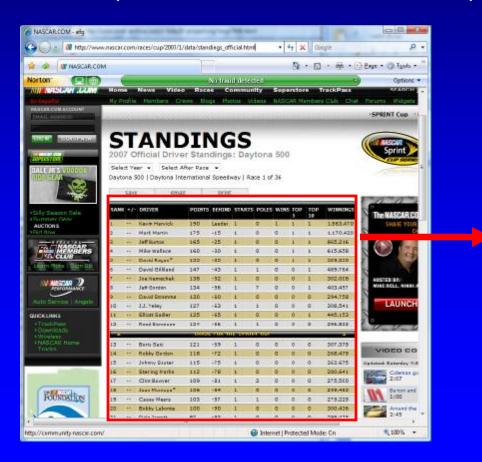
XML and RCurl Packages

Extracting a data.frame from HTML code

http://www.mail-archive.com/r-help@r-project.org/msg17496.html



DIVINITION DELIVED DEL
···RANK·+/-········DRIVER·POINTS·BEHIND·STARTS·POLES·WINS·TOP·5·TOP·10·WINNINGS¶
11
22Mark.Martin1751510001.1,170,420¶
33
44Mike-Wallace1603010011
55David.Ragan*1553510011.
66David.Gilliland14743110001489,764¶
77
8899.ff.Gordon1345617001403,497¶
99David.Stremme13060100000.
10···10··········.J.J.·Yeley····127····-63······1·····1····0····0····0···308,541¶
1111Elliott.Sadler12565100001445,153¶
12···12······Reed·Sorenson···124···-66·····1····1····0····0····0···0··296,833¶
1313Boris Said12169100000307,375¶
14···14······Robby·Gordon····118····-72·····1····0····0···0····0···268,475¶
1515
1616Sterling Marlin11278100000280,641¶
1717
1818
19···19·····Casey·Mears····103····-87·····1····1···0···0···0···0··275,225¶
2020Bobby.Labonte1009010000.
21···21·······Dale·Jarrett····97···-93·····1····0···0···0···0··295,475¶
2222
2323
2424000273,383¶
2525Greg.Biffle8810211000317,075¶
2626Ricky-Rudd8510510000293,091¶
2727Martin.Truex.Jr8110911000290,820¶
2828Denny.Hamlin7911111000.
2929Jamie.McMurray7012011000265,058¶
3030Dale-Earnhardt-Jr67123110000355,733¶
3131
32···32··· Dave·Blaney····61··-129·····1···0···0··0··269,447¶
33···33······Ken·Schrader····58··-132·····1····0···0···0···0···314,189¶
34···34······Jeff·Green····55··135····-1····0···0····0····0···259,025¶
35···35·······Ryan·Newman····54···-136·····1····5···0····0···0··316,133¶
3636Kurt.Busch5014011000365,316¶
37···37····.Jimmie·Johnson····46···-144·····1····4···0····0····0···353,386¶
3838David.Reutimann*43147100000249,583¶
39390
40···40······Matt·Kenseth·····37···-153······1·····0····0····0····0···309,099¶
41···41·········Kyle·Petty·····37···-153······1·····0····0····0····0···248,050¶
42···42········Scott·Riggs·····27···-163······1·····0····0····0····0···304,158¶
43···43·····Michael·Waltrip···-27···-217·····1····1····0····0····0···269,708¶

XML and RCurl Packages Extracting a data.frame from HTML code

```
library(XML)
url <- 'http://www.nascar.com/races/cup/2007/1/data/standings_official.html'
xml <- htmlTreeParse(url, useInternal=TRUE)

q <- "//tbody/tr[position()!=13]/td"
dat <- unlist(xpathApply(xml, q, xmlValue))

df <- as.data.frame(t(matrix(dat, 11)))

# Get the headers
q2 <- "//table/tr/th"
dat2 <- unlist(xpathApply(xml, q2, xmlValue))

colnames(df) <- dat2</pre>
```

	RANK	+/-	DRIVER	POINTS	BEHIND	STARTS	POLES	WINS	тор	5	TOP	10	WINNINGS
1	1		Kevin Harvick		Leader		0	1		ī		1	1,563,470
2	2		Mark Martin	175	-15	1	0	0		1		1	1,170,420
3	3		Jeff Burton	165	-25	1	0	0		1		1	865,216
4	4		Mike Wallace	160	-30	1	0	0		1		1	615,658
5	5		David Ragan*	155	-35	1	0	0		1		1	529,350
6	6		David Gilliland	147	-43	1	1	Ω		Ω		1	489.764

XML and RCurl Packages Extracting a data.frame from HTML code

```
> unlist(xpathApply(xml,
                                       "//*", xmlName))
  [1] "html"
                  "head"
                             "title"
                                        "meta"
                                                    "meta"
                                                               "link"
                                                                           "link"
                                                                                      "link"
  [9] "link"
                 "script"
                             "script"
                                        "body"
                                                    "div"
                                                               "script"
                                                                           "stvle"
                                                                                      "script"
                 "script"
                             "div"
                                        "div"
                                                    "div"
                                                               "script"
                                                                           "map"
                                                                                      "area"
 [17] "script"
                             "script"
                                        "noscript" "div"
                                                               "form"
                                                                           "input"
 [25] "area"
                 "area"
                                                                                      "input"
[945] "a"
                 "dixr"
                             "a"
                                        "dix"
                                                    "a"
                                                               "div"
                                                                           "a"
                                                                                      "div"
[953] "a"
                                                    "a"
                                                               "a"
                 "imer"
                                        "imq"
                                                    "ല"
                                                               "imer"
                                                                           "p"
                                                                                      "script"
[969] "script"
                 "script"
                             "script"
                                        "script"
                                                    "ima"
                                                               "div"
                                                                           "imer"
```

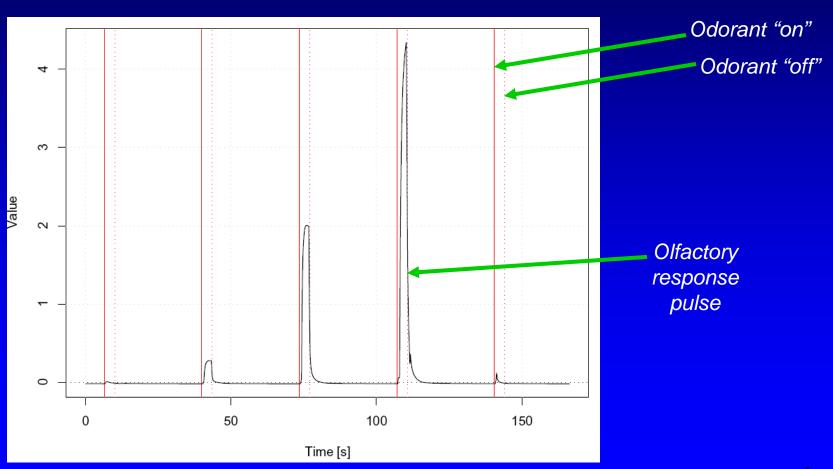
Analyzing Olfactory Response Data in ABF Files

Stowers Institute for Medical Research R/Bioconductor Discussion Group

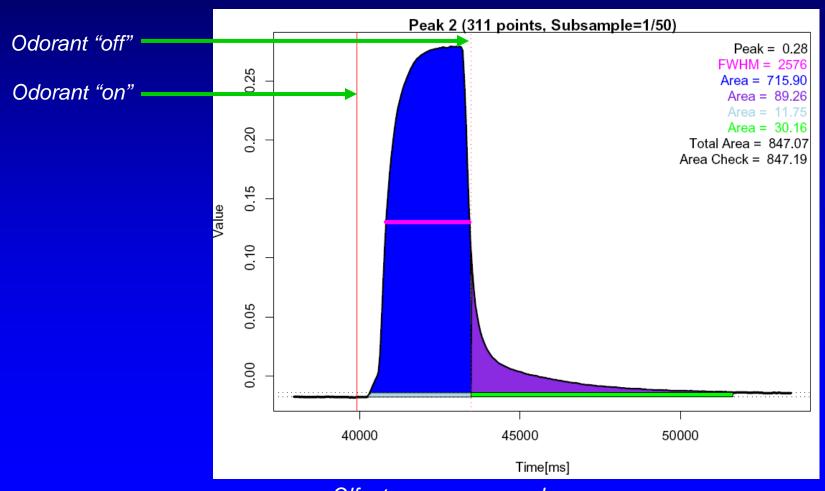
Earl F. Glynn Scientific Programmer 25 Sept 2008

- Converting Axon Binary File to CSV
- Processing directory of ABF files in R
- Finding events in TTL channel
- •Finding features and areas in olfactory response "Value" channel
- Reporting results in file and charts

 $U: \efg\Research\RonYu\Limei\R\071225Z-AA-200cm-3s.pdf$



U:\efg\Research\RonYu\Limei\R\071225Z-AA-200cm-3s.pdf



Converting Axon Binary File to CSV

U:\efg\Research\RonYu\ABF\Converting-abf-to-csv.doc

- Developed "C" program to extract data from binary ABF file
- Only process "Gap free files" at present
- Only process needed subset of data
- Requires proprietary abffio.dll at run-time
- CSV files are ~4X larger than ABF files
- Many programs can read CSVs; few programs can read ABFs

Converting Axon Binary File to CSV

U:\efg\Research\RonYu\Limei\071225-Length

Use system to run command-line program

e.g., abf2csv 071225A-AA-25cm-1s.abf 071225A-AA-25cm-1s.csv

```
read.abf.file <- function(abffile, delete.csv=TRUE)
{
  basedir <- substr(abffile,1,nchar(abffile)-3)
  csvfile <- paste(basedir, "csv", sep="")

  system(paste("abf2csv", abffile, csvfile))

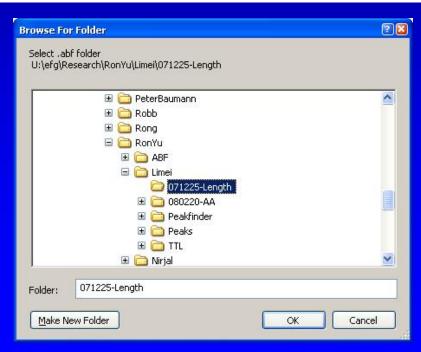
  raw <- read.csv(csvfile, as.is=TRUE)
  colnames(raw) <- c("Value", "TTL")
  raw$Time <- 0:(nrow(raw)-1)

  if (delete.csv)
  {
    file.remove(csvfile)
  }

  return(raw)
}</pre>
```

Processing directory of files in R

U:\efg\Research\RonYu\Limei\R\ComputeAreas.R



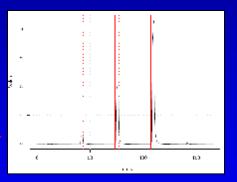
Processing directory of ABF files in R

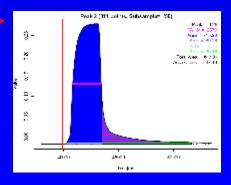
```
process.directory <- function(abf.folder)
{
  abflist <- dir(path=abf.folder, pattern="\\.abf$")
  . . .

  for (file.index in 1:length(abflist))
  {
    abffile <- file.path(abf.folder, abflist[file.index])
    . . .
  }
}</pre>
```

Processing directory of files in R

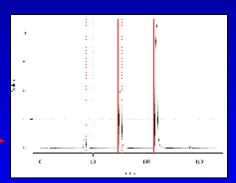
```
process.directory <- function(abf.folder)</pre>
  abflist <- dir(path=abf.folder, pattern="\\.abf$")
  basefile <- substr(abflist,1,nchar(abflist)-3)</pre>
  pdflist <- paste(basefile, "pdf", sep="")</pre>
  for (file.index in 1:length(abflist))
    abffile <- file.path(abf.folder, abflist[file.index])</pre>
    raw <- read.abf.file(abffile)</pre>
    TTL <- process.TTL.data(raw)
    subsample <- subsample.raw.data(raw, SUBSAMPLE.FACTOR)
    pdf(file.path(abf.folder, pdflist[file.index]), width=8, height=10)
      par(oma=c(2,0,3,0))
      plot.subsample(subsample, TTL)
      plot.header.and.footer(abffile)
      for (i in 1:length(TTL$start))
        peak.results <- plot.peak(abffile, i, subsample, TTL)</pre>
        plot.header.and.footer(abffile)
    dev.off()
```

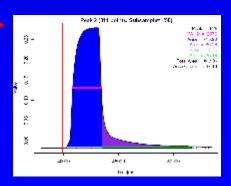




Processing directory of files in R

```
process.directory <- function(abf.folder)</pre>
  abflist <- dir(path=abf.folder, pattern="\\.abf$")
  basefile <- substr(abflist,1,nchar(abflist)-3)</pre>
  pdflist <- paste(basefile, "pdf", sep="")</pre>
  for (file.index in 1:length(abflist))
    abffile <- file.path(abf.folder, abflist[file.index])</pre>
    raw <- read.abf.file(abffile)
    TTL <- process.TTL.data(raw)
    subsample <- subsample.raw.data(raw, SUBSAMPLE.FACTOR)
    pdf(file.path(abf.folder, pdflist[file.index]), width=8, height=10)
      par(oma=c(2,0,3,0))
      plot.subsample(subsample, TTL)
      plot.header.and.footer(abffile)
      for (i in 1:length(TTL$start))
        peak.results <- plot.peak(abffile, i, subsample, TTL)</pre>
        plot.header.and.footer(abffile)
    dev.off()
```



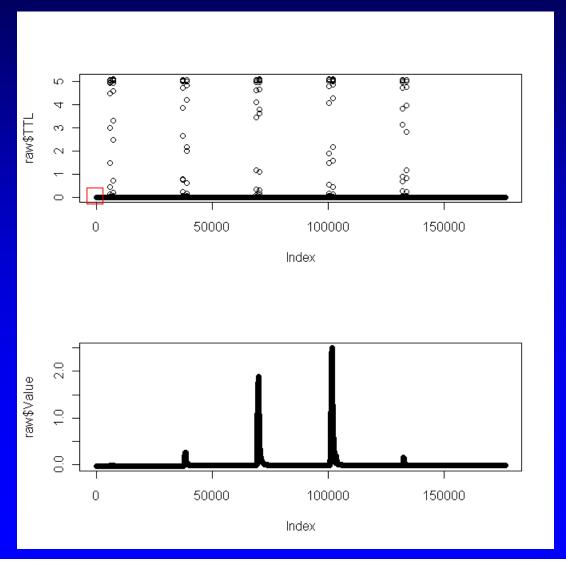


Finding events in TTL channel

raw <- read.abf.file(abffile)</pre>

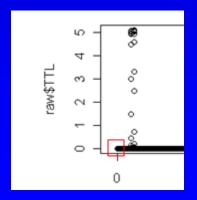
par(mfrow=c(2,1))
plot(raw\$TTL)
plot(raw\$Value)

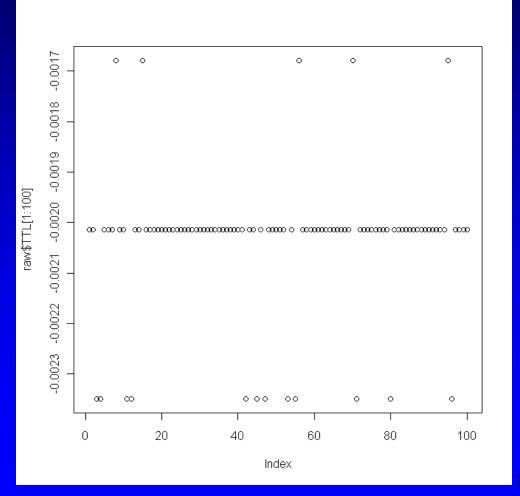
Use TTL events to process peaks in olfactory response "Value" data



Finding events in TTL channel

plot(raw\$TTL[1:100])

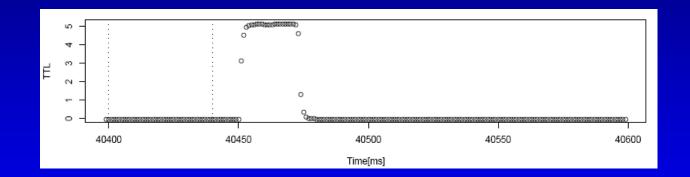




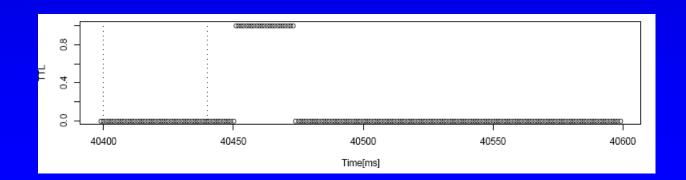
Finding events in TTL channel

TTL.midpoint <- (max(raw\$TTL) - min(raw\$TTL)) / 2
fixed.TTL <- ifelse(raw\$TTL <= TTL.midpoint, 0, 1)</pre>

Raw



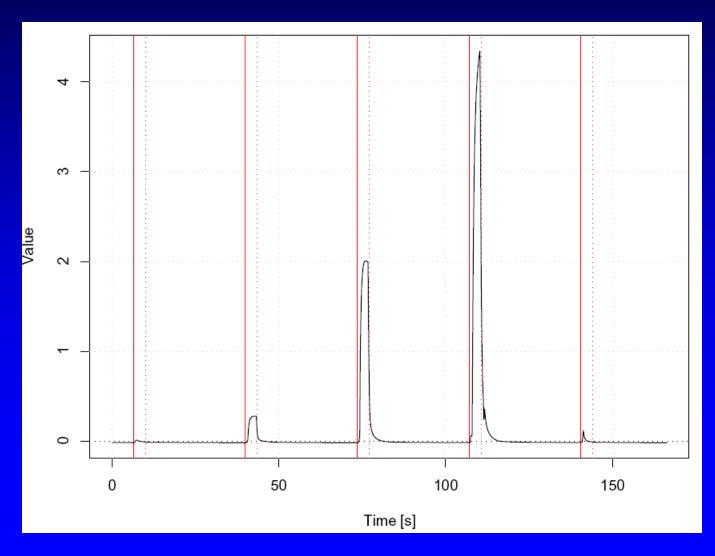
Fixed



Finding events in TTL channel

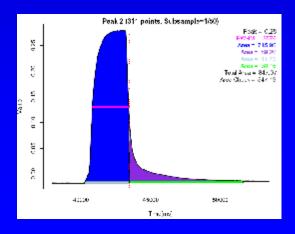
Intervals of Interest

Finding events in TTL channel



Finding features and areas in Value channel

- Need high sampling rate for exact timing of events in TTL channel
- Do not need high sampling rate for most olfactory response features in the Value channel, e.g., area.
- Considerable speedup after subsampling



SUBSAMPLE FACTOR

Subsampling

```
subsample <- subsample.raw.data(raw, SUBSAMPLE.FACTOR)

subsample.raw.data <- function(raw, subsample.frequency)
{
    # Subsample data -- millisecond resolution too high
    Subsample.Time <- subsample.frequency * 0:((nrow(raw) %/% subsample.frequency) - 1)
    Subsample.Value <- raw$Value[Subsample.Time]</pre>
```

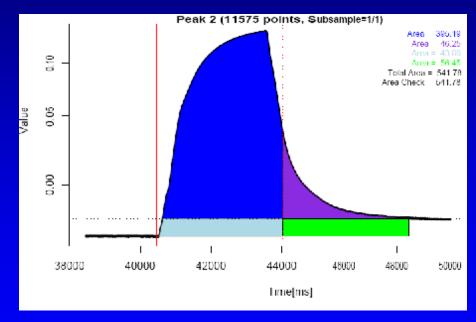
return(list(Time=Subsample.Time, Value=Subsample.Value, frequency=subsample.frequency))

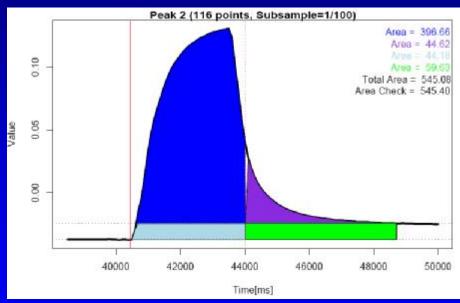
Pick every 50th point to speed up processing. Output PDFs are much smaller with subsampling.

How does Subsampling affect area?

11,575 points

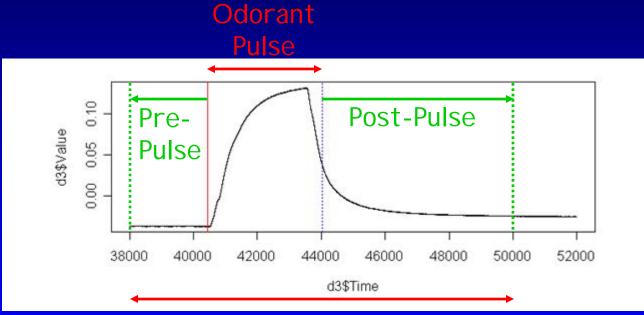
116 points





<1% difference on large areas up to 6% difference on small areas

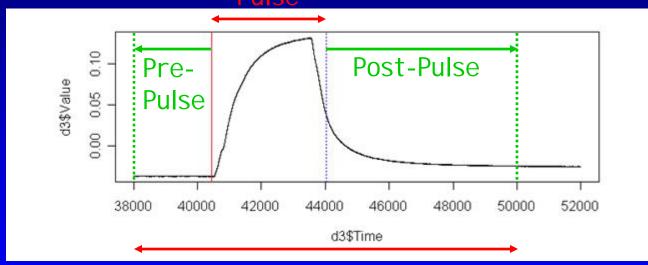
Finding features and areas in Value channel



Analysis Interval

Finding features and areas in Value channel

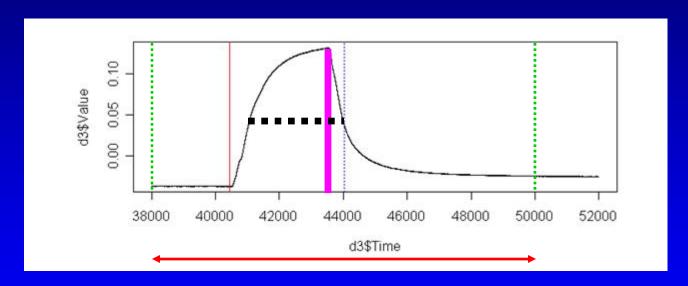
Odorant Pulse



Analysis Interval

```
interval.Time <- subsample$Time[interval.range]
interval.Value <- subsample$Value[interval.range]
```

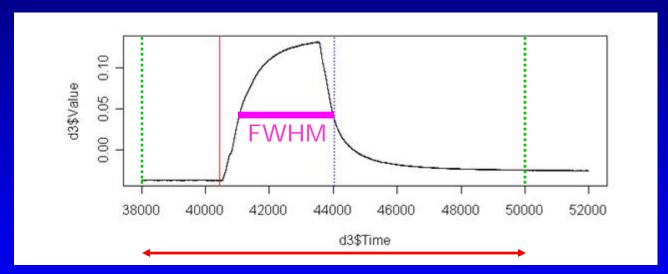
Peak and Full-Width at Half Max (FWHM)



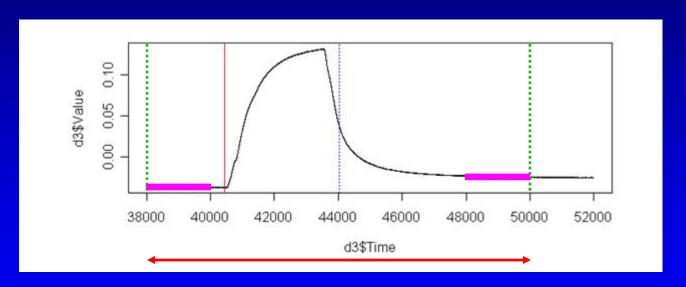
```
# Compute FWHM
Value.max <- max(interval.Value)
Value.min <- min(interval.Value)

Value.halfmax <- (Value.max + Value.min) / 2
# Pick first if more than one
Index.max <- which(interval.Value == Value.max)[1]</pre>
```

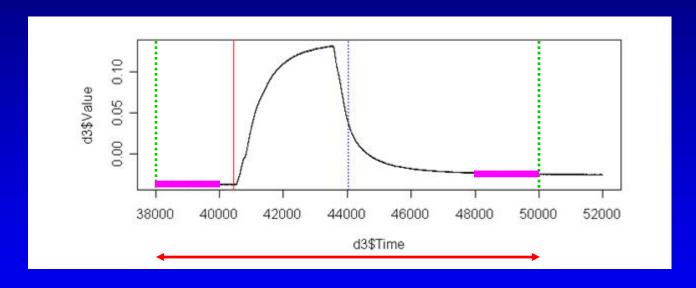
Finding features and areas in Value channel Full-Width at Half Max (FWHM)



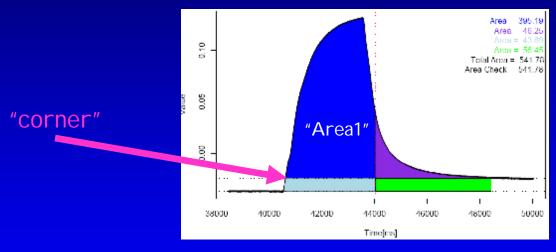
Left and Right "Plateaus"



Left and Right "Plateaus"

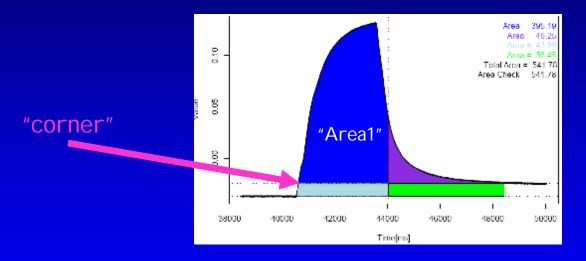


Areas



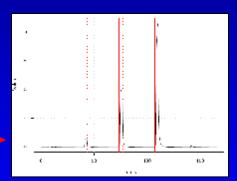
Finding features and areas in Value channel

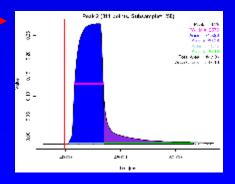
Areas



Reporting results in charts

```
process.directory <- function(abf.folder)</pre>
  abflist <- dir(path=abf.folder, pattern="\\.abf$")
  basefile <- substr(abflist,1,nchar(abflist)-3)</pre>
  pdflist <- paste(basefile, "pdf", sep="")</pre>
  for (file.index in 1:length(abflist))
    abffile <- file.path(abf.folder, abflist[file.index])</pre>
    raw <- read.abf.file(abffile)</pre>
    TTL <- process.TTL.data(raw)
    subsample <- subsample.raw.data(raw, SUBSAMPLE.FACTOR)
    pdf(file.path(abf.folder, pdflist[file.index]), width=8, height=10)
      par(oma=c(2,0,3,0))
      plot.subsample(subsample, TTL)
      plot.header.and.footer(abffile)
      for (i in 1:length(TTL$start))
        peak.results <- plot.peak(abffile, i, subsample, TTL)</pre>
        plot.header.and.footer(abffile)
    dev.off()
```





Reporting results in file

```
process.directory <- function(abf.folder)
  abflist <- dir(path=abf.folder, pattern="\\.abf$")
 basefile <- substr(abflist,1,nchar(abflist)-3)</pre>
 pdflist <- paste(basefile, "pdf", sep="")</pre>
 All.Results <- NULL
  for (file.index in 1:length(abflist))
    abffile <- file.path(abf.folder, abflist[file.index])
    cat( format(Sys.time(), "%Y-%m-%d %H:%M:%S"), " Reading", abffile, "\n")
    flush.console()
    raw <- read.abf.file(abffile)
   TTL <- process.TTL.data(raw)
    subsample <- subsample.raw.data(raw, SUBSAMPLE.FACTOR)
    pdf(file.path(abf.folder, pdflist[file.index]), width=8, height=10)
     par(oma=c(2,0,3,0)) # Leave room for footer
     plot.subsample(subsample, TTL)
     plot.header.and.footer(abffile)
      for (i in 1:length(TTL$start))
        peak.results <- plot.peak(abffile, i, subsample, TTL)</pre>
        plot.header.and.footer(abffile)
        All.Results <- rbind(All.Results, peak.results)
    dev.off()
  cat( format(Sys.time(), "%Y-%m-%d %H:%M:%S"), "\n")
 write.csv(All.Results, file=file.path(abf.folder, "PeakSummary.csv"), row.names=FALSE)
```

Reporting results in file

FilePeakSummary.csv												
	А	В	С	D	Е	F	G	Н	I	J		
1	file	peak.index	peak	FWHM	area1	area2	area3	area4	area.total	area.check		
2	071225A-AA-25cm-1s-clamp9.abf	1	0.0	2541.2	3.0	1.1	2.4	2.5	9.0	9.0		
3	071225A-AA-25cm-1s-clamp9.abf	2	0.3	717.9	188.6	42.9	9.3	34.7	275.6	276.0		
4	071225A-AA-25cm-1s-clamp9.abf	3	1.9	769.0	1420.8	213.8	15.0	52.0	1701.6	1701.6		
5	071225A-AA-25cm-1s-clamp9.abf	4	2.5	674.6	1639.8	426.5	13.1	46.1	2125.5	2125.6		
6	071225A-AA-25cm-1s-clamp9.abf	5	0.2	444.6	87.0	12.7	3.9	12.1	115.6	115.6		
7	071225A-AA-25cm-1s.abf	1	0.0	2541.2	3.0	1.1	2.4	2.5	9.0	9.0		
8	071225A-AA-25cm-1s.abf	2	0.3	717.9	188.6	42.9	9.3	34.7	275.6	276.0		
9	071225A-AA-25cm-1s.abf	3	1.9	769.0	1420.8	213.8	15.0	52.0	1701.6	1701.6		
10	071225A-AA-25cm-1s.abf	4	2.5	674.6	1639.8	426.5	13.1	46.1	2125.5	2125.6		
11	071225A-AA-25cm-1s.abf	5	0.2	444.6	87.0	12.7	3.9	12.1	115.6	115.6		

Take Home: "R" and Analysis Tips

- system
- processing directory of files
 - choose.dir
 - dir
 - file.path
 - rbind (form composite data.frame)
 - write.csv
- cleanup noise in data: threshold, median
- subsampling data
- area computations
- approx to interpolate
- suppressWarnings
- FWHM (full width at half max)
- polygon

Acknowledgments Yu Lab

- Nirjal Sapkota (now at North Carolina State University)
- Limei Ma
- Ron Yu