Survey of R Packages

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Top 10 Cran Packages

Package	What does it do?
ggplot2	An implementation of the Grammar of Graphics
Rcpp	Seamless R and C++ Integration
plyr	Tools for splitting, applying and combining data
digest	Create cryptographic hash digests of R objects
stringr	Make it easier to work with strings
reshape2	Flexibly reshape data: a reboot of the reshape package
RColorBrewer	ColorBrewer palettes
BayHaz	Bayesian estimation of smooth hazard rates via CPP and BPS priors
colorspace	Color Space Manipulation
scales	Scale functions for graphics

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): conversion failure
## on '→' in 'mbcsToSbcs': dot substituted for <e2>
```

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```

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## on '→' in 'mbcsToSbcs': dot substituted for <92>
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## Warning in plot.xy(xy.coords(x, y), type = type, ...): font metrics
## unknown for Unicode character U+2192
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```
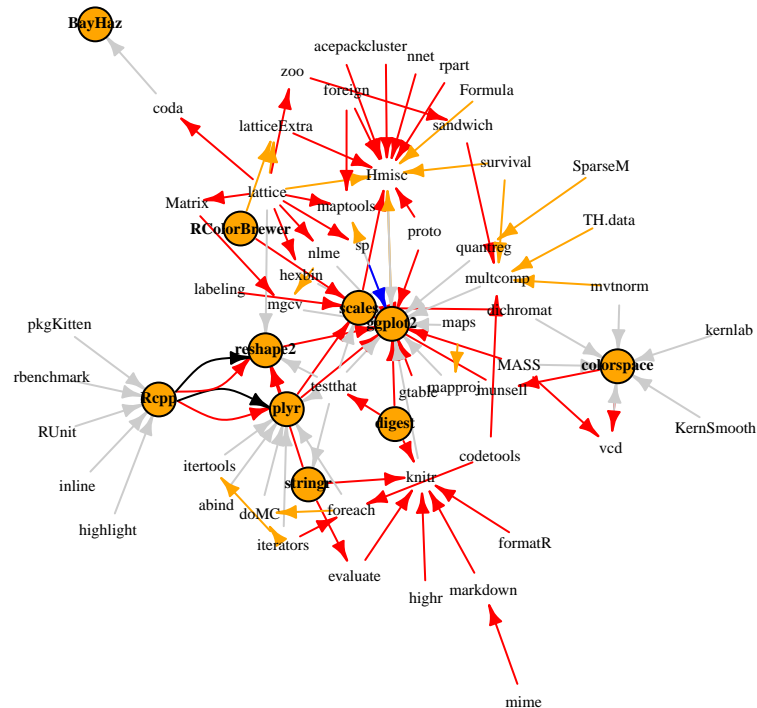
Rcpp, plyr, digest, stringr, reshape2, RColorBrewer, BayHaz, colorspac

ggplot2 Functions

```
##    [1] ".__C__Scales"            ".__global__"
##    [3] ".__NAMESPACE__."         ".__S3MethodsTable__."
##    [5] ".all_aesthetics"         ".base_to_ggplot"
##    [7] ".element_tree"           ".onAttach"
##    [9] ".packageName"            ".plot_store"
##   [11] ".pt"                     ".requireCachedGenerics"
##   [13] ".store"                  ".theme"
##   [15] ".zeroGrob"               "[.uneval"
##   [17] "%+%"                     "%+replace%"
##   [19] "%||%"                    "%inside%"
##   [21] "+.gg"                    "absoluteGrob"
##   [23] "add_ggplot"              "add_group"
##   [25] "add_theme"               "aes"
##   [27] "aes_all"                 "aes_auto"
##   [29] "aes_q"                   "aes_string"
##   [31] "aes_to_scale"            "aesdefaults"
##   [33] "aesthetics"              "annotate"
##   [35] "annotation_custom"       "annotation_logticks"
##   [37] "annotation_map"          "annotation_raster"
##   [39] "as.character.uneval"     "assign_viewports"
##   [41] "autoplot"                "autoplot.default"
##   [43] "benchplot"               "bin"
##   [45] "bolus"                   "bolus.ggplot"
##   [47] "bolus.proto"             "borders"
##   [49] "breaks"                  "build_guides"
##   [51] "build_strip"             "calc_element"
```

```
##  [53] "calc_logticks"                  "calculate_ellipse"
##  [55] "calculate_stats"                "check_required_aesthetics"
##  [57] "clist"                          "collide"
##  [59] "combine_elements"               "compute_grob_dimensions"
##  [61] "compute_grob_heights"           "compute_grob_widths"
##  [63] "compute_intercept"              "continuous_scale"
##  [65] "contour_lines"                  "coord"
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##  [69] "coord_aspect.fixed"             "coord_aspect.map"
##  [71] "coord_aspect.polar"             "coord_aspect.quickmap"
##  [73] "coord_cartesian"                "coord_distance"
##  [75] "coord_distance.cartesian"       "coord_distance.map"
##  [77] "coord_distance.polar"           "coord_distance.trans"
##  [79] "coord_equal"                    "coord_expand_defaults"
##  [81] "coord_expand_defaults.default"  "coord_expand_defaults.polar"
##  [83] "coord_fixed"                    "coord_flip"
##  [85] "coord_labels"                   "coord_labels.default"
##  [87] "coord_labels.flip"              "coord_labels.polar"
##  [89] "coord_map"                      "coord_munch"
##  [91] "coord_polar"                    "coord_quickmap"
##  [93] "coord_range"                    "coord_range.default"
##  [95] "coord_range.flip"               "coord_range.polar"
##  [97] "coord_render_axis_h"            "coord_render_axis_h.default"
##  [99] "coord_render_axis_h.map"        "coord_render_axis_h.polar"
## [101] "coord_render_axis_v"            "coord_render_axis_v.default"
## [103] "coord_render_axis_v.map"        "coord_render_axis_v.polar"
## [105] "coord_render_bg"                "coord_render_bg.default"
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## [111] "coord_render_fg.polar"          "coord_train"
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## [115] "coord_train.map"                "coord_train.polar"
## [117] "coord_train.trans"              "coord_trans"
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## [123] "coord_transform.polar"          "coord_transform.trans"
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## [127] "cut_number"                     "cweave"
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## [149] "element_grob.element_text"      "element_line"
## [151] "element_rect"                   "element_render"
## [153] "element_text"                   "equal_dims"
## [155] "expand_default"                 "expand_limits"
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## [159] "facet_axes.grid"                "facet_axes.wrap"
```

```
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## [225] "geom_errorbarh"                     "geom_freqpoly"
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## [241] "geom_ribbon"                        "geom_rug"
## [243] "geom_segment"                       "geom_smooth"
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## [249] "geom_vline"                         "GeomAbline"
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## [257] "GeomContour"                        "GeomCrossbar"
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## [263] "GeomErrorbar"                       "GeomErrorbarh"
## [265] "GeomFreqpoly"                       "GeomHex"
## [267] "GeomHistogram"                      "GeomHline"
```

```
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## [285] "GeomSmooth"                    "GeomStep"
## [287] "GeomText"                      "GeomTile"
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## [295] "ggorder"                       "ggpcp"
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## [313] "grobY.absoluteGrob"            "guide_axis"
## [315] "guide_colorbar"                "guide_colourbar"
## [317] "guide_gengrob"                 "guide_gengrob.colorbar"
## [319] "guide_gengrob.legend"          "guide_geom"
## [321] "guide_geom.colorbar"           "guide_geom.legend"
## [323] "guide_grid"                    "guide_legend"
## [325] "guide_merge"                   "guide_merge.colorbar"
## [327] "guide_merge.legend"            "guide_train"
## [329] "guide_train.colorbar"          "guide_train.legend"
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## [335] "guides_merge"                  "guides_train"
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```

```
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## [413] "pos_stack"                     "Position"
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## [439] "print.theme"                  "print.uneval"
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## [449] "rel"                           "remove_missing"
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## [465] "scale_alpha_manual"           "scale_apply"
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```

```
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## [489] "scale_color_gradientn"       "scale_color_grey"
## [491] "scale_color_hue"             "scale_color_identity"
## [493] "scale_color_manual"          "scale_colour_brewer"
## [495] "scale_colour_continuous"     "scale_colour_discrete"
## [497] "scale_colour_distiller"      "scale_colour_gradient"
## [499] "scale_colour_gradient2"      "scale_colour_gradientn"
## [501] "scale_colour_grey"           "scale_colour_hue"
## [503] "scale_colour_identity"       "scale_colour_manual"
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## [509] "scale_dimension.discrete"    "scale_dimension.position_d"
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## [515] "scale_fill_discrete"         "scale_fill_distiller"
## [517] "scale_fill_gradient"         "scale_fill_gradient2"
## [519] "scale_fill_gradientn"        "scale_fill_grey"
## [521] "scale_fill_hue"              "scale_fill_identity"
## [523] "scale_fill_manual"           "scale_is_empty"
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## [559] "scale_size_identity"         "scale_size_manual"
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## [565] "scale_train.identity"        "scale_train.position_d"
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## [577] "scale_type.numeric"          "scale_type.POSIXt"
## [579] "scale_x_continuous"          "scale_x_date"
## [581] "scale_x_datetime"            "scale_x_discrete"
## [583] "scale_x_log10"               "scale_x_reverse"
## [585] "scale_x_sqrt"                "scale_y_continuous"
## [587] "scale_y_date"                "scale_y_datetime"
## [589] "scale_y_discrete"            "scale_y_log10"
## [591] "scale_y_reverse"             "scale_y_sqrt"
```

```
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## [597] "scales_train_df"            "scales_transform_df"
## [599] "set_last_plot"              "setup_viewports"
## [601] "should_stop"                "spiral_arc_length"
## [603] "stairstep"                  "Stat"
## [605] "stat_abline"                "stat_aesthetics"
## [607] "stat_bin"                   "stat_bin2d"
## [609] "stat_bindot"                "stat_binhex"
## [611] "stat_boxplot"               "stat_contour"
## [613] "stat_density"               "stat_density2d"
## [615] "stat_ecdf"                  "stat_ellipse"
## [617] "stat_function"              "stat_hline"
## [619] "stat_identity"              "stat_qq"
## [621] "stat_quantile"              "stat_smooth"
## [623] "stat_spoke"                 "stat_sum"
## [625] "stat_summary"               "stat_summary_hex"
## [627] "stat_summary2d"             "stat_unique"
## [629] "stat_vline"                 "stat_ydensity"
## [631] "StatAbline"                 "StatBin"
## [633] "StatBin2d"                  "StatBindot"
## [635] "StatBinhex"                 "StatBoxplot"
## [637] "StatContour"                "StatDensity"
## [639] "StatDensity2d"              "StatEcdf"
## [641] "StatEllipse"                "StatFunction"
## [643] "StatHline"                  "StatIdentity"
## [645] "StatQq"                     "StatQuantile"
## [647] "StatSmooth"                 "StatSpoke"
## [649] "StatSum"                    "StatSummary"
## [651] "StatSummary2d"              "StatSummaryhex"
## [653] "StatUnique"                 "StatVline"
## [655] "StatYdensity"               "str.uneval"
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## [665] "theme_gray"                 "theme_grey"
## [667] "theme_light"                "theme_line"
## [669] "theme_linedraw"             "theme_minimal"
## [671] "theme_rect"                 "theme_segment"
## [673] "theme_set"                  "theme_text"
## [675] "theme_update"               "theta_rescale"
## [677] "theta_rescale_no_clip"      "TopLevel"
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## [681] "train_position"             "train_ranges"
## [683] "train_trans"                "transform_position"
## [685] "transform_value"            "try_require"
## [687] "ulevels"                    "unique_combs"
## [689] "uniquecols"                 "update_element"
## [691] "update_geom_defaults"       "update_guides"
## [693] "update_labels"              "update_stat_defaults"
## [695] "update_theme"               "validate_element"
## [697] "validate_guide"             "vp_name"
## [699] "vp_path"                    "waiver"
```

```
## [701] "width_cm"                        "widthDetails.zeroGrob"
## [703] "wrap_dims"                        "wrap_hmisc"
## [705] "xlab"                             "xlabel"
## [707] "xlim"                             "ylab"
## [709] "ylabel"                           "ylim"
## [711] "zeroGrob"
```

Rcpp Functions

```
##   [1] ".__C__C++Class"                   ".__C__C++Constructor"
##   [3] ".__C__C++Field"                   ".__C__C++Function"
##   [5] ".__C__C++Object"                  ".__C__C++OverloadedMethods"
##   [7] ".__C__Module"                     ".__C__RcppClass"
##   [9] ".__C__refClassGeneratorFunction"  ".__C__refGenerator"
##  [11] ".__global__"                      ".__NAMESPACE__."
##  [13] ".__S3MethodsTable__."             ".__T__.DollarNames:utils"
##  [15] ".__T__$:base"                     ".__T__complete:Rcpp"
##  [17] ".__T__formals<-:base"             ".__T__functions:Rcpp"
##  [19] ".__T__initialize:methods"         ".__T__prompt:utils"
##  [21] ".__T__show:methods"               ".asString"
##  [23] ".badModulePointer"                ".buildClinkCppFlags"
##  [25] ".callBuildCompleteHook"           ".callBuildHook"
##  [27] ".checkDevelTools"                 ".classes_map"
##  [29] ".CppClassName"                    ".cppfunction_formals_gets"
##  [31] ".DollarNames"                     ".DollarNames.C++Object"
##  [33] ".DollarNames.Module"              ".dummyInstancePointer"
##  [35] ".DummyModule"                     ".findPlugin"
##  [37] ".get_Module_Class"                ".get_Module_function"
##  [39] ".getHooksList"                    ".getInlinePlugin"
##  [41] ".getModulePointer"                ".getSourceCppDependencies"
##  [43] ".hasDevelTools"                   ".isPackageSourceFile"
##  [45] ".linkingToIncludes"               ".makeCppFields"
##  [47] ".makeCppMethods"                  ".makeFieldsList"
##  [49] ".moduleMetaName"                  ".moduleNames"
##  [51] ".onLoad"                          ".packageName"
##  [53] ".parseLinkingTo"                  ".pathWithRtools"
##  [55] ".pluginIncludes"                  ".plugins"
##  [57] ".printVerboseOutput"              ".rcpp_cache"
##  [59] ".rcpp_collect_warnings"           ".rcpp_error_recorder"
##  [61] ".rcpp_warning_recorder"           ".RcppClass"
##  [63] ".readPkgDescField"                ".requireCachedGenerics"
##  [65] ".restoreEnvironment"              ".setModulePointer"
##  [67] ".setupBuildEnvironment"           ".showBuildFailureDiagnostics"
##  [69] ".specifyItems"                    ".splitDepends"
##  [71] ".stdHeader"                       ".strings"
##  [73] ".type_manipulate"                 ".validatePackages"
##  [75] ".warningsEnv"                     ".writeFieldFunction"
##  [77] ".writeMethodFunction"             "areMacrosDefined"
##  [79] "as_character_externalptr"         "asBuildPath"
##  [81] "bib"                              "binding_maker"
##  [83] "canUseCXX0X"                      "capabilities"
##  [85] "class__dummyInstance"             "Class__has_default_constructor"
##  [87] "Class__name"                      "class__newInstance"
```

```
##  [89] "compileAttributes"           "complete"
##  [91] "cpp_fields"                  "cpp_hasDefaultConstructor"
##  [93] "cpp_object_dummy"            "cpp_object_initializer"
##  [95] "cpp_object_maker"            "cpp_refMethods"
##  [97] "CppClass__complete"          "CppClass__methods"
##  [99] "CppField__get"               "CppField__set"
## [101] "cppFunction"                 "CppMethod__invoke"
## [103] "CppMethod__invoke_notvoid"   "CppMethod__invoke_void"
## [105] "CppObject__finalize"         "CxxOxFlags"
## [107] "CxxFlags"                    "dealWith"
## [109] "demangle"                    "evalCpp"
## [111] "exposeClass"                 "externalptr_address"
## [113] "forceAssignInNamespace"      "formals<-"
## [115] "functions"                   "gctortureRUnitTest"
## [117] "get_rcpp_cache"              "inlineCxxPlugin"
## [119] "internal_function"           "InternalFunction_invoke"
## [121] "isBotchedSession"            "LdFlags"
## [123] "loadModule"                  "loadRcppClass"
## [125] "loadRcppModules"             "method_wrapper"
## [127] "Module"                      "Module__classes_info"
## [129] "Module__complete"            "Module__functions_arity"
## [131] "Module__functions_names"     "Module__get_class"
## [133] "Module__get_function"        "Module__has_class"
## [135] "Module__has_function"        "Module__invoke"
## [137] "Module__name"                "moduleIsLoaded"
## [139] "new_CppObject_xp"            "new_dummyObject"
## [141] "populate"                    "print.bytes"
## [143] "prompt"                      "rcpp_can_use_cxxOx"
## [145] "rcpp_can_use_cxx11"          "rcpp_capabilities"
## [147] "rcpp_error_recorder"         "Rcpp.package.skeleton"
## [149] "Rcpp.plugin.maker"           "Rcpp.system.file"
## [151] "RcppCapabilities"            "RcppCxxOxFlags"
## [153] "RcppCxxFlags"                "RcppLdFlags"
## [155] "RcppLdPath"                  "registerPlugin"
## [157] "setRcppClass"                "sizeof"
## [159] "sourceCpp"                   "sourceCppFunction"
## [161] "test"                        "unitTestSetup"
```

plyr Functions

```
##   [1] "."                   ".__NAMESPACE__."
##   [3] ".__S3MethodsTable__."  ".join_all"
##   [5] ".join_first"           ".matrix_to_df"
##   [7] ".onUnload"             ".packageName"
##   [9] ".rlply_worker"         ".wrapped_expr_to_fun"
##  [11] "[.idf"                 "[.indexed"
##  [13] "[.quoted"              "[.split"
##  [15] "[[.idf"                "[[.indexed_array"
##  [17] "[[.indexed_df"         "%||%"
##  [19] "a_ply"                 "aaply"
##  [21] "adply"                 "allocate_column"
##  [23] "alply"                 "amv_dim"
##  [25] "amv_dimnames"          "arrange"
```

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```
##  [27] "as.data.frame.function" "as.data.frame.idf"
##  [29] "as.list.indexed"        "as.list.split"
##  [31] "as.quoted"              "as.quoted.call"
##  [33] "as.quoted.character"    "as.quoted.factor"
##  [35] "as.quoted.formula"      "as.quoted.name"
##  [37] "as.quoted.NULL"         "as.quoted.numeric"
##  [39] "as.quoted.quoted"       "c.quoted"
##  [41] "cat_line"               "catcolwise"
##  [43] "colwise"                "compact"
##  [45] "count"                  "create_progress_bar"
##  [47] "d_ply"                  "daply"
##  [49] "ddply"                  "defaults"
##  [51] "desc"                   "dim.idf"
##  [53] "dims"                   "dlply"
##  [55] "dots"                   "each"
##  [57] "empty"                  "eval.quoted"
##  [59] "extract_col_rows"       "extract_rows"
##  [61] "failwith"               "here"
##  [63] "id"                     "id_var"
##  [65] "idata.frame"            "indexed_array"
##  [67] "indexed_df"             "is.discrete"
##  [69] "is.formula"             "is.quoted"
##  [71] "isplit2"                "join"
##  [73] "join_all"               "join_ids"
##  [75] "join.keys"              "l_ply"
##  [77] "laply"                  "ldply"
##  [79] "length.indexed"         "length.indexed_array"
##  [81] "liply"                  "list_to_array"
##  [83] "list_to_dataframe"      "list_to_vector"
##  [85] "llply"                  "loop_apply"
##  [87] "m_ply"                  "make_assignment_call"
##  [89] "make_names"             "maply"
##  [91] "mapvalues"              "match_df"
##  [93] "mdply"                  "mlply"
##  [95] "mutate"                 "name_rows"
##  [97] "names.idf"              "names.indexed"
##  [99] "names.indexed_array"    "names.quoted"
## [101] "ninteraction"           "nlevels"
## [103] "numcolwise"             "nunique"
## [105] "output_template"        "parallel_fe"
## [107] "print.indexed"          "print.quoted"
## [109] "print.split"            "progress_none"
## [111] "progress_text"          "progress_time"
## [113] "progress_tk"            "progress_win"
## [115] "quickdf"                "r_ply"
## [117] "raply"                  "rbind.fill"
## [119] "rbind.fill.matrix"      "rdply"
## [121] "reduce_dim"             "rename"
## [123] "revalue"                "rlply"
## [125] "round_any"              "round_any.numeric"
## [127] "round_any.POSIXct"      "setup_parallel"
## [129] "show_time"              "splat"
## [131] "split_indices"          "split_labels"
## [133] "splitter_a"             "splitter_d"
```

```
## [135] "str_rep"              "strip_splits"
## [137] "summarise"            "summarize"
## [139] "take"                 "true"
## [141] "try_default"          "tryapply"
## [143] "tryNULL"              "txtTimerBar"
## [145] "ulevels"              "unrowname"
## [147] "vaggregate"
```

digest Functions

```
##  [1] ".__NAMESPACE__."     ".__S3MethodsTable__." ".packageName"
##  [4] "AES"                 "AESdecryptECB"        "AESencryptECB"
##  [7] "AESinit"             "digest"               "digest_impl"
## [10] "hmac"                "makeRaw"              "makeRaw.character"
## [13] "makeRaw.default"     "makeRaw.digest"       "makeRaw.raw"
## [16] "modes"               "padWithZeros"         "print.AES"
```

stringr Functions

```
##  [1] ".__NAMESPACE__."     ".__S3MethodsTable__." ".packageName"
##  [4] "case.ignored"        "check_pattern"        "check_string"
##  [7] "compact"             "fixed"                "ignore.case"
## [10] "invert_match"        "is.fixed"             "is.perl"
## [13] "match_to_matrix"     "perl"                 "re_call"
## [16] "re_mapply"           "recyclable"           "str_c"
## [19] "str_count"           "str_detect"           "str_dup"
## [22] "str_extract"         "str_extract_all"      "str_join"
## [25] "str_length"          "str_locate"           "str_locate_all"
## [28] "str_match"           "str_match_all"        "str_pad"
## [31] "str_replace"         "str_replace_all"      "str_split"
## [34] "str_split_fixed"     "str_sub"              "str_sub<-"
## [37] "str_trim"            "str_wrap"             "word"
```

reshape2 Functions

```
##  [1] ".__NAMESPACE__."         ".__S3MethodsTable__."
##  [3] ".packageName"            "%||%"
##  [5] "acast"                   "add_margins"
##  [7] "all_identical"           "array_names"
##  [9] "cast"                    "colsplit"
## [11] "dcast"                   "downto"
## [13] "guess_value"             "is.string"
## [15] "margins"                 "melt"
## [17] "melt_check"              "melt_dataframe"
## [19] "melt.array"              "melt.data.frame"
## [21] "melt.default"            "melt.list"
## [23] "melt.matrix"             "melt.table"
## [25] "normalize_melt_arguments" "parse_formula"
## [27] "recast"                  "upto"
```

RColorBrewer Functions

```
##  [1] ".__NAMESPACE__."      ".__S3MethodsTable__." ".packageName"
##  [4] "brewer.pal"           "brewer.pal.info"      "catlist"
##  [7] "colorblind"           "colorblindlist"       "display.brewer.all"
## [10] "display.brewer.pal"   "divlist"              "divnum"
## [13] "maxcolors"            "namelist"             "quallist"
## [16] "qualnum"              "seqlist"              "seqnum"
```

colorspace Functions

```
##  [1] ".__C__color"          ".__C__HLS"
##  [3] ".__C__HSV"            ".__C__LAB"
##  [5] ".__C__LUV"            ".__C__polarLAB"
##  [7] ".__C__polarLUV"       ".__C__RGB"
##  [9] ".__C__sRGB"           ".__C__XYZ"
## [11] ".__NAMESPACE__."      ".__S3MethodsTable__."
## [13] ".__T__[:base"         ".__T__coerce:methods"
## [15] ".__T__coords:colorspace" ".__T__plot:graphics"
## [17] ".__T__show:methods"   ".packageName"
## [19] ".WhitePoint"          "CheckBounds"
## [21] "CheckMatrix"          "choose_palette"
## [23] "coords"               "desaturate"
## [25] "diverge_hcl"          "diverge_hsv"
## [27] "heat_hcl"             "hex"
## [29] "hex2RGB"              "HLS"
## [31] "HSV"                  "LAB"
## [33] "LUV"                  "mixcolor"
## [35] "plot"                 "polarLAB"
## [37] "polarLUV"             "rainbow_hcl"
## [39] "readhex"              "readRGB"
## [41] "RGB"                  "sequential_hcl"
## [43] "sRGB"                 "terrain_hcl"
## [45] "writehex"             "XYZ"
```

scales Functions

```
##  [1] ".__C__Continuous"     ".__C__DiscreteRange"
##  [3] ".__C__Range"          ".__global__"
##  [5] ".__NAMESPACE__."      ".__S3MethodsTable__."
##  [7] ".packageName"         ".requireCachedGenerics"
##  [9] "%||%"                 "abs_area"
## [11] "alpha"                "area_pal"
## [13] "as.trans"             "asn_trans"
## [15] "atanh_trans"          "boxcox_trans"
## [17] "brewer"               "brewer_pal"
## [19] "cbreaks"              "ceiling_date"
## [21] "ceiling_time"         "censor"
## [23] "clevels"              "col2hcl"
## [25] "comma"                "comma_format"
## [27] "ContinuousRange"      "cscale"
## [29] "date_breaks"          "date_format"
```

```
##  [31] "date_trans"          "dichromat_pal"
##  [33] "dichromat_schemes"   "discard"
##  [35] "discrete_range"      "DiscreteRange"
##  [37] "div_gradient_pal"    "dollar"
##  [39] "dollar_format"       "dscale"
##  [41] "exp_trans"           "expand_range"
##  [43] "extended_breaks"     "floor_date"
##  [45] "floor_time"          "format_format"
##  [47] "from_date"           "fullseq"
##  [49] "fullseq.Date"        "fullseq.numeric"
##  [51] "fullseq.POSIXt"      "gradient_n_pal"
##  [53] "grey_pal"            "hue_pal"
##  [55] "identity_pal"        "identity_trans"
##  [57] "is.trans"            "linetype_pal"
##  [59] "log_breaks"          "log_trans"
##  [61] "log10_trans"         "log1p_trans"
##  [63] "log2_trans"          "logit_trans"
##  [65] "manual_pal"          "map_continuous"
##  [67] "map_discrete"        "math_format"
##  [69] "muted"               "nice_rgb"
##  [71] "pal_name"            "parse_format"
##  [73] "parse_unit_spec"     "percent"
##  [75] "percent_format"      "precision"
##  [77] "pretty_breaks"       "print.trans"
##  [79] "probability_trans"   "probit_trans"
##  [81] "Range"               "reciprocal_trans"
##  [83] "rescale"             "rescale_max"
##  [85] "rescale_mid"         "rescale_none"
##  [87] "rescale_pal"         "reverse_trans"
##  [89] "scientific"          "scientific_format"
##  [91] "seealso"             "seealso_pal"
##  [93] "seealso_trans"       "seq_gradient_pal"
##  [95] "shape_pal"           "show_col"
##  [97] "sqrt_trans"          "squish"
##  [99] "squish_infinite"     "time_trans"
## [101] "to_date"             "train_continuous"
## [103] "train_discrete"      "trans_breaks"
## [105] "trans_format"        "trans_new"
## [107] "trans_range"         "zero_range"
```

Top 100 Cran Packages

Package	What does it do?
ggplot2	An implementation of the Grammar of Graphics
Rcpp	Seamless R and C++ Integration
plyr	Tools for splitting, applying and combining data
digest	Create cryptographic hash digests of R objects
stringr	Make it easier to work with strings
reshape2	Flexibly reshape data: a reboot of the reshape package

Package	What does it do?
RColorBrewer	ColorBrewer palettes
BayHaz	Bayesian estimation of smooth hazard rates via CPP and BPS priors
colorspace	Color Space Manipulation
scales	Scale functions for graphics
clhs	implements the conditioned Latin hypercube sampling, as published by Minasny and McBratney (2006)
labeling	Axis Labeling
proto	Prototype object-based programming
rJava	Low-level R to Java interface
munsell	Munsell colour system
gtable	Arrange grobs in tables
dichromat	Color Schemes for Dichromats
bitops	Bitwise Operations
DBI	R Database Interface
RCurl	General network (HTTP/FTP/. . .) client interface for R
car	Companion to Applied Regression
knitr	A general-purpose package for dynamic report generation in R
zoo	S3 Infrastructure for Regular and Irregular Time Series (Z's ordered observations)
evaluate	Parsing and evaluation tools that provide more details than the default
markdown	Markdown rendering for R
Hmisc	Harrell Miscellaneous
mime	guesses the MIME type from a filename extension using the data derived from /etc/mime.types in UNIX-type systems
formatR	Format R Code Automatically
highr	provides syntax highlighting for R source code
mvtnorm	Multivariate Normal and t Distributions
GPseq	modeling sequence read counts as a generalized poisson model and to use this model for detecting differentially expressed genes in different conditions and differentially spliced exons
caTools	Tools: moving window statistics, GIF, Base64, ROC AUC, etc
httr	tools for working with HTTP organised by HTTP verbs (GET(), POST(), etc)
OPI	Open Perimetry Interface (OPI) for simulating and controlling visual field machines using R
RcppArmadillo	Rcpp integration for Armadillo templated linear algebra library
YaleToolkit	tools developed at Yale University for the graphical exploration of complex multivariate data; barcode and gpairs now have their own packages
MASS	Support Functions and Datasets for Venables and Ripley's MASS
Formula	Infrastructure for extended formulas with multiple parts on the right-hand side and/or

Package	What does it do?
	multiple responses on the left-hand side
foreach	Foreach looping construct for R
latticeExtra	Extra Graphical Utilities Based on Lattice
gtools	Various R programming tools
iterators	Iterator construct for R
XML	Tools for parsing and generating XML within R and S-Plus
devtools	Tools to make developing R code easier
lme4	Linear mixed-effects models using S4 classes
lattice	Lattice Graphics
xtable	Export tables to LaTeX or HTML
yaml	This package implements the libyaml YAML 1.1 parser and emitter
sandwich	Robust Covariance Matrix Estimators
e1071	Misc Functions of the Department of Statistics (e1071), TU Wien
jsonlite	A fast JSON parser and generator optimized for statistical data and the web
rgl	3D visualization device system (OpenGL)
gdata	Various R programming tools for data manipulation
mgcv	Mixed GAM Computation Vehicle with GCV/AIC/REML smoothness estimation
SparseM	Sparse Linear Algebra
RJSONIO	Serialize R objects to JSON, JavaScript Object Notation
Matrix	Sparse and Dense Matrix Classes and Methods
minqa	Derivative-free optimization by quadratic approximation based on an interface to Fortran implementations
htmltools	Tools for HTML generation and output
RcppEigen	R and Eigen integration using Rcpp
sp	classes and methods for spatial data
quantreg	Quantile Regression
dplyr	A fast, consistent tool for working with data frame like objects, both in memory and out of memory
memoise	Memoise functions
shiny	Easy interactive web applications with R
reshape	Flexibly reshape data
foreign	Read Data Stored by Minitab, S, SAS, SPSS, Stata, Systat, dBase,..
gplots	Various R programming tools for plotting data
survsim	Simulation of simple and complex survival data
xlsx	Read, write, format Excel 2007 and Excel 97/2000/XP/2003 files
R6	The R6 package allows the creation of classes with reference semantics,

Package	What does it do?
	similar to R's built-in reference classes
nlme	Linear and Nonlinear Mixed Effects Models
testthat	A testing package specifically tailored for R that's fun, flexible and easy to set up
data.table	Fast aggregation of large data (e.g. 100GB in RAM), fast ordered joins,
	fast add/modify/delete of columns by group using no copies at all,
	list columns and a fast file reader (fread)
maps	Draw Geographical Maps
multcomp	Simultaneous Inference in General Parametric Models
nloptr	NLopt is a free/open-source library for nonlinear optimization,
	providing a common interface for a number of different free optimization routines
	available online as well as original implementations of various other algorithms
psych	Procedures for Psychological, Psychometric, and Personality Research
igraph	Network analysis and visualization
KernSmooth	Functions for kernel smoothing for Wand &amp Jones (1995)
survival	Survival Analysis
lmtest	Testing Linear Regression Models
cluster	Cluster Analysis Extended Rousseeuw et al
manipulate	The manipulate function accepts a plotting expression and a set of controls
	(e.g. slider, picker, checkbox, or button) which are used to dynamically
	change values within the expression
chron	Chronological objects which can handle dates and times
xts	eXtensible Time Series
RSQLite	SQLite interface for R
rpart	Recursive Partitioning
boot	Functions and datasets for bootstrapping from the book
	"Bootstrap Methods and Their Applications" by A. C. Davison and D. V. Hinkley
BH	A large part of Boost is provided as C++ template code which is resolved
	entirely at compile-time without linking
xlsxjars	The xlsxjars package collects all the external jars required for the xlxs package
quadprog	Functions to solve Quadratic Programming Problems
whisker	logicless templating, reuse templates in many programming languages including R
swirl	swirl turns the R console into an interactive learning environment
httpuv	httpuv provides low-level socket and protocol support for handling HTTP and
	WebSocket requests directly from within R
LPCM	Fitting multivariate data patterns with local principal curves;
	including simple tools for data compression (projection),

Package	What does it do?
	bandwidth selection, and measuring goodness-of-fit
magrittr	Provides a mechanism for chaining commands with a new forward-pipe operator, %>%
acepack	ACE and AVAS methods for choosing regression transformations
RMySQL	Implements DBI-compliant Interface to MySQL and MariaDB Databases
TH.data	Contains data sets used in other packages Torsten Hothorn maintains

rOpenSci Packages

Data Publication

Package	What does it do?
dataone	Search across repositories, and read and write data and metadata from the DataONE federation of data repositories from R. Includes repositories such as the KNB and Dryad.
dvn	Programmatic interface to the DataVerse Network.
EML	An R package for reading, writing, integrating and publishing data using the Ecological Metadata Language (EML) format.
rfigshare	Push data, figures, and text to, and search and retrieve data from, Figshare from R
RNeXML	Semantically rich NeXML I/O in R - next generation XML for Phylogenetic data.

Data Access

Package	What does it do?
AntWeb	Access data from the world's largest ant database. Maintained and developed by the California Academy of Science
BEFdata	Connects to instances of BEFdata portals for collaborative data management (e.g BEF-China and FUNdiv)
bold	R client for BOLD Systems (Barcode Of Life Database).
ckanr	R client for CKAN RESTful API. In early development
chromer	Interact with the chromosome counts database (CCDB) at http://ccdb.tau.ac.il
clifro	An R client for New Zealand's National Climate Database
ecoengine	Retrieve 3+ MM records, checklists and photos from Berkeley's ecoengine
ecoretriever	R client wrapping the Python Ecoretriever software.
gender	gender is an R package to encode gender based on names and dates of birth
geonames	Grab data from the GeoNames geographical database which covers all countries and contains over eight million placenames
historydata	An R package with datasets of interest to historians. It is primarily intended for pedagogic

Package	What does it do?
	purposes in teaching historians how to use R.
internetarchive	This API client for the Internet Archive is intended primarily for searching for items,
	retrieving metadata for items, and downloading the files associated with the items.
musemeta	R Client for Scraping Museum Metadata, including The Metropolitan Museum of Art,
	the Canadian Science & Technology Museum Corporation, the National Gallery of Art, and the Getty Mu
	and more to come. In early development
neotoma	Search for sites and download data for use in analytical workflows of paleoecological research
	using the Neotoma Paleoecological Database
paleobioDB	Access data from the Paleobiology Database, a warehouse of paleobiology database
pangaear	An R client to interact with the Pangaea database. In early development
parasiteR	Access parasite occurrences from the London Natural History Museum's Host-Parasite database,
	which contains over a quarter-million helminth records
pleiades	Search for and retrieve metadata and spatial location data on archeological
	places and names from Pleiades. In early development
rAvis	Download occurrence data for bird species, and associated metadata from ProyectoAvis,
	a citizen science bird project in Spain.
rbhl	Access full text and metadata on scanned and OCR text for biodiversity literature from
	Biodiversity Heritage Library
rbison	R client for USGS's BISON (Biodiversity Information Serving Our Nation).
RCryptsy	Allows data to be pulled from the Cryptsy exchange into R via the Cryptsy Public API.
	For more infomation about Cryptsy see https://www.cryptsy.com
rdpla	An R client to interact with Digital Public Library of America (DPLA) metadata.
	In early development
rdryad	Get data from Dryad a repository of data associated with published scholarly papers.
	Development pending upcoming API changes.
rebird	Search and acquire occurrence records of bird sightings collated in the eBird database
rentrez	rentrez provides functions that work with the NCBI eutils to search or download
	data from various NCBI databases
reol	R client to the Encyclopedia of Life a website and database of data/images/descriptions of species.
rerddap	General purpose R client for working with ERDDAP servers. More infomation on ERDDAP.
	ERDDAP is a specific case of OPeNDAP. In early development
reuropeana	An R client to interact with Europeana metadata. In early development
rfishbase	Access any fish data from Fishbase.org, including occurrence records, habitat data, and more
rfisheries	Search and retrieve data from the OpenFisheries.org, currently providing access to global
	capture fishing landings from the Food and Agriculture Organization (FAO) of the United Nations
rgbif	Access more than 400 million species occurrence records from across the globe in one place,

Package	What does it do?
	from the Global Biodiversity Information Facility
rglobi	R interface to the aggregated biotic interaction data of GloBI In early development
rif	R client for Neuroscience Information Network In early development
rinat	A programmatic interface to the API provided by iNaturalist.
RMendeley	This package is now deprecated. Programmatic interface to the Mendeley network - push up data to Mendeley as well as search and retrieve data from your private data and public Mendeley records. Updates pending upcoming API changes.
rnoaa	Access climate data from NOAA, including temperature and precipitation, as well as sea ice cover data, and extreme weather events
rnbn	Acess to the United Kingdom's National Biodiversity Network data.
rnpn	Access phenological data from US National Phenology Network for plants and animals
RSelenium	An R client for Selenium Remote WebDriver
rsnps	Search and retrieve Single Nucleotide Polymorphism data from openSNP, a repository of direct-to-customer genetic test results
RStars	Access to the Digital Universe Data set at http://star-api.herokuapp.com/ In early development
rvertnet	Access to specimen records for vertebrates across many museums though VertNet
rWBClimate	Programmatic interface to the World Bank climate data used in the World Bank climate knowledge portal.
spocc	Collect and map species occurrence data from GBIF, iNaturalist, Ecoengine, AntWeb, eBird, and USGS's BISON.
taxize	Get taxonomic identifiers from many different databases; taxonomic synonyms; taxonomic hierarchies; retrieve common names, and more. Access to a dozen different sources
traits	A high level R package to acquire species trait data from many sources, including Polytraits, BETTYdb, NCBI, Phylomatic, and more. In early development
treebase	Programmatic interface to Treebase - a database of phylogenetic trees
USAboundaries	Historical boundaries of the United States. Map the United States (or the colonies that became the United States) on any date from 1629 to 2000. Contains both county and state/territory level polygons.
webchem	webchem is a R package to retrieve chemical information from many sources. Currently includes: Chemical Identifier Resolver, ChemSpider, PubChem, and Chemical Translation Service.

Literature

Package	What does it do?
aRxiv	Access to the aRxiv preprint repository
bmc	An R interface to Biomed Central (BMC) search API and full text XML. In early development

Package	What does it do?
csl	Explore CSL styles and locales.
elife	R interface to the eLife API Deprecated - eLife is shutting their API down soon. See the package fulltext for eLife access
fulltext	An high level R interface to many different sources for full text (or nearly) scholarly texts, including PLOS, PMC, PeerJ, eLife, arXiv, and many more. In early development
IEEER	Interface to the IEEE Xplore Gateway. In early development
rcrossref	An R interface to Crossref metadata search API.
rdatacite	Wrapper to DataCite metadata. In early development
rebi	Access to the European PubMed Central database of papers and metadata
rhindawi	R interface to the Hindawi Journals metadata and corpus. No further development - See package fulltext for full text data access.
rmetadata	A high level R interface to many different scholarly metadata sources, which will include Crossref, any OAI-PMH provider, Digital Public Library of America, Hathi Trust, Europeana, and more. In early development
rorcid	A programmatic interface the Orcid.org API In early development
rpensoft	Access to Pensoft journals full text and metadata. No further development - See package fulltext for full text data access.
rplos	Connects to the full-text API of the Public Library of Science (PLOS). They provide a powerful search engine by exposing Solr search endpoints
rspringer	Full-text access to Springer journals. Development pending upcoming API changes.

Altmetrics

Package	What does it do?
alm	R wrapper to the almetrics API platform developed by PLoS API - other publishers have built on this and work out of the box: CrossRef, Copernicus Publishers, and the Public Knowledge Project (PKP)
Citeulike	R interface to CiteULike. Not in active development.
rAltmetric	Programmatic interface to article-level metrics data from Altmetric.com
rImpactStory	Programmatic interface to ImpactStory Package deprecated.

Reproducibility

Package	What does it do?
gistr	gistr is a light interface to GitHub's gists for R.
git2r	Git bindings from R

Package	What does it do?
testdat	A test suite to ensure that tabular data are correctly formatted.

Databases

Package	What does it do?
elastic	An R client for Elasticsearch
etseed	R client for etcd, a key-value store from the folks at CoreOS
solr	An R client for Apache Solr

Data Visualization

Package	What does it do?
plotly	Programmatic interface to the Plot.ly API - construct plots with ggplot2 and push to Plot.ly for an interactive plot with a few lines of code
rMaps	Generate interactive Javascript maps from R, using Mapbox, Leaflet, CrossLet, DataMaps, and more - and share maps on the interwebs

Geospatial Spatial data I/O and mapping.

Package	What does it do?
cartographer	Cartographer provides interactive maps in R Markdown documents or at the R console. These maps are suitable for data exploration. It wraps Elijah Meeks's d3-carto-map.
geojsonio	A package to convert many data formats to geoJSON or Bostock's topoJSON
lawn	An R client for turf.js, a Javascript library for advanced geospatial analysis
proj	An R client for proj4js, a Javascript library for transforming coordinates from one coordinate system to another, including datum transformations
wellknown	Convert WKT to GeoJSON and vice versa. Inspired by Python's geomet.

yHat Suggested Packages

Package	What does it do?
sqldf	Description: Manipulate R data frames using SQL
forecast	Forecasting functions for time series and linear models
plyr	Tools for splitting, applying and combining data

Package	What does it do?
stringr	Make it easier to work with strings
RPostgreSQL	Database interface and PostgreSQL driver for R
RMySQL	Implements DBI-compliant Interface to MySQL and MariaDB Databases
RMongo	MongoDB Database interface for R. The interface is provided via Java calls to the mongo-java-driver
RODBC	ODBC Database Access
RSQLite	SQLite interface for R
lubridate	Lubridate makes it easier to work with dates and times by providing functions to identify and parse date-time data ext
ggplot2	An implementation of the Grammar of Graphics
qcc Shewhart	quality control charts for continuous, attribute and count data
reshape2	Flexibly reshape data: a reboot of the reshape package
randomForest	Breiman and Cutler's random forests for classification and regression

Matt's Recently Used Packages

Package	What does it do?
ape	ape provides functions for reading, writing, plotting, and manipulating phylogenetic trees, analyses of comparative data in a phylogenetic framework, ext.
berndbischl/BBmisc	Miscellaneous helper functions for and from B. Bischl and some other guys at TU Dortmund, mainly for package development
berndbischl/parallel	Map R package to interface some popular parallelization back-ends with a unified interface
berndbischl/ParamHelpers	Helpers for parameters in black-box optimization, tuning and machine learning
BH	A large part of Boost is provided as C++ template code which is resolved entirely at compile-time without linking
caret	Misc functions for training and plotting classification and regression models
class	Various functions for classification
data.table	Fast aggregation of large data (e.g. 100GB in RAM), fast ordered joins, fast add/modify/delete of columns
digest	Create cryptographic hash digests of R objects
forecast	Forecasting functions for time series and linear models
fpp	All data sets required for the examples and exercises in the book "Forecasting: principles and practice"
HH	This contemporary presentation of statistical methods features extensive use of graphical displays for exploring data and for displaying the analysis
httr	tools for working with HTTP organised by HTTP verbs (GET(), POST(), etc)

Package	What does it do?
ISLR	The collection of datasets used in the book "An Introduction to Statistical Learning with Applications in R"
jsonlite	A fast JSON parser and generator optimized for statistical data and the web
kernlab	Kernel-based Machine Learning Lab
knitr	A general-purpose package for dynamic report generation in R
manipulate	The manipulate function accepts a plotting expression and a set of controls (e.g. slider, picker, checkbox, or button)
markdown	Markdown rendering for R
MASS	Support Functions and Datasets for Venables and Ripley's MASS
Matrix	Sparse and Dense Matrix Classes and Methods
mgcv	Mixed GAM Computation Vehicle with GCV/AIC/REML smoothness estimation
mime	This package guesses the MIME type from a filename extension using the data derived from /etc/mime.types in UNIX-type systems
mlr	Interface to a large number of classification and regression techniques, including machine-readable parameter descriptions
multcomp	Simultaneous Inference in General Parametric Models
mvtnorm	Multivariate Normal and t Distributions
OpenCL	This package provides an interface to OpenCL, allowing R to leverage computing power of GPUs and other HPC accelerator devices
party	A computational toolbox for recursive partitioning
rattle	Rattle (the R Analytic Tool To Learn Easily) provides a Gnome (RGtk2) based interface to R functionality for data mining
Rcmdr	R Commander
RColorBrewer	ColorBrewer palettes
Rcpp	Seamless R and C++ Integration
RcppArmadillo	Rcpp integration for Armadillo templated linear algebra library
RcppEigen	R and Eigen integration using Rcpp
Rcurl	General network (HTTP/FTP/. . .) client interface for R
reshape2	Flexibly reshape data: a reboot of the reshape package
rjson	Converts R object into JSON objects and vice-versa
RJSONIO	Serialize R objects to JSON, JavaScript Object Notation
rmarkdown	Convert R Markdown documents into a variety of formats including HTML, MS Word, PDF, and Beamer
ROAuth	Provides an interface to the OAuth 1.0 specification allowing users to authenticate via OAuth to the server of their choice
rpart.plot	Plot rpart models. Extends plot.rpart and text.rpart in the rpart package

Package	What does it do?
seriation	Infrastructure for seriation with an implementation of several seriation/sequencing techniques to reorder matrices, dissimilarity matrices, and dendrograms
shiny	Easy interactive web applications with R
swirl	swirl turns the R console into an interactive learning environment
tcltk2	A series of additional Tcl commands and Tk widgets with style and various functions to supplement the tcltk package
tools	
twitteR	Provides an interface to the Twitter web API
UsingR	A collection of data sets to accompany the textbook "Using R for Introductory Statistics"
yaml	This package implements the libyaml YAML 1.1 parser and emitter

Matt's Installed Packages

Package What does it do? ——————- ————————————————————

Apendix

Bioconductor Packages

Package	What does it do?
a4	Automated Affymetrix Array Analysis Umbrella Package
a4Base	Automated Affymetrix Array Analysis Base Package
a4Classif	Automated Affymetrix Array Analysis Classification Package
a4Core	Automated Affymetrix Array Analysis Core Package
a4Preproc	Automated Affymetrix Array Analysis Preprocessing Package
a4Reporting	Automated Affymetrix Array Analysis Reporting Package
ABarray	Microarray QA and statistical data analysis for Applied Biosystems Genome Survey Microrarray (AB1700) gene expression data
ABSSeq	ABSSeq: a new RNA-Seq analysis method based on absolute expression differences and generalized Poisson model
aCGH	Classes and functions for Array Comparative Genomic Hybridization data
ACME	Algorithms for Calculating Microarray Enrichment (ACME)
ADaCGH2	Analysis of big data from aCGH experiments using parallel computing and ff objects
adSplit	Annotation-Driven Clustering
affxparser	Affymetrix File Parsing SDK
affy	Methods for Affymetrix Oligonucleotide Arrays

Package	What does it do?
affycomp	Graphics Toolbox for Assessment of Affymetrix Expression Measures
AffyCompatible	Affymetrix GeneChip software compatibility
affyContam	Structured corruption of affymetrix cel file data
affycoretools	Functions useful for those doing repetitive analyses with Affymetrix GeneChips
AffyExpress	Affymetrix Quality Assessment and Analysis Tool
affyILM	Linear Model of background subtraction and the Langmuir isotherm
affyio	Tools for parsing Affymetrix data files
affylmGUI	GUI for affy analysis using limma package
affyPara	Parallelized preprocessing methods for Affymetrix Oligonucleotide Arrays
affypdnn	Probe Dependent Nearest Neighbours (PDNN) for the affy package
affyPLM	Methods for fitting probe-level models
affyQCReport	QC Report Generation for affyBatch objects
AffyRNADegradation	Analyze and correct probe positional bias in microarray data due to RNA degradation
AffyTiling	Easy extraction of individual probes in Affymetrix tiling arrays
AGDEX	Agreement of Differential Expression Analysis
agilp	Agilent expression array processing package
AgiMicroRna	Processing and Differential Expression Analysis of Agilent microRNA chips
ALDEx2	Analysis of differential abundance taking sample variation into account
AllelicImbalance	Investigates allele specific expression
alsace	ALS for the Automatic Chemical Exploration of mixtures
altcdfenvs	Alternative CDF environments (aka probeset mappings)
ampliQueso	Analysis of amplicon enrichment panels
annaffy	Annotation tools for Affymetrix biological metadata
annmap	Genome annotation and visualisation package pertaining to Affymetrix arrays and NGS analysis
annotate	Annotation for microarrays
AnnotationDbi	Annotation Database Interface
AnnotationForge	Code for Building Annotation Database Packages
AnnotationFuncs	Annotation translation functions
AnnotationHub	A client for retrieving Bioconductor objects from AnnotationHub
annotationTools	Annotate microarrays and perform cross-species gene expression analyses using flat file databases
anota	ANalysis Of Translational Activity (ANOTA)
antiProfiles	Implementation of gene expression anti-profiles
apComplex	Estimate protein complex membership using AP-MS protein data
aroma.light	Light-weight methods for normalization and visualization of microarray

Package	What does it do?
	data using only basic R data types
ArrayExpress	Access the ArrayExpress Microarray Database at EBI and build Bioconductor
	data structures: ExpressionSet, AffyBatch, NChannelSet
ArrayExpressHTS	ArrayExpress High Throughput Sequencing Processing Pipeline
arrayMvout	Multivariate outlier detection for expression array QA
arrayQuality	Assessing array quality on spotted arrays
arrayQualityMetrics	Quality metrics report for microarray data sets
ArrayTools	GeneChip Analysis Package
ArrayTV	Implementation of wave correction for arrays
ARRmNormalization	Adaptive Robust Regression normalization for Illumina methylation data
ASEB	Predict Acetylated Lysine Sites
ASGSCA	Association Studies for multiple SNPs and multiple traits using
	Generalized Structured Equation Models
asmn	All sample mean normalization
ASSET	An R package for subset-based association analysis of heterogeneous traits and subtypes
ASSIGN	Adaptive Signature Selection and InteGratioN (ASSIGN)
AtlasRDF	Gene Expression Atlas query and gene set enrichment package
attract	Methods to Find the Gene Expression Modules that Represent the
	Drivers of Kauffman's Attractor Landscape
BAC	Bayesian Analysis of Chip-chip experiment
BADER	Bayesian Analysis of Differential Expression in RNA Sequencing Data
BAGS	A Bayesian Approach for Geneset Selection
ballgown	Flexible, isoform-level differential expression analysis
BaseSpaceR	R SDK for BaseSpace RESTful API
Basic4Cseq	Basic4Cseq: an R/Bioconductor package for analyzing 4C-seq data
BayesPeak	Bayesian Analysis of ChIP-seq Data
baySeq	Empirical Bayesian analysis of patterns of differential expression in count data
BCRANK	Predicting binding site consensus from ranked DNA sequences
beadarray	Quality assessment and low-level analysis for Illumina BeadArray data
beadarraySNP	Normalization and reporting of Illumina SNP bead arrays
BeadDataPackR	Compression of Illumina BeadArray data
BEAT	BEAT - BS-Seq Epimutation Analysis Toolkit
betr	Identify differentially expressed genes in microarray time-course data
bgafun	BGAfun A method to identify specifity determining residues in protein families
BGmix	Bayesian models for differential gene expression
bgx	Bayesian Gene eXpression

Package	What does it do?
BHC	Bayesian Hierarchical Clustering
BicARE	Biclustering Analysis and Results Exploration
BiGGR	Constraint based modeling in R using metabolic reconstruction databases
bigmemoryExtras	An extension of the bigmemory package with added safety, convenience, and a factor class
bioassayR	R library for Bioactivity analysis
Biobase	Biobase: Base functions for Bioconductor
BiocCaseStudies	BiocCaseStudies: Support for the Case Studies Monograph
BiocCheck	Bioconductor-specific package checks
BiocGenerics	S4 generic functions for Bioconductor
biocGraph	Graph examples and use cases in Bioinformatics
BiocInstaller	Install/Update Bioconductor and CRAN Packages
BiocParallel	Bioconductor facilities for parallel evaluation
BiocStyle	Standard styles for vignettes and other Bioconductor documents
biocViews	Categorized views of R package repositories
bioDist	Different distance measures
biomaRt	Interface to BioMart databases (e.g. Ensembl, COSMIC ,Wormbase and Gramene)
BioMVCClass	Model-View-Controller (MVC) Classes That Use Biobase
biomvRCNS	Copy Number study and Segmentation for multivariate biological data
BioNet	Routines for the functional analysis of biological networks
BioSeqClass	Classification for Biological Sequences
Biostrings	String objects representing biological sequences, and matching algorithms
biosvd	Package for high-throughput data processing, outlier detection, noise removal and dynamic modeling
biovizBase	Basic graphic utilities for visualization of genomic data
BiRewire	High-performing routines for the randomization of a bipartite graph (or a binary event matrix) preserving degree distribution (or marginal totals)
birta	Bayesian Inference of Regulation of Transcriptional Activity
BiSeq	Processing and analyzing bisulfite sequencing data
BitSeq	Transcript expression inference and differential expression analysis for RNA-seq data
blima	Package for the preprocessing and analysis of the Illumina microarrays on the detector (bead) level
BRAIN	Baffling Recursive Algorithm for Isotope distributioN calculations
BrainStars	Query gene expression data and plots from BrainStars (B*)
bridge	Bayesian Robust Inference for Differential Gene Expression
BridgeDbR	Code for using BridgeDb identifier mapping framework from within R

Package	What does it do?
BSgenome	Infrastructure for Biostrings-based genome data packages
bsseq	Analyze, manage and store bisulfite sequencing data
BufferedMatrix	A matrix data storage object held in temporary files
BufferedMatrixMethods	Microarray Data related methods that utlize BufferedMatrix objects
bumphunter	Bump Hunter
BUS	Gene network reconstruction
CAFE	Chromosmal Aberrations Finder in Expression data
CAGEr	Analysis of CAGE (Cap Analysis of Gene Expression) sequencing data for precise mapping of transcription start sites and promoterome mining
CALIB	Calibration model for estimating absolute expression levels from microarray data
CAMERA	Collection of annotation related methods for mass spectrometry data
cancerclass	Development and validation of diagnostic tests from high-dimensional molecular data
CancerMutationAnalysis	Cancer mutation analysis
casper	Characterization of Alternative Splicing based on Paired-End Reads
Category	Category Analysis
categoryCompare	Meta-analysis of high-throughput experiments using feature annotations
ccrepe	Ccrepe and nc.score
cellGrowth	Fitting cell population growth models
cellHTS	Analysis of cell-based screens
cellHTS2	Analysis of cell-based screens - revised version of cellHTS
CellNOptR	Training of boolean logic models of signalling networks using prior knowledge networks and perturbation data
CexoR	An R package to uncover high-resolution protein-DNA interactions in ChIP-exo replicates
CFAssay	Statistical analysis for the Colony Formation Assay
CGEN	An R package for analysis of case-control studies in genetic epidemiology
CGHbase	CGHbase: Base functions and classes for arrayCGH data analysis
CGHcall	Calling aberrations for array CGH tumor profiles
cghMCR	Find chromosome regions showing common gains/losses
CGHnormaliter	Normalization of array CGH data with imbalanced aberrations
CGHregions	Dimension Reduction for Array CGH Data with Minimal Information Loss
ChAMP	Chip Analysis Methylation Pipeline for Illumina HumanMethylation450
charm	Analysis of DNA methylation data from CHARM microarrays
ChemmineOB	R interface to a subset of OpenBabel functionalities
ChemmineR	Cheminformatics Toolkit for R
chimera	A package for secondary analysis of fusion products
chipenrich	Gene set enrichment for ChIP-seq peak data

Package	What does it do?
ChIPpeakAnno	Batch annotation of the peaks identified from either ChIP-seq,
	ChIP-chip experiments or any experiments resulted in large number of chromosome ranges
ChIPQC	Quality metrics for ChIPseq data
ChIPseeker	ChIPseeker for ChIP peak Annotation, Comparison, and Visualization
chipseq	Chipseq: A package for analyzing chipseq data
ChIPseqR	Identifying Protein Binding Sites in High-Throughput Sequencing Data
ChIPsim	Simulation of ChIP-seq experiments
ChIPXpress	ChIPXpress: enhanced transcription factor target gene identification from
	ChIP-seq and ChIP-chip data using publicly available gene expression profiles
chopsticks	The snp.matrix and X.snp.matrix classes
chroGPS	ChroGPS: visualizing the epigenome
ChromHeatMap	Heat map plotting by genome coordinate
cisPath	Visualization and management of the protein-protein interaction networks
ClassifyR	A framework for two-class classification problems, with applications to
	differential variability and differential distribution testing
cleanUpdTSeq	This package classifies putative polyadenylation sites as true or
	false/internally oligodT primed
cleaver	Cleavage of Polypeptide Sequences
clippda	A package for the clinical proteomic profiling data analysis
clipper	Gene set analysis exploiting pathway topology
Clomial	Infers clonal composition of a tumor
Clonality	Clonality testing
clonotypeR	High throughput analysis of T cell antigen receptor sequences
clst	Classification by local similarity threshold
clstutils	Tools for performing taxonomic assignment
clusterProfiler	Statistical analysis and visulization of functional profiles for genes and gene clusters
clusterStab	Compute cluster stability scores for microarray data
CMA	Synthesis of microarray-based classification
cn.farms	Cn.FARMS - factor analysis for copy number estimation
cn.mops	Cn.mops - Mixture of Poissons for CNV detection in NGS data
CNAnorm	A normalization method for Copy Number Aberration in cancer samples
CNEr	CNE detection and visualization.
CNORdt	Add-on to CellNOptR: Discretized time treatments
CNORfeeder	Integration of CellNOptR to add missing links
CNORfuzzy	Addon to CellNOptR: Fuzzy Logic
CNORode	ODE add-on to CellNOptR

Package	What does it do?
CNTools	Convert segment data into a region by sample matrix to allow for other high level computational analyses.
cnvGSA	Gene Set Analysis of (Rare) Copy Number Variants
CNVrd2	CNVrd2: a read depth-based method to detect and genotype complex common copy number variants from next generation sequencing data
CNVtools	A package to test genetic association with CNV data
cobindR	Finding Co-occuring motifs of transcription factor binding sites
CoCiteStats	Different test statistics based on co-citation
codelink	Manipulation of Codelink microarray data
CoGAPS	Coordinated Gene Activity in Pattern Sets
coGPS	Cancer outlier Gene Profile Sets
COHCAP	CpG Island Analysis Pipeline for Illumina Methylation Array and Targeted BS-Seq Data
COMPASS	Combinatorial Polyfunctionality Analysis of Single Cells
compcodeR	RNAseq data simulation, differential expression analysis and performance comparison of differential expression methods
compEpiTools	Tools for computational epigenomics
CompGO	An R pipeline for .bed file annotation, comparing GO term enrichment between gene sets and data visualisation
ConsensusClusterPlus	ConsensusClusterPlus
convert	Convert Microarray Data Objects
copa	Functions to perform cancer outlier profile analysis
COPDSexualDimorphism	Sexual dimorphic and COPD differential analysis for gene expression and methylation.
copynumber	Segmentation of single- and multi-track copy number data by penalized least squares regression.
CopyNumber450k	R package for calling CNV from Illumina 450k methylation microarrays
CoRegNet	CoRegNet : reconstruction and integrated analysis of co-regulatory networks
Cormotif	Correlation Motif Fit
CorMut	Detect the correlated mutations based on selection pressure
coRNAi	Analysis of co-knock-down RNAi data
CORREP	Multivariate Correlation Estimator and Statistical Inference Procedures
cosmiq	Cosmiq - COmbining Single Masses Into Quantities
COSNet	COSNet: Cost-Senstitive network for node label prediction
CoverageView	Coverage visualization package for R
cqn	Conditional quantile normalization
CRImage	CRImage a package to classify cells and calculate tumour cellularity
CRISPRseek	Design of target-specific guide RNAs in CRISPR-Cas9, genome-editing systems

Package	What does it do?
crlmm	Genotype Calling (CRLMM) and Copy Number Analysis tool for Affymetrix SNP 5.0 and 6.0 and Illumina arrays
CSAR	Statistical tools for the analysis of ChIP-seq data
csaw	ChIP-seq analysis with windows
CSSP	ChIP-Seq Statistical Power
ctc	Cluster and Tree Conversion.
cummeRbund	Analysis, exploration, manipulation, and visualization of Cufflinks high-throughput sequencing data.
customProDB	Generate customized protein database from NGS data, with a focus on RNA-Seq data, for proteomics search.
cycle	Significance of periodic expression pattern in time-series data
dagLogo	DagLogo
daMA	Efficient design and analysis of factorial two-colour microarray data
DART	Denoising Algorithm based on Relevance network Topology
DASiR	Distributed Annotation System in R
DAVIDQuery	Retrieval from the DAVID bioinformatics data resource into R
DBChIP	Differential Binding of Transcription Factor with ChIP-seq
ddCt	The ddCt Algorithm for the Analysis of Quantitative Real-Time PCR (qRT-PCR)
ddgraph	Distinguish direct and indirect interactions with Graphical Modelling
DECIPHER	Database Enabled Code for Ideal Probe Hybridization Employing R
DeconRNASeq	Deconvolution of Heterogeneous Tissue Samples for mRNA-Seq data
DEDS	Differential Expression via Distance Summary for Microarray Data
deepSNV	Detection of subclonal SNVs in deep sequencing data
DEGraph	Two-sample tests on a graph
DEGreport	Report of DEG analysis
DEGseq	Identify Differentially Expressed Genes from RNA-seq data
deltaGseg	DeltaGseg
derfinder	Annotation-agnostic differential expression analysis of RNA-seq data at base-pair resolution
derfinderHelper	Derfinder helper package
derfinderPlot	Plotting functions for derfinder
DESeq	Differential gene expression analysis based on the negative binomial distribution
DESeq2	Differential gene expression analysis based on the negative binomial distribution
DEXSeq	Inference of differential exon usage in RNA-Seq
dexus	DEXUS - Identifying Differential Expression in RNA-Seq Studies with Unknown Conditions or without Replicates
DFP	Gene Selection

Package	What does it do?
DiffBind	Differential Binding Analysis of ChIP-Seq peak data
diffGeneAnalysis	Performs differential gene expression Analysis
DirichletMultinomial	Dirichlet-Multinomial Mixture Model Machine Learning for Microbiome Data
dks	The double Kolmogorov-Smirnov package for evaluating multiple testing procedures
DMRcate	Illumina 450K methylation array spatial analysis methods
DMRforPairs	DMRforPairs: identifying Differentially Methylated Regions between unique samples using array based methylation profiles
DNAcopy	DNA copy number data analysis
DNaseR	DNase I footprinting analysis of DNase-seq data
domainsignatures	Geneset enrichment based on InterPro domain signatures
DOQTL	Genotyping and QTL Mapping in DO Mice
DOSE	Disease Ontology Semantic and Enrichment analysis
DriverNet	Drivernet: uncovering somatic driver mutations modulating transcriptional networks in cancer
DrugVsDisease	Comparison of disease and drug profiles using Gene set Enrichment Analysis
DSS	Dispersion shrinakge for sequencing data
DTA	Dynamic Transcriptome Analysis
dualKS	Dual KS Discriminant Analysis and Classification
DupChecker	A package for checking high-throughput genomic data redundancy in meta-analysis
dyebias	The GASSCO method for correcting for slide-dependent gene-specific dye bias
DynDoc	Dynamic document tools
EasyqpcR	EasyqpcR for low-throughput real-time quantitative PCR data analysis
easyRNASeq	Count summarization and normalization for RNA-Seq data
EBarrays	Unified Approach for Simultaneous Gene Clustering and Differential Expression Identification
EBcoexpress	EBcoexpress for Differential Co-Expression Analysis
EBImage	Image processing and analysis toolbox for R
EBSeq	An R package for gene and isoform differential expression analysis of RNA-seq data
EBSeqHMM	Bayesian analysis for identifying gene or isoform expression changes in ordered RNA-seq experiments
ecolitk	Meta-data and tools for E. coli
EDASeq	Exploratory Data Analysis and Normalization for RNA-Seq
EDDA	Experimental Design in Differential Abundance analysis
edgeR	Empirical analysis of digital gene expression data in R
eiR	Accelerated similarity searching of small molecules
eisa	Expression data analysis via the Iterative Signature Algorithm

Package	What does it do?
ELBOW	ELBOW - Evaluating foLd change By the lOgit Way
EnrichmentBrowser	Seamless navigation through combined results of set-based and network-based enrichment analysis
ensemblVEP	R Interface to Ensembl Variant Effect Predictor
ENVISIONQuery	Retrieval from the ENVISION bioinformatics data portal into R
epigenomix	Epigenetic and gene transcription data normalization and integration with mixture models
epivizr	R Interface to epiviz web app
erccdashboard	Assess Differential Gene Expression Experiments with ERCC Controls
ExiMiR	R functions for the normalization of Exiqon miRNA array data
exomeCopy	Copy number variant detection from exome sequencing read depth
exomePeak	Exome-based anlaysis of MeRIP-Seq data: peak calling and differential analysis
explorase	GUI for exploratory data analysis of systems biology data
ExpressionView	Visualize biclusters identified in gene expression data
fabia	FABIA: Factor Analysis for Bicluster Acquisition
facopy	Feature-based association and gene-set enrichment for copy number alteration analysis in cancer
factDesign	Factorial designed microarray experiment analysis
farms	FARMS - Factor Analysis for Robust Microarray Summarization
fastLiquidAssociation	Functions for genome-wide application of Liquid Association
fastseg	Fastseg - a fast segmentation algorithm
fdrame	FDR adjustments of Microarray Experiments (FDR-AME)
FEM	Identification of FunctionalEpigenetic Modules
ffpe	Quality assessment and control for FFPE microarray expression data
FGNet	Functional Gene Networks derived from biological enrichment analyses
flagme	Analysis of Metabolomics GC/MS Data
flipflop	Fast lasso-based isoform prediction as a flow problem
flowBeads	FlowBeads: Analysis of flow bead data
flowBin	Combining multitube flow cytometry data by binning
flowcatchR	Tools to analyze in vivo microscopy imaging data focused on tracking flowing blood cells
flowCHIC	Analyze flow cytometric data using histogram information
flowCL	Semantic labelling of flow cytometric cell populations
flowClean	FlowClean
flowClust	Clustering for Flow Cytometry
flowCore	FlowCore: Basic structures for flow cytometry data
flowCyBar	Analyze flow cytometric data using gate information
flowDensity	Sequential Flow Cytometry Data Gating

Package	What does it do?
flowFit	Estimate proliferation in cell-tracking dye studies
flowFlowJo	Tools for extracting information from a FlowJo workspace and working with the data in the flowCore paradigm
flowFP	Fingerprinting for Flow Cytometry
flowMap	A probabilistic algorithm for matching and comparing multiple flow cytometry samples
flowMatch	Matching and meta-clustering in flow cytometry
flowMeans	Non-parametric Flow Cytometry Data Gating
flowMerge	Cluster Merging for Flow Cytometry Data
flowPeaks	An R package for flow data clustering
flowPhyto	Methods for Continuous Flow Cytometry
flowPlots	FlowPlots: analysis plots and data class for gated flow cytometry data
flowQ	Quality control for flow cytometry
flowQB	Automated Quadratic Characterization of Flow Cytometer Instrument Sensitivity: Q, B and CVinstrinsic calculations
flowStats	Statistical methods for the analysis of flow cytometry data
flowTrans	Parameter Optimization for Flow Cytometry Data Transformation
flowType	Phenotyping Flow Cytometry Assays
flowUtils	Utilities for flow cytometry
flowViz	Visualization for flow cytometry
flowWorkspace	Import flowJo Workspaces into BioConductor and replicate flowJo gating with flowCore
fmcsR	Mismatch Tolerant Maximum Common Substructure Searching
focalCall	Detection of focal aberrations in DNA copy number data
FourCSeq	Package analyse 4C sequencing data
FRGEpistasis	Epistasis Analysis for Quantitative Traits by Functional Regression Model
frma	Frozen RMA and Barcode
frmaTools	Frozen RMA Tools
FunciSNP	Integrating Functional Non-coding Datasets with Genetic Association Studies to Identify Candidate Regulatory SNPs
gaga	GaGa hierarchical model for high-throughput data analysis
gage	Generally Applicable Gene-set Enrichment for Pathway Analysis
gaggle	Broadcast data between R and Gaggle
gaia	GAIA: An R package for genomic analysis of significant chromosomal aberrations.
gaucho	Genetic Algorithms for Understanding Clonal Heterogeneity and Ordering
gCMAP	Tools for Connectivity Map-like analyses
gCMAPWeb	A web interface for gene-set enrichment analyses
gcrma	Background Adjustment Using Sequence Information

Package	What does it do?
gdsfmt	R Interface to CoreArray Genomic Data Structure (GDS) files
geecc	Gene set Enrichment analysis Extended to Contingency Cubes
genArise	Microarray Analysis tool
GENE.E	Interact with GENE-E from R
GeneAnswers	Integrated Interpretation of Genes
GeneExpressionSignature	Gene Expression Signature based Similarity Metric
genefilter	Genefilter: methods for filtering genes from high-throughput experiments
genefu	Relevant Functions for Gene Expression Analysis, Especially in Breast Cancer
GeneGA	Design gene based on both mRNA secondary structure and codon usage bias using Genetic algorithm
GeneMeta	MetaAnalysis for High Throughput Experiments
GeneNetworkBuilder	Build Regulatory Network from ChIP-chip/ChIP-seq and Expression Data
GeneOverlap	Test and visualize gene overlaps
geneplotter	Graphics related functions for Bioconductor
geneRecommender	A gene recommender algorithm to identify genes coexpressed with a query set of genes
GeneRegionScan	GeneRegionScan
geneRxCluster	GRx Differential Clustering
GeneSelectMMD	Gene selection based on the marginal distributions of gene profiles that characterized by a mixture of three-component multivariate distributions
GeneSelector	Stability and Aggregation of ranked gene lists
geNetClassifier	Classify diseases and build associated gene networks using gene expression profiles
GeneticsDesign	Functions for designing genetics studies
GeneticsPed	Pedigree and genetic relationship functions
genoCN	Genotyping and copy number study tools
GenomeGraphs	Plotting genomic information from Ensembl
GenomeInfoDb	Utilities for manipulating chromosome and other 'seqname' identifiers
genomeIntervals	Operations on genomic intervals
genomes	Genome sequencing project metadata
GenomicAlignments	Representation and manipulation of short genomic alignments
GenomicFeatures	Tools for making and manipulating transcript centric annotations
GenomicFiles	Distributed computing by file or by range
GenomicInteractions	R package for handling genomic interaction data
GenomicRanges	Representation and manipulation of genomic intervals
GenomicTuples	Representation and manipulation of genomic tuples
Genominator	Analyze, manage and store genomic data
genoset	Provides classes similar to ExpressionSet for copy number analysis

Package	What does it do?
GenoView	Condensed, overlapped plotting of genomic data tracks
GEOmetadb	A compilation of metadata from NCBI GEO
GEOquery	Get data from NCBI Gene Expression Omnibus (GEO)
GEOsubmission	Prepares microarray data for submission to GEO
GEWIST	Gene Environment Wide Interaction Search Threshold
GGBase	GGBase infrastructure for genetics of gene expression package GGtools
ggbio	Visualization tools for genomic data
GGtools	Software and data for analyses in genetics of gene expression
girafe	Genome Intervals and Read Alignments for Functional Exploration
GLAD	Gain and Loss Analysis of DNA
GlobalAncova	Calculates a global test for differential gene expression between groups
globaltest	Testing groups of covariates/features for association with a response variable,
	with applications to gene set testing
gmapR	Provides convenience methods to work with GMAP and GSNAP from within R
GOexpress	Visualise microarray and RNAseq data using gene ontology annotations
GOFunction	GO-function: deriving biologcially relevant functions from statistically significant functions
goProfiles	GoProfiles: an R package for the statistical analysis of functional profiles
GOSemSim	GO-terms Semantic Similarity Measures
goseq	Gene Ontology analyser for RNA-seq and other length biased data
GOSim	Computation of functional similarities between GO terms and gene products;
	GO enrichment analysis
GOstats	Tools for manipulating GO and microarrays
GOsummaries	Word cloud summaries of GO enrichment analysis
GOTHiC	Binomial test for Hi-C data analysis
goTools	Functions for Gene Ontology database
gpls	Classification using generalized partial least squares
gprege	Gaussian Process Ranking and Estimation of Gene Expression time-series
graph	Graph: A package to handle graph data structures
GraphAlignment	GraphAlignment
GraphAT	Graph Theoretic Association Tests
graphite	GRAPH Interaction from pathway Topological Environment
GraphPAC	Identification of Mutational Clusters in Proteins via a Graph Theoretical Approach
GRENITS	Gene Regulatory Network Inference Using Time Series
groHMM	GRO-seq Analysis Pipeline
GSAR	Gene Set Analysis in R
GSCA	GSCA: Gene Set Context Analysis

Package	What does it do?
GSEABase	Gene set enrichment data structures and methods
GSEAlm	Linear Model Toolset for Gene Set Enrichment Analysis
GSReg	Gene Set Regulation (GS-Reg)
GSRI	Gene Set Regulation Index
GSVA	Gene Set Variation Analysis for microarray and RNA-seq data
Gviz	Plotting data and annotation information along genomic coordinates
gwascat	Representing and modeling data in the NHGRI GWAS catalog
GWASTools	Tools for Genome Wide Association Studies
h5vc	Managing alignment tallies using a hdf5 backend
hapFabia	HapFabia: Identification of very short segments of identity by descent (IBD) characterized by rare variants in large sequencing data
Harshlight	A "corrective make-up" program for microarray chips
HCsnip	Semi-supervised adaptive-height snipping of the Hierarchical Clustering tree
HDTD	Statistical Inference about the Mean Matrix and the Covariance Matrices in High-Dimensional Transposable Data (HDTD)
Heatplus	Heatmaps with row and/or column covariates and colored clusters
HELP	Tools for HELP data analysis
HEM	Heterogeneous error model for identification of differentially expressed genes under multiple conditions
hiAnnotator	Functions for annotating GRanges objects
HilbertVis	Hilbert curve visualization
HilbertVisGUI	HilbertVisGUI
hiReadsProcessor	Functions to process LM-PCR reads from 454/Illumina data
HiTC	High Throughput Chromosome Conformation Capture analysis
HMMcopy	Copy number prediction with correction for GC and mappability bias for HTS data
hopach	Hierarchical Ordered Partitioning and Collapsing Hybrid (HOPACH)
hpar	Human Protein Atlas in R
HTqPCR	Automated analysis of high-throughput qPCR data
HTSanalyzeR	Gene set over-representation, enrichment and network analyses for high-throughput screens
HTSeqGenie	A NGS analysis pipeline
htSeqTools	Quality Control, Visualization and Processing for High-Throughput Sequencing data
HTSFilter	Filter replicated high-throughput transcriptome sequencing data
HybridMTest	Hybrid Multiple Testing
hyperdraw	Visualizing Hypergaphs
hypergraph	A package providing hypergraph data structures
iASeq	IASeq: integrating multiple sequencing datasets for detecting allele-specific events

Package	What does it do?
iBBiG	Iterative Binary Biclustering of Genesets
ibh	Interaction Based Homogeneity for Evaluating Gene Lists
iBMQ	Integrated Bayesian Modeling of eQTL data
Icens	NPMLE for Censored and Truncated Data
iChip	Bayesian Modeling of ChIP-chip Data Through Hidden Ising Models
iClusterPlus	Integrative clustering of multi-type genomic data
IdeoViz	Plots data (continuous/discrete) along chromosomal ideogram
idiogram	Idiogram
IdMappingAnalysis	ID Mapping Analysis
IdMappingRetrieval	ID Mapping Data Retrieval
illuminaio	Parsing Illumina microarray output files
imageHTS	Analysis of high-throughput microscopy-based screens
IMPCdata	Retrieves data from IMPC database
impute	Impute: Imputation for microarray data
INPower	An R package for computing the number of susceptibility SNPs
inSilicoDb	Access to the InSilico Database
inSilicoMerging	Collection of Merging Techniques for Gene Expression Data
intansv	Integrative analysis of structural variations
interactiveDisplay	Package for enabling powerful shiny web displays of Bioconductor objects
interactiveDisplayBase	Base package for enabling powerful shiny web displays of Bioconductor objects
inveRsion	Inversions in genotype data
iontree	Data management and analysis of ion trees from ion-trap mass spectrometry
iPAC	Identification of Protein Amino acid Clustering
IPPD	Isotopic peak pattern deconvolution for Protein Mass Spectrometry by template matching
IRanges	Infrastructure for manipulating intervals on sequences
iSeq	Bayesian Hierarchical Modeling of ChIP-seq Data Through Hidden Ising Models
isobar	Analysis and quantitation of isobarically tagged MSMS proteomics data
IsoGeneGUI	A graphical user interface to conduct a dose-response analysis of microarray data
ITALICS	ITALICS
iterativeBMA	The Iterative Bayesian Model Averaging (BMA) algorithm
iterativeBMAsurv	The Iterative Bayesian Model Averaging (BMA) Algorithm For Survival Analysis
jmosaics	Joint analysis of multiple ChIP-Seq data sets
joda	JODA algorithm for quantifying gene deregulation using knowledge
KCsmart	Multi sample aCGH analysis package using kernel convolution
kebabs	Kernel-Based Analysis Of Biological Sequences
KEGGgraph	KEGGgraph: A graph approach to KEGG PATHWAY in R and Bioconductor

Package	What does it do?
keggorthology	Graph support for KO, KEGG Orthology
KEGGprofile	An annotation and visualization package for multi-types and multi-groups expression data in KEGG pathway
KEGGREST	Client-side REST access to KEGG
lapmix	Laplace Mixture Model in Microarray Experiments
LBE	Estimation of the false discovery rate
les	Identifying Differential Effects in Tiling Microarray Data
limma	Linear Models for Microarray Data
limmaGUI	GUI for limma package
LiquidAssociation	LiquidAssociation
lmdme	Linear Model decomposition for Designed Multivariate Experiments
LMGene	LMGene Software for Data Transformation and Identification of Differentially Expressed Genes in Gene Expression Arrays
logicFS	Identification of SNP Interactions
logitT	logit-t Package
lol	Lots Of Lasso
LPE	Methods for analyzing microarray data using Local Pooled Error (LPE) method
LPEadj	A correction of the local pooled error (LPE) method to replace the asymptotic variance adjustment with an unbiased adjustment based on sample size
lpNet	Linear Programming Model for Network Inference
lumi	BeadArray Specific Methods for Illumina Methylation and Expression Microarrays
LVSmiRNA	LVS normalization for Agilent miRNA data
M3D	Identifies differentially methylated regions across testing groups
maanova	Tools for analyzing Micro Array experiments
macat	MicroArray Chromosome Analysis Tool
maCorrPlot	Visualize artificial correlation in microarray data
made4	Multivariate analysis of microarray data using ADE4
maigesPack	Functions to handle cDNA microarray data, including several methods of data analysis
MAIT	Statistical Analysis of Metabolomic Data
makecdfenv	CDF Environment Maker
MANOR	CGH Micro-Array NORmalization
manta	Microbial Assemblage Normalized Transcript Analysis
MantelCorr	Compute Mantel Cluster Correlations
maPredictDSC	Phenotype prediction using microarray data: approach of the best overall team in the IMPROVER Diagnostic Signature Challenge
marray	Exploratory analysis for two-color spotted microarray data

Package	What does it do?
maSigPro	Significant Gene Expression Profile Differences in Time Course Microarray Data
maskBAD	Masking probes with binding affinity differences
MassArray	Analytical Tools for MassArray Data
massiR	MassiR: MicroArray Sample Sex Identifier
MassSpecWavelet	Mass spectrum processing by wavelet-based algorithms
matchBox	Utilities to compute, compare, and plot the agreement between ordered vectors of features (ie. distinct genomic experiments). The package includes Correspondence-At-the-TOP (CAT) analysis
MBAmethyl	Model-based analysis of DNA methylation data
MBASED	Package containing functions for ASE analysis using Meta-analysis Based Allele-Specific Expression Detection
MBCB	MBCB (Model-based Background Correction for Beadarray)
mBPCR	Bayesian Piecewise Constant Regression for DNA copy number estimation
mcaGUI	Microbial Community Analysis GUI
MCRestimate	Misclassification error estimation with cross-validation
mdqc	Mahalanobis Distance Quality Control for microarrays
MeasurementError.cor	Measurement Error model estimate for correlation coefficient
MEDIPS	(MeD)IP-seq data analysis
MEDME	Modelling Experimental Data from MeDIP Enrichment
MEIGOR	MEIGO - MEtaheuristics for bIoinformatics Global Optimization
MergeMaid	Merge Maid
MeSHDbi	DBI to construct MeSH-related package from sqlite file
meshr	Tools for conducting enrichment analysis of MeSH
messina	Single-gene classifiers and outlier-resistant detection of differential expression for two-group and survival problems
metaArray	Integration of Microarray Data for Meta-analysis
Metab	Metab: An R Package for a High-Throughput Analysis of Metabolomics Data Generated by GC-MS
metabomxtr	A package to run mixture models for truncated metabolomics data with normal or lognormal distributions
metagene	A package to produce metagene plots
metagenomeSeq	Statistical analysis for sparse high-throughput sequencing
metahdep	Hierarchical Dependence in Meta-Analysis
metaMS	MS-based metabolomics annotation pipeline
metaSeq	Meta-analysis of RNA-Seq count data in multiple studies
metaseqR	An R package for the analysis and result reporting of RNA-Seq data by

Package	What does it do?
	combining multiple statistical algorithms
methVisual	Methods for visualization and statistics on DNA methylation data
methyAnalysis	DNA methylation data analysis and visualization
MethylAid	Visual and interactive quality control of large Illumina 450k data sets
MethylMix	MethylMix: Identifying methylation driven cancer genes
methylMnM	Detect different methylation level (DMR)
methylPipe	Base resolution DNA methylation data analysis
MethylSeekR	Segmentation of Bis-seq data
methylumi	Handle Illumina methylation data
Mfuzz	Soft clustering of time series gene expression data
MGFM	Marker Gene Finder in Microarray gene expression data
mgsa	Model-based gene set analysis
MiChip	MiChip Parsing and Summarizing Functions
microRNA	Data and functions for dealing with microRNAs
MIMOSA	Mixture Models for Single-Cell Assays
MineICA	Analysis of an ICA decomposition obtained on genomics data
minet	Mutual Information NETworks
minfi	Analyze Illumina's 450k methylation arrays
MinimumDistance	A package for de novo CNV detection in case-parent trios
MiPP	Misclassification Penalized Posterior Classification
MiRaGE	MiRNA Ranking by Gene Expression
miRNApath	MiRNApath: Pathway Enrichment for miRNA Expression Data
miRNAtap	MiRNAtap: microRNA Targets - Aggregated Predictions
miRNAtap.db	Data for miRNAtap
Mirsynergy	Mirsynergy
missMethyl	Analysis of methylation array data
mitoODE	Implementation of the differential equation model described in
	"Dynamical modelling of phenotypes in a genome-wide RNAi live-cell imaging assay"
MLInterfaces	Uniform interfaces to R machine learning procedures for data in Bioconductor containers
MLP	MLP
MLSeq	Machine learning interface for RNA-Seq data
MMDiff	Statistical Testing for ChIP-Seq data sets
mmnet	A metagenomic pipeline for systems biology
MmPalateMiRNA	Murine Palate miRNA Expression Analysis
monocle	Analysis tools for single-cell expression experiments
MoPS	MoPS - Model-based Periodicity Screening

Package	What does it do?
mosaics	MOSAiCS (MOdel-based one and two Sample Analysis and Inference for ChIP-Seq)
MotifDb	An Annotated Collection of Protein-DNA Binding Sequence Motifs
motifRG	A package for discriminative motif discovery, designed for high throuput sequencing dataset
motifStack	Plot stacked logos for single or multiple DNA, RNA and amino acid sequence
MotIV	Motif Identification and Validation
MPFE	Estimation of the amplicon methylation pattern distribution from bisulphite sequencing data
mQTL.NMR	Metabolomic Quantitative Trait Locus Mapping for 1H NMR data
MSGFgui	A shiny GUI for MSGFplus
MSGFplus	An interface between R and MS-GF+
msmsEDA	Exploratory Data Analysis of LC-MS/MS data by spectral counts
msmsTests	LC-MS/MS Differential Expression Tests
MSnbase	MSnbase: Base Functions and Classes for MS-based Proteomics
MSnID	Utilities for Exploration and Assessment of Confidence of LC-MSn Proteomics Identifications
MSstats	Protein Significance Analysis in DDA, SRM and DIA for Label-free or Label-based Proteomics Experiments
Mulcom	Calculates Mulcom test
MultiMed	Testing multiple biological mediators simultaneously
multiscan	R package for combining multiple scans
multtest	Resampling-based multiple hypothesis testing
MVCClass	Model-View-Controller (MVC) Classes
mvGST	Multivariate and directional gene set testing
mygene	Access MyGene.Info services
mzID	An mzIdentML parser for R
mzR	Parser for netCDF, mzXML, mzData and mzML and mzIdentML files (mass spectrometry data)
NarrowPeaks	Shape-based Analysis of Variation in ChIP-Seq using Functional PCA
ncdfFlow	NcdfFlow: A package that provides ncdf based storage for flow cytometry data
NCIgraph	Pathways from the NCI Pathways Database
neaGUI	An R package to perform the network enrichment analysis (NEA)
nem	(Dynamic) Nested Effects Models and Deterministic Effects Propagation Networks to reconstruct phenotypic hierarchies
netbiov	A package for visualizing complex biological network
NetPathMiner	NetPathMiner for Biological Network Construction, Path Mining and Visualization

Package	What does it do?
netresponse	Netresponse: functional network analysis
NetSAM	Network Seriation And Modularization
networkBMA	Regression-based network inference using Bayesian Model Averaging
NGScopy	NGScopy: Detection of copy number variations in next generation sequencing
nnNorm	Spatial and intensity based normalization of cDNA microarray data based on robust neural nets
NOISeq	Exploratory analysis and differential expression for RNA-seq data
nondetects	Non-detects in qPCR data
NormqPCR	Functions for normalisation of RT-qPCR data
npGSEA	Permutation approximation methods for gene set enrichment analysis (non-permutation GSEA)
NTW	Predict gene network using an Ordinary Differential Equation (ODE) based method
nucleR	Nucleosome positioning package for R
nudge	Normal Uniform Differential Gene Expression detection
NuPoP	An R package for nucleosome positioning prediction
occugene	Functions for Multinomial Occupancy Distribution
OCplus	Operating characteristics plus sample size and local fdr for microarray experiments
oligo	Preprocessing tools for oligonucleotide arrays
oligoClasses	Classes for high-throughput arrays supported by oligo and crlmm
OLIN	Optimized local intensity-dependent normalisation of two-color microarrays
OLINgui	Graphical user interface for OLIN
omicade4	Multiple co-inertia analysis of omics datasets
OmicCircos	High-quality circular visualization of omic data
OncoSimulR	Simulation of cancer progresion with order restrictions
oneChannelGUI	A graphical interface designed to facilitate analysis of microarrays and miRNA/RNA-seq data on laptops
ontoCAT	Ontology traversal and search
openCyto	Hierarchical Gating Pipeline for flow cytometry data
oposSOM	Comprehensive analysis of transciptome data
OrderedList	Similarities of Ordered Gene Lists
OrganismDbi	Software to enable the smooth interfacing of different database packages
OSAT	OSAT: Optimal Sample Assignment Tool
OTUbase	Provides structure and functions for the analysis of OTU data
OutlierD	Outlier detection using quantile regression on the M-A scatterplots of high-throughput data
PAA	PAA (Protein Array Analyzer)
PADOG	Pathway Analysis with Down-weighting of Overlapping Genes (PADOG)

Package	What does it do?
paircompviz	Multiple comparison test visualization
PAnnBuilder	Protein annotation data package builder
panp	Presence-Absence Calls from Negative Strand Matching Probesets
PANR	Posterior association networks and functional modules inferred from rich phenotypes of gene perturbations
PAPi	Predict metabolic pathway activity based on metabolomics data
parody	Parametric And Resistant Outlier DYtection
pathifier	Quantify deregulation of pathways in cancer
PathNet	An R package for pathway analysis using topological information
pathRender	Render molecular pathways
pathview	A tool set for pathway based data integration and visualization
paxtoolsr	PaxtoolsR: Access Pathways from Multiple Databases through BioPAX and Pathway Commons
Pbase	Manipulating and exploring protein and proteomics data
pcaGoPromoter	PcaGoPromoter is used to analyze DNA micro array data
pcaMethods	A collection of PCA methods
pcot2	Principal Coordinates and Hotelling's T-Square method
PCpheno	Phenotypes and cellular organizational units
pdInfoBuilder	Platform Design Information Package Builder
pdmclass	Classification of Microarray Samples using Penalized Discriminant Methods
PECA	Probe-level Expression Change Averaging
pepStat	Statistical analysis of peptide microarrays
pepXMLTab	Parsing pepXML files and filter based on peptide FDR
PGSEA	Parametric Gene Set Enrichment Analysis
phenoDist	Phenotypic distance measures
phenoTest	Tools to test association between gene expression and phenotype in a way that is efficient, structured, fast and scalable. We also provide tools to do GSEA (Gene set enrichment analysis) and copy number variation
PhenStat	Statistical analysis of phenotypic data
phyloseq	Handling and analysis of high-throughput microbiome census data
piano	Platform for integrative analysis of omics data
pickgene	Adaptive Gene Picking for Microarray Expression Data Analysis
PICS	Probabilistic inference of ChIP-seq
PING	Probabilistic inference for Nucleosome Positioning with MNase-based or Sonicated Short-read Data
pint	Pairwise INTegration of functional genomics data

Package	What does it do?
pkgDepTools	Package Dependency Tools
plateCore	Statistical tools and data structures for plate-based flow cytometry
plethy	R framework for exploration and analysis of respirometry data
plgem	Detect differential expression in microarray and proteomics datasets with the Power Law Global Error Model (PLGEM)
plier	Implements the Affymetrix PLIER algorithm
PLPE	Local Pooled Error Test for Differential Expression with Paired High-throughput Data
plrs	Piecewise Linear Regression Splines (PLRS) for the association between DNA copy number and gene expression
plw	Probe level Locally moderated Weighted t-tests
polyester	Simulate RNA-seq reads
Polyfit	Add-on to DESeq to improve p-values and q-values
ppiStats	Protein-Protein Interaction Statistical Package
prada	Data analysis for cell-based functional assays
prebs	Probe region expression estimation for RNA-seq data for improved microarray comparability
PREDA	Position RElated Data Anlysis
predictionet	Inference for predictive networks designed for (but not limited to) genomic data
preprocessCore	A collection of pre-processing functions
proBAMr	Generating SAM file for PSMs in shotgun proteomics data
PROcess	Ciphergen SELDI-TOF Processing
procoil	Prediction of Oligomerization of Coiled Coil Proteins
ProCoNA	Protein co-expression network analysis (ProCoNA)
pRoloc	A unifying bioinformatics framework for spatial proteomics
pRolocGUI	Interactive visualisation of spatial proteomics data
PROMISE	PRojection Onto the Most Interesting Statistical Evidence
prot2D	Statistical Tools for volume data from 2D Gel Electrophoresis
proteinProfiles	Protein Profiling
proteoQC	An R package for proteomics data quality control
PSEA	Population-Specific Expression Analysis
PSICQUIC	Protemics Standard Initiative Common QUery InterfaCe
puma	Propagating Uncertainty in Microarray Analysis(including Affymetrix tranditional 3' arrays and exon arrays and Human Transcriptome Array 2.0)
pvac	PCA-based gene filtering for Affymetrix arrays
pvca	Principal Variance Component Analysis (PVCA)
Pviz	Peptide Annotation and Data Visualization using Gviz
PWMEnrich	PWM enrichment analysis

Package	What does it do?
qcmetrics	A Framework for Quality Control
QDNAseq	Quantitative DNA sequencing for chromosomal aberrations
qpcrNorm	Data-driven normalization strategies for high-throughput qPCR data
qpgraph	Estimation of genetic and molecular regulatory networks from high-throughput genomics data
qrqc	Quick Read Quality Control
QUALIFIER	Quality Control of Gated Flow Cytometry Experiments
quantro	A test for when to use quantile normalization
quantsmooth	Quantile smoothing and genomic visualization of array data
QuasR	Quantify and Annotate Short Reads in R
qusage	Qusage: Quantitative Set Analysis for Gene Expression
qvalue	Q-value estimation for false discovery rate control
r3Cseq	Analysis of Chromosome Conformation Capture and Next-generation Sequencing (3C-seq)
R453Plus1Toolbox	A package for importing and analyzing data from Roche's Genome Sequencer System
rain	Rhythmicity Analysis Incorporating Non-parametric Methods
rama	Robust Analysis of MicroArrays
RamiGO	AmiGO visualize R interface
randPack	Randomization routines for Clinical Trials
RankProd	Rank Product method for identifying differentially expressed genes with application in meta-analysis
Rariant	Identification and Assessment of Single Nucleotide Variants through Shifts in Non-Consensus Base Call Frequencies
RbcBook1	Support for Springer monograph on Bioconductor
RBGL	An interface to the BOOST graph library
RBioinf	RBioinf
rBiopaxParser	Parses BioPax files and represents them in R
Rbowtie	R bowtie wrapper
rbsurv	Robust likelihood-based survival modeling with microarray data
Rcade	R-based analysis of ChIP-seq And Differential Expression - a tool for integrating a count-based ChIP-seq analysis with differential expression summary data
RCASPAR	A package for survival time prediction based on a piecewise baseline hazard Cox regression model
Rchemcpp	Similarity measures for chemical compounds
RchyOptimyx	Optimyzed Cellular Hierarchies for Flow Cytometry
Rcpi	Toolkit for Compound-Protein Interaction in Drug Discovery
RCytoscape	Display and manipulate graphs in Cytoscape

Package	What does it do?
RDAVIDWebService	An R Package for retrieving data from DAVID into R objects using Web Services API
Rdisop	Decomposition of Isotopic Patterns
RDRToolbox	A package for nonlinear dimension reduction with Isomap and LLE
ReactomePA	Reactome Pathway Analysis
ReadqPCR	Read qPCR data
reb	Regional Expression Biases
RedeR	Interactive visualization and manipulation of nested networks
REDseq	Analysis of high-throughput sequencing data processed by restriction enzyme digestion
RefNet	A queryable collection of molecular interactions, from many sources
RefPlus	A function set for the Extrapolation Strategy (RMA+) and Extrapolation Averaging (RMA++) methods
regionReport	Generate HTML reports for exploring a set of regions
Repitools	Epigenomic tools
ReportingTools	Tools for making reports in various formats
ReQON	Recalibrating Quality Of Nucleotides
rfPred	Assign rfPred functional prediction scores to a missense variants list
rGADEM	De novo motif discovery
RGalaxy	Make an R function available in the Galaxy web platform
Rgraphviz	Provides plotting capabilities for R graph objects
RGSEA	Random Gene Set Enrichment Analysis
rhdf5	HDF5 interface to R
rHVDM	Hidden Variable Dynamic Modeling
riboSeqR	Analysis of sequencing data from ribosome profiling experiments
Ringo	R Investigation of ChIP-chip Oligoarrays
RIPSeeker	RIPSeeker: a statistical package for identifying protein-associated transcripts from RIP-seq experiments
Risa	Converting experimental metadata from ISA-tab into Bioconductor data structures
RLMM	A Genotype Calling Algorithm for Affymetrix SNP Arrays
Rmagpie	MicroArray Gene-expression-based Program In Error rate estimation
RMassBank	Workflow to process tandem MS files and build MassBank records
rMAT	R implementation from MAT program to normalize and analyze tiling arrays and ChIP-chip data
RmiR	Package to work with miRNAs and miRNA targets with R
RmiR.Hs.miRNA	Various databases of microRNA Targets
RmiR.hsa	Various databases of microRNA Targets
RNAinteract	Estimate Pairwise Interactions from multidimensional features

Package	What does it do?
RNAither	Statistical analysis of high-throughput RNAi screens
rnaSeqMap	RnaSeq secondary analyses
RNASeqPower	Sample size for RNAseq studies
Rnits	R Normalization and Inference of Time Series data
roar	Identify differential APA usage from RNA-seq alignments
ROC	Utilities for ROC, with uarray focus
Roleswitch	Infer miRNA-mRNA interactions using paired expression data from a single sample
Rolexa	Statistical analysis of Solexa sequencing data
rols	An R interface to the Ontology Lookup Service
ROntoTools	R Onto-Tools suite
RPA	RPA: Robust Probabilistic Averaging for probe-level analysis
RpsiXML	R interface to PSI-MI 2.5 files
rpx	R Interface to the ProteomeXchange Repository
Rqc	Quality Control Tool for High-Throughput Sequencing Data
rqubic	Qualitative biclustering algorithm for expression data analysis in R
rRDP	Interface to the RDP Classifier
RRHO	Inference on agreement between ordered lists
Rsamtools	Binary alignment (BAM), FASTA, variant call (BCF), and tabix file import
rsbml	R support for SBML, using libsbml
rSFFreader	RSFFreader reads in sff files generated by Roche 454 and
	Life Sciences Ion Torrent sequencers
Rsubread	Rsubread package: high-performance read alignment, quantification
	and mutation discovery
RSVSim	RSVSim: an R/Bioconductor package for the simulation of structural variations
rTANDEM	Interfaces the tandem protein identification algorithm in R
RTCA	Open-source toolkit to analyse data from xCELLigence System (RTCA)
RTN	Reconstruction of transcriptional networks and analysis of master regulators
RTopper	This package is designed to perform Gene Set Analysis across multiple genomic platforms
rtracklayer	R interface to genome browsers and their annotation tracks
Rtreemix	Rtreemix: Mutagenetic trees mixture models
rTRM	Identification of transcriptional regulatory modules from PPI networks
rTRMui	A shiny user interface for rTRM
RUVnormalize	RUV for normalization of expression array data
RUVSeq	Remove Unwanted Variation from RNA-Seq Data
RWebServices	Expose R functions as web services through Java/Axis/Apache
S4Vectors	S4 implementation of vectors and lists

Package	What does it do?
safe	Significance Analysis of Function and Expression
sagenhaft	Collection of functions for reading and comparing SAGE libraries
SAGx	Statistical Analysis of the GeneChip
SamSPECTRAL	Identifies cell population in flow cytometry data
sangerseqR	Tools for Sanger Sequencing Data in R
SANTA	Spatial Analysis of Network Associations
sapFinder	A package for variant peptides detection and visualization in shotgun proteomics
savR	Parse and analyze Illumina SAV files
SBMLR	SBML-R Interface and Analysis Tools
SCAN.UPC	Single-channel array normalization (SCAN) and Universal exPression Codes (UPC)
ScISI	In Silico Interactome
scsR	SiRNA correction for seed mediated off-target effect
segmentSeq	Methods for identifying small RNA loci from high-throughput sequencing data
SemDist	Information Accretion-based Function Predictor Evaluation
SeqArray	Big Data Management of Genome-wide Sequencing Variants
seqbias	Estimation of per-position bias in high-throughput sequencing data
seqCNA	Copy number analysis of high-throughput sequencing cancer data
SeqGSEA	Gene Set Enrichment Analysis (GSEA) of RNA-Seq Data: integrating differential expression and splicing
seqLogo	Sequence logos for DNA sequence alignments
seqplots	An interactive tool for visualizing NGS signals and sequence motif densities along genomic features using average plots and heatmaps
seqTools	Analysis of nucleotide, sequence and quality content on fastq files
SeqVarTools	Tools for variant data
SGSeq	Prediction, quantification and visualization of alternative transcript events from RNA-seq data
shinyMethyl	Interactive visualization for Illumina's 450k methylation arrays
shinyTANDEM	Provides a GUI for rTANDEM
ShortRead	FASTQ input and manipulation
sigaR	Statistics for integrative genomics analyses in R
SigCheck	Check a gene signature's classification performance against random signatures, permuted data, and known signatures
SigFuge	SigFuge
siggenes	Multiple testing using SAM and Efron's empirical Bayes approaches
sigPathway	Pathway Analysis
SIM	Integrated Analysis on two human genomic datasets

Package	What does it do?
SimBindProfiles	Similar Binding Profiles
simpleaffy	Very simple high level analysis of Affymetrix data
simulatorZ	Simulator for Collections of Independent Genomic Data Sets
sizepower	Sample Size and Power Calculation in Micorarray Studies
SJava	The Omegahat interface for R and Java
SLGI	Synthetic Lethal Genetic Interaction
SLqPCR	Functions for analysis of real-time quantitative PCR data at SIRS-Lab GmbH
SMAP	A Segmental Maximum A Posteriori Approach to Array-CGH Copy Number Profiling
SNAGEE	Signal-to-Noise applied to Gene Expression Experiments
snapCGH	Segmentation, normalisation and processing of aCGH data
snm	Supervised Normalization of Microarrays
SNPchip	Visualizations for copy number alterations
SNPRelate	Parallel computing toolset for relatedness and principal component analysis of SNP data
snpStats	SnpMatrix and XSnpMatrix classes and methods
SomatiCA	SomatiCA: identifying, characterizing, and quantifying somatic copy number aberrations from cancer genome sequencing
SomaticSignatures	Somatic Signatures
SpacePAC	Identification of Mutational Clusters in 3D Protein Space via Simulation
spade	SPADE – An analysis and visualization tool for Flow Cytometry
specL	SpecL - Prepare Peptide Spectrum Matches for Use in Targeted Proteomics
SpeCond	Condition specific detection from expression data
SPEM	S-system parameter estimation method
SPIA	Signaling Pathway Impact Analysis (SPIA) using combined evidence of pathway over-representation and unusual signaling perturbations
spikeLI	Affymetrix Spike-in Langmuir Isotherm Data Analysis Tool
spkTools	Methods for Spike-in Arrays
splicegear	Splicegear
spliceR	Classification of alternative splicing and prediction of coding potential from RNA-seq data.
spliceSites	Manages align gap positions from RNA-seq data
SplicingGraphs	Create, manipulate, visualize splicing graphs, and assign RNA-seq reads to them
splots	Visualization of high-throughput assays in microtitre plate or slide format
spotSegmentation	Microarray Spot Segmentation and Gridding for Blocks of Microarray Spots
SQUADD	Add-on of the SQUAD Software
SRAdb	A compilation of metadata from NCBI SRA and tools
sRAP	Simplified RNA-Seq Analysis Pipeline
sscore	S-Score Algorithm for Affymetrix Oligonucleotide Microarrays

Package	What does it do?
sSeq	Shrinkage estimation of dispersion in Negative Binomial models for RNA-seq experiments with small sample size
ssize	Estimate Microarray Sample Size
SSPA	General Sample Size and Power Analysis for Microarray and Next-Generation Sequencing Data
ssviz	A small RNA-seq visualizer and analysis toolkit
STAN	STrand-specific ANnotation of genomic data
staRank	Stability Ranking
Starr	Simple tiling array analysis of Affymetrix ChIP-chip data
STATegRa	Classes and methods for multi-omics data integration
stepNorm	Stepwise normalization functions for cDNA microarrays
stepwiseCM	Stepwise Classification of Cancer Samples using High-dimensional Data Sets
Streamer	Enabling stream processing of large files
STRINGdb	STRINGdb (Search Tool for the Retrieval of Interacting proteins database)
supraHex	A supra-hexagonal map for analysing tabular omics data
survcomp	Performance Assessment and Comparison for Survival Analysis
Sushi	Tools for visualizing genomics data
sva	Surrogate Variable Analysis
SwimR	SwimR: A Suite of Analytical Tools for Quantification of C. elegans Swimming Behavior
switchBox	Utilities to train and validate classifiers based on pair switching using the K-Top-Scoring-Pair (KTSP) algorithm
synapter	Label-free data analysis pipeline for optimal identification and quantitation
systemPipeR	SystemPipeR: NGS workflow and report generation environment
TargetScore	TargetScore: Infer microRNA targets using microRNA-overexpression data and sequence information
TargetSearch	A package for the analysis of GC-MS metabolite profiling data
TCC	TCC: Differential expression analysis for tag count data with robust normalization strategies
TDARACNE	Network reverse engineering from time course data
TEQC	Quality control for target capture experiments
ternarynet	Ternary Network Estimation
TFBSTools	Software package for transcription factor binding site (TFBS) analysis
tigre	Transcription factor Inference through Gaussian process Reconstruction of Expression
tilingArray	Transcript mapping with high-density oligonucleotide tiling arrays
timecourse	Statistical Analysis for Developmental Microarray Time Course Data
TitanCNA	Subclonal copy number and LOH prediction from whole genome sequencing of tumours
tkWidgets	R based tk widgets

Package	What does it do?
ToPASeq	Package for Topology-based Pathway Analysis of RNASeq data
topGO	TopGO: Enrichment analysis for Gene Ontology
tracktables	Build IGV tracks and HTML reports
trackViewer	A bioconductor package with minimalist design for plotting elegant track layers
tRanslatome	Comparison between multiple levels of gene expression.
TransView	Read density map construction and accession. Visualization of ChIPSeq and RNASeq data sets.
triform	Triform finds enriched regions (peaks) in transcription factor ChIP-sequencing data
trigger	Transcriptional Regulatory Inference from Genetics of Gene ExpRession
trio	Testing of SNPs and SNP Interactions in Case-Parent Trio Studies
triplex	Search and visualize intramolecular triplex-forming sequences in DNA
TSCAN	TSCAN: Tools for Single-Cell ANalysis
tspair	Top Scoring Pairs for Microarray Classification
TSSi	Transcription Start Site Identification
TurboNorm	A fast scatterplot smoother suitable for microarray normalization
tweeDEseq	RNA-seq data analysis using the Poisson-Tweedie family of distributions
twilight	Estimation of local false discovery rate
TypeInfo	Optional Type Specification Prototype
UNDO	Unsupervised Deconvolution of Tumor-Stromal Mixed Expressions
unifiedWMWqPCR	Unified Wilcoxon-Mann Whitney Test for testing differential expression in qPCR data
UniProt.ws	R Interface to UniProt Web Services
VanillaICE	A Hidden Markov Model for high throughput genotyping arrays
VariantAnnotation	Annotation of Genetic Variants
VariantFiltering	Filtering of coding and non-coding genetic variants
VariantTools	Tools for Working with Genetic Variants
vbmp	Variational Bayesian Multinomial Probit Regression
Vega	An R package for copy number data segmentation
VegaMC	VegaMC: A Package Implementing a Variational Piecewise Smooth Model for Identification of Driver Chromosomal Imbalances in Cancer
viper	Virtual Inference of Protein-activity by Enriched Regulon analysis
vsn	Variance stabilization and calibration for microarray data
vtpnet	Variant-transcription factor-phenotype networks
wateRmelon	Illumina 450 methylation array normalization and metrics
wavClusteR	WavClusteR
waveTiling	Wavelet-Based Models for Tiling Array Transcriptome Analysis
weaver	Tools and extensions for processing Sweave documents

Package	What does it do?
webbioc	Bioconductor Web Interface
widgetTools	Creates an interactive tcltk widget
xcms	LC/MS and GC/MS Data Analysis
XDE	XDE: a Bayesian hierarchical model for cross-study analysis of differential gene expression
xmapbridge	Export plotting files to the xmapBridge for visualisation in X:Map
xps	Processing and Analysis of Affymetrix Oligonucleotide Arrays including Exon Arrays, Whole Genome Arrays and Plate Arrays
XVector	Representation and manpulation of external sequences
yaqcaffy	Affymetrix expression data quality control and reproducibility analysis
zlibbioc	An R packaged zlib-1.2.5