Clustered Recognition of Interrupted Bouts (CRIB)

Paul R. Hibbing

Introduction and Installation

This vignette will show you how to implement the CRIB method. The first step is making sure you have the PBpatterns package installed on your computer. Here's how:

Copy and paste the above into your R console, then hit enter to run it.

Preparation

Once you have the package installed, all you need is some activity data and the analyze_bouts function. For this demonstration, let's use some sample NHANES data.

```
data(example_data, package = "PBpatterns")
```

This dataset has activity counts that we can use to look at bouts of moderate-to-vigorous physical activity (MVPA). For illustration, let's say we initially coded our data as sedentary behavior ($PAXINTEN \leq 100$), light physical activity (PAXINTEN 101 - 759), or MVPA ($PAXINTEN \geq 760$).

```
## Determine minute-by-minute intensity
intensity <- cut(
  example_data$PAXINTEN,
  breaks = c(-Inf, 101, 760, Inf),
  labels = c("SB", "LPA", "MVPA"),
  right = FALSE
)</pre>
```

Running the Code

Once we have our data (intensity in this case), we can plug it into analyze_bouts. Let's see the code first, then go over what it means.

```
mvpa_bouts <- PBpatterns::analyze_bouts(
    x = intensity,
    target = "MVPA",
    method = "CRIB",
    target_buffer_mins = 10,
    longest_allowable_interruption_mins = 2,
    required_percent = 80,
    max_n_interruptions = Inf,
    minimum_bout_duration_minutes = 10,
    epoch_length_sec = 60
)</pre>
```

Here is what each piece means:

- mvpa_bouts <- Store the function results in an object called mvpa_bouts
- PBpatterns::analyze_bouts This tells R to find the analyze_bouts function in the PBpatterns package. In fact, if you run PBpatterns::analyze_bouts in your console, R will print the source code.
- x = intensity Here we specify that our input datastream is intensity, as defined in the earlier code.
- target = "MVPA" Here we specify which behavior we are interested in. The input data (intensity) has values in the set {SB, LPA, MVPA}, and we would like to look specifically at bouts of MVPA, with the other behaviors being lumped together in a single group called other.
- method = "CRIB" Here we specify that R should run the CRIB method. To explore the other options, check out the Bout Analysis and Sedentary Patterns vignette.
- target_buffer_mins = 10 Here we specify how our data should be stratified/partitioned. In this case, intensity will be stratified/partitioned anytime we see ≥ 10 consecutive minutes of other behavior.
- longest_allowable_interruption_mins = 2 Here we specify that a valid bout should not include any single interruption lasting longer than 2 minutes.
- required_percent = 80 Here we specify that a valid bout should be interrupted for no more than 20% of its full duration.
- max_n_interruptions = Inf Here we specify that a valid bout can have unlimited interruptions as long as the criteria for longest_allowable_interruption_mins and required_percent are met.
- minimum_bout_duration_minutes = 10 Here we specify that only bouts lasting \geq 10 min should be included in the output.
- epoch length sec = 60 Here we specify what the epoch length of intensity is.

The above elements are set up to allow flexible bout criteria depending on the research question and the variable of interest. In our example, we set max_n_interruptions = Inf to avoid a restriction in that area – similar approaches can be taken for other settings as well, by setting them to 0 or Inf as appropriate. (For required_percent, 100 is the upper limit rather than Inf.) Notably, minimum_bout_duration_minutes is a filtering criterion. It has no direct effect on how the bouts are defined; it simply affects which ones are retained after they have been defined.

Interpreting the Output

Now let's take a look at the output and go over what it means:

mvpa	_bouts							
#>	$start_index$	end_index	values	n_total_event	s n_value_e	vents		
#> 1	912	932	MVPA		7	4		
#> 2	998	1011	MVPA		5	3		
#> 3	1022	1039	MVPA		1	1		
#> 4	1042	1063	MVPA		5	3		
#> 5	2212	2221	MVPA		1	1		
#> 6	3910	3922	MVPA		3	2		
#> 7	4166	4188	MVPA		5	3		
#>	$n_interrupto$	ion_events	overall	L_minutes enga	$ged_minutes$	percen	$t_time_engaged$	
#> 1		3		21	17	•	80.95238	
#> 2	?	2		14	12		85.71429	
#> 3		0		18	18		100.00000	
#> 4		2		22	20		90.90909	
#> 5	5	0		10	10		100.00000	
#> 6	3	1		13	12		92.30769	
#> 7		2		23	21		91.30435	
#>	$total_interruption_minutes$ $longest_interruption_minutes$							
#> 1			4			2		
#> 2			2			1		
#> 3			0			0		
#> 4			2			1		
#> 5			0			0		
#> 6			1			1		
#> 7	7		2			1		

This is a data frame with one row per bout. The variables are:

- start_index The starting point of the bout (e.g., intensity[912] for the first bout in this example)
- end_index The ending point of the bout (e.g., intensity[932] for the first bout in this example)
- values A meaningless constant (equal to the setting of target), left over from run length encoding
- n_total_events The number of distinct behavior events occurring between start_index and end_index
- n_value_events The number of distinct target behavior events occurring between start_index and end_index (referred to as value events in reference to the values column)
- n_interruption_events The number of distinct interruption events occurring between start_index and end_index
- overall minutes The combined duration of all value and interruption events
- engaged_minutes The combined duration of all value events
- percent_time_engaged Percentage of length_total comprised by length_value
- total interruption minutes The combined duration of all interruption events
- longest_interruption_minutes The duration of the single longest interruption event

Expanding the Output

In some cases we may want to convert our bout information back to the original length of the input (i.e., intensity). We can use the expand_bouts function to accomplish that.

```
expanded <- PBpatterns::expand_bouts(mvpa_bouts)
str(expanded)
#> Factor w/ 3 levels "other","MVPA",..: 1 1 1 1 1 1 1 1 1 1 1 1 1 ...
table(expanded)
#> expanded
#> other MVPA interruption
#> 9959 110 11
```

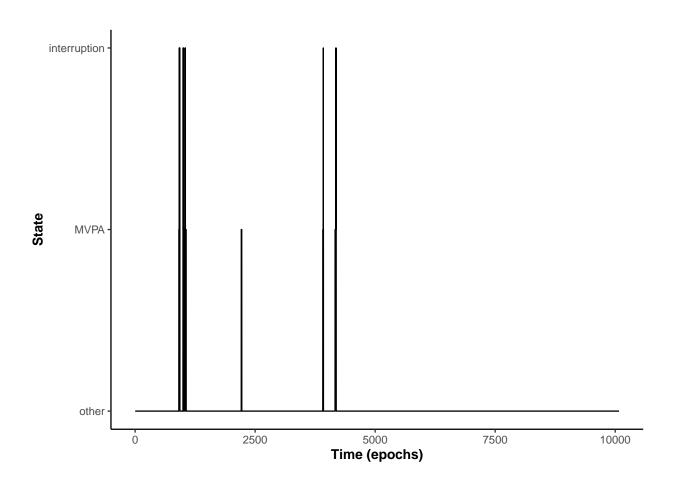
And we can also append that new variable into our original dataset as well.

```
example_data$intensity <- expanded</pre>
head(example_data)
      SEQN PAXSTAT PAXCAL PAXDAY PAXN PAXHOUR PAXMINUT PAXINTEN intensity
#> 1 21010
                 1
                        1
                                7
                                     1
                                             0
                                                       0
                                                                1
                                                                      other
                 1
                                7
                                     2
                                             0
                                                       1
                                                                0
#> 2 21010
                        1
                                                                      other
                                     3
                                                       2
                                                                0
#> 3 21010
                 1
                        1
                               7
                                             0
                                                                      other
                                7
                                     4
                                             0
                                                       3
                                                                0
#> 4 21010
                 1
                        1
                                                                      other
                                7
#> 5 21010
                 1
                                     5
                                             0
                                                       4
                                                                0
                        1
                                                                      other
                                     6
#> 6 21010
                                                       5
```

Plotting the output

If you want to visualize the results of your bout analysis, you can use a basic plot function.

plot(mvpa_bouts)



Conclusion

This should give you a broad sense of how to use the CRIB method and what else you can do with it. Feel free to post an issue on the GitHub page if any of the above gives you trouble. Good luck!