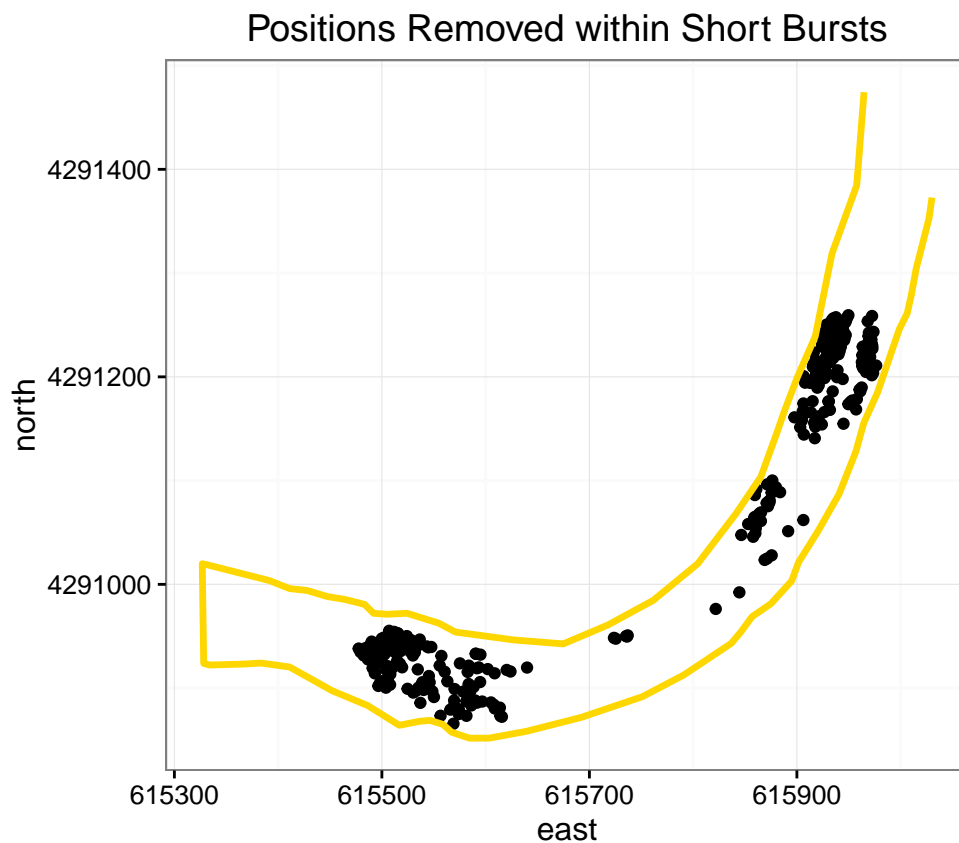```

## [1] 74

```
    sum(bursts.rem$ndet) # 373 positions removed
```

[1] 373

```
  red.br =  red7[(red7$burst %in% bursts.rem$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 = red7[!(red7$burst %in% bursts.rem$burst),]

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

```
# discretize in space
redlt.ssrdz = (redisltraj(red8.ltraj, u=25, type="space", nnew=5))
  # u=25 is the smallest distance where the code will work.

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

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

  dim(red8.ssrdz) # 10796 detections after discretization
```

[1] 10796   15

```
   length(unique(red8.ssrdz$id))   # 439
```

[1] 430

```
   ndetects.discr = summarize(group_by(red8.ssrdz, id), ndet = n())
     mean(ndetects.discr$ndet) # 28.75 per fish
```

[1] 25.10698

```
   range(ndetects.discr$ndet) # ranges from 10 - 41
```

[1] 6 37

```
   max(red8.ssrdz$spd_mps, na.rm=T)  # 73.11 mps
```

[1] 20.49389

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

Note: In 2015 I removed tracks which had < 10 positions after spatial discretization. However, this year's anaysis is slightly different since I'm working with bursts -> we should have already controlled for sparse tracks (i.e., those where interpolation might be inapporpriate). Plus, above I've removed any burst with < 10 positions. Therefore, I'm imposing no additional filtering after discretization.
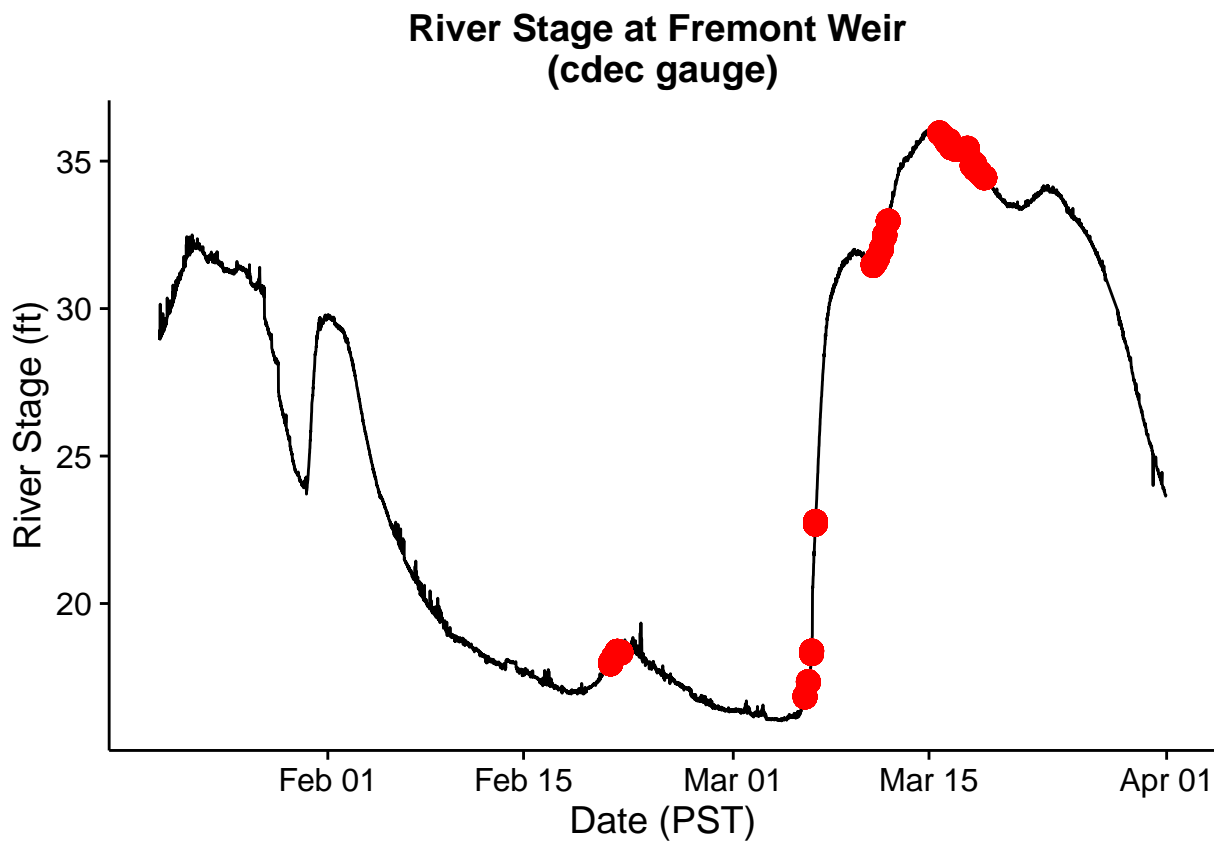
[1] -1.27 -1.26 -1.28 -0.85 -0.79 -1.84 -1.88 -1.58 -1.56 -1.41 -1.43
[12] -1.45 -0.71   NA

3

Histogram of compare$stage_ft.x − compare$stage_ft.y

compare$stage_ft.x − compare$stage_ft.y

```
## [1] -1.331538
```

```
## [1] 0.3681224
```

River Stage at Fremont Weir
(cdec gauge)
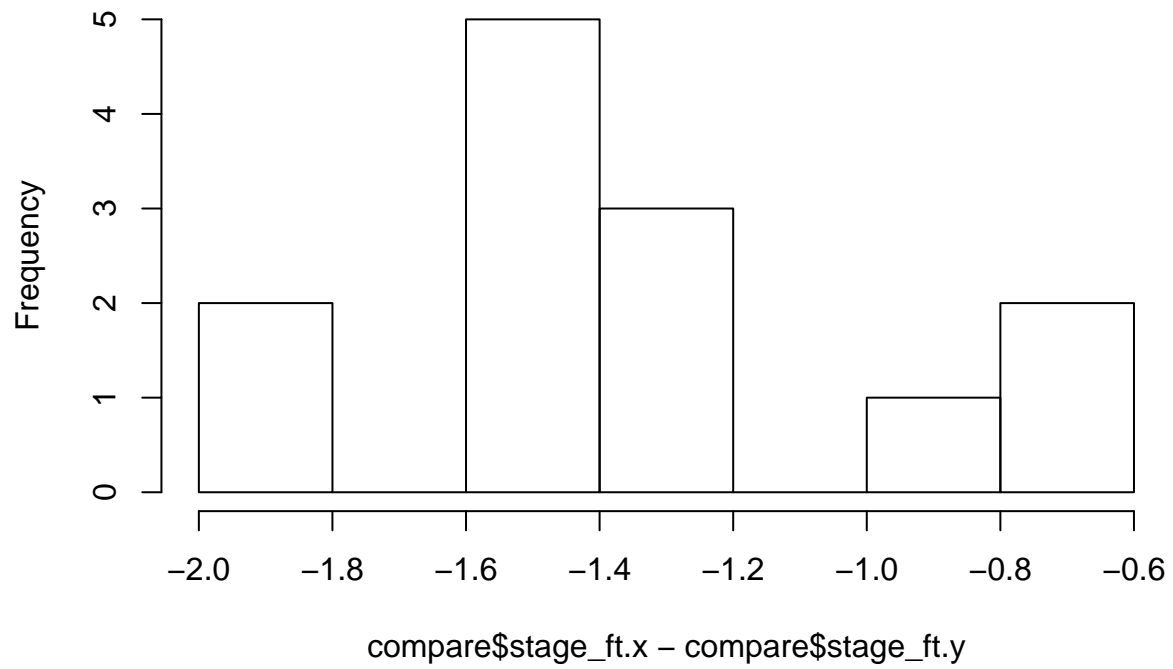
And finally, output the general metrics about the remaining dataset

```
dim(red8.ssrdz) # 10796 detections after discretization
```

```
## [1] 10796    22
```

```
length(unique(red8.ssrdz$id))  # 430
```

```
## [1] 430
```

```
ndetects.discr = summarize(group_by(red8.ssrdz, id), ndet = n())
  mean(ndetects.discr$ndet) # 28.11 per fish
```

```
## [1] 25.10698
```

```
range(ndetects.discr$ndet) # ranges from 6 - 37
```

```
## [1]  6 37
```

```
max(red8.ssrdz$spd_mps, na.rm=T)  # 20.49 mps
```

```
## [1] 20.49389
```