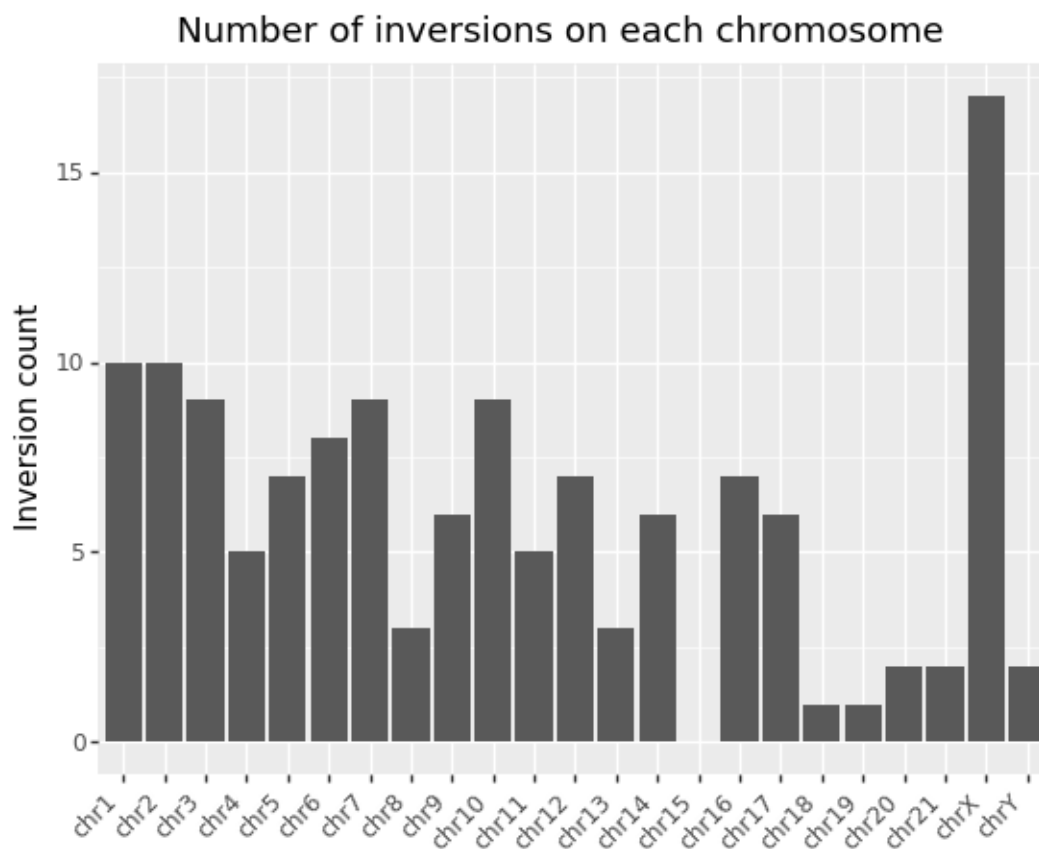# 20211117_LocationPatterns1

November 23, 2021

1 Location patterns 1 - global chromosome characteristics

This notebook explores the relationship between inversion coordinates and chromosome characteristics related to recombination rates.

1.1 Raw data upload

```
We will be analyzing 135 inversions
```

1.2 General distribution by chromosomes

[15]: <ggplot: (8747774513475)>

1.3 Relationship with chromosome size

```
␣
↪--------------------------------------------------------------------------

    PlotnineError                             Traceback (most recent call␣
↪last)

    <ipython-input-70-614e42e6abf5> in <module>
     16     stat_smooth(aes(x = "chromEnd", y = "Chr"), method = "lm") +
     17     geom_point(aes(x = "chromEnd", y = "Chr")) +
 ---> 18     annotate('text', x = math.inf, y = -math.inf, label = "hello",␣
↪hjust = 0, vjust = 1)
     19
     20 )


    ~/anaconda3/lib/python3.8/site-packages/plotnine/geoms/annotate.py in␣
↪__init__(self, geom, x, y, xmin, xmax, xend, ymin, ymax, yend, **kwargs)
     94
     95             # The positions are mapped, the rest are manual settings
 ---> 96             self._annotation_geom = geom(mappings,
     97                                           data=data,
     98                                           stat='identity',


    ~/anaconda3/lib/python3.8/site-packages/plotnine/geoms/geom_text.py in␣
↪__init__(self, mapping, data, **kwargs)
     110               mapping['va'] = mapping.pop('vjust')
     111
 --> 112           geom.__init__(self, mapping, data, **kwargs)
     113
     114     def setup_data(self, data):


    ~/anaconda3/lib/python3.8/site-packages/plotnine/geoms/geom.py in␣
↪__init__(self, mapping, data, **kwargs)
     45             self._stat = stat.from_geom(self)
     46             self._position = position.from_geom(self)
 ---> 47             self._verify_arguments(kwargs)     # geom, stat, layer
     48
```

```
     49        @staticmethod


     ~/anaconda3/lib/python3.8/site-packages/plotnine/geoms/geom.py in␣
 ↪_verify_arguments(self, kwargs)
     381                  msg = ("Parameters {}, are not understood by "
     382                       "either the geom, stat or layer.")
  --> 383                  raise PlotnineError(msg.format(unknown))
     384
     385       def handle_na(self, data):


     PlotnineError: "Parameters {'hjust', 'vjust'}, are not understood by␣
 ↪either the geom, stat or layer."
```

[45]: pandas.core.series.Series

1.4 Relative position within chromosome

1.5 Distribution within chromosome and inversion groups

1.6 Relationship with chromosome mean recombination rate