

ggbio: extending the grammar of graphics for genomic data

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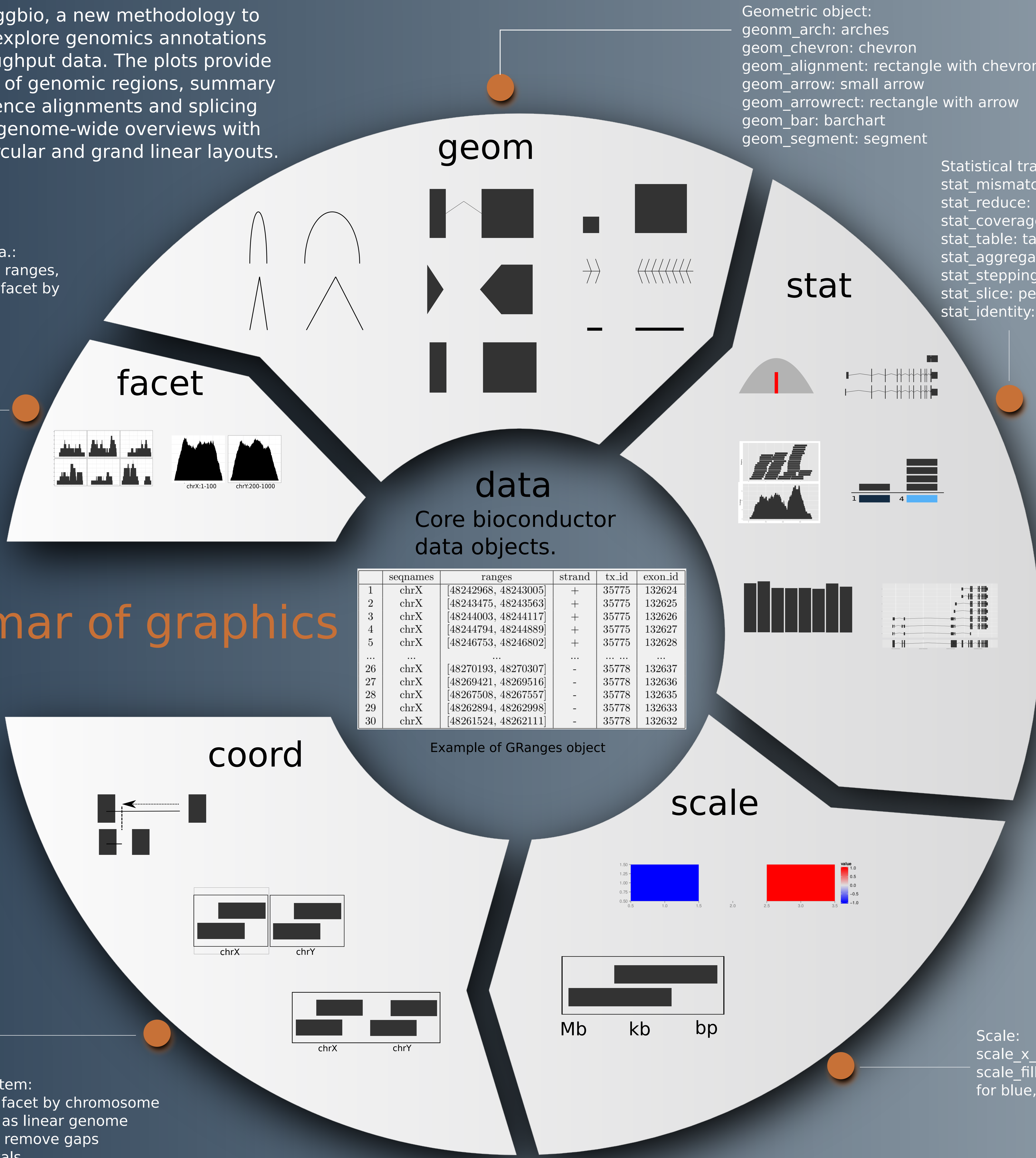
We introduce ggbio, a new methodology to visualize and explore genomics annotations and high-throughput data. The plots provide detailed views of genomic regions, summary views of sequence alignments and splicing patterns, and genome-wide overviews with karyogram, circular and grand linear layouts.

Subset of the data.:
facet_gr: facet by ranges,
facet_seqnames: facet by
seqnames

Geometric object:
geom_arch: arches
geom_chevron: chevron
geom_alignment: rectangle with chevron
geom_arrow: small arrow
geom_arrowrect: rectangle with arrow
geom_bar: barchart
geom_segment: segment

Statistical transformation:
stat_mismatch: mismatch summary
stat_reduce: single gene structure
stat_coverage: coverage
stat_table: tabulate intervals
stat_aggregate: summary over bins
stat_stepping: avoid overlapping
stat_slice: peak finding
stat_identity: do nothing

Grammar of graphics



Layout and tracks

Specialized plots

