

# Sliding Window

## 1 Method definition

The sliding window method estimates the local recombination rates by carrying out linear regressions within a sliding window of a given physical size.

In `MareyMapOnline`, the threshold markers number in a window is 8.

Then, we automatically compute the size of the window which is fixed for all chromosomes: we take the maximal size which includes 8 markers.

## 2 R code

The `calcRecomRates_slidingWindow` (see below) allows to build the sliding window model from the physical (`physcoord`) and genetical (`gencoord`) coordinates and to calculate recombination rates at some physical positions (`physpos`).

This function is based on the R `lm` function.

The `windowsize` value is computed for all available chromosome of a specific species and returns the maximal size (in bp) of a window containing 8 markers.

```
calcRecomRates_slidingWindow <- function(physpos, windowsize, physcoord, gencoord) {  
  out <- sapply(physpos, function(pp) {  
    btm <- pp - windowsize / 2  
    top <- pp + windowsize / 2  
    idx <- which((physcoord >= btm) & (physcoord <= top))  
    if(length(idx) << 8)  
      return(NA)  
    mkrphys <- physcoord[idx]  
    mkrgen <- gencoord[idx]  
    modelSlidingWindow <- lm(mkrgen ~ mkrphys)  
    round(modelSlidingWindow$coef[[2]] * 1000000, digits = 2)  
  })  
  return(out)  
}
```

## 3 Bibliography