

# Suggested changes to *biocViews*

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## 1 Introduction

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A list of *biocViews* terms can be found at :

[http://bioconductor.org/packages/release/BiocViews.html#\\_\\_\\_Software](http://bioconductor.org/packages/release/BiocViews.html#___Software)

The tree structure on the left are all the *biocViews* terms. We always direct users who are looking for packages to use, to this page and ask them to navigate through the tree to find packages that best fit their task. By adding *biocViews* terms to your package - your package will show up automatically on this page and in this list in the next release of Bioconductor.

## 2 Aim

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We have been working to revise the *biocViews* with the aim of :

- Allowing all packages to be searched for, more effectively
- Allowing the package contributors to define their package more accurately with the help of *biocViews*.

Please note -

- We are suggesting changes only to the software branch
- Henceforth - Package contributors can add *biocViews* from only one category per package. For example- software packages will not be allowed to have *biocViews* from *ExperimentData* and *AnnotationData* and vice-versa.
- **You do NOT need to make changes to your existing packages in the bioconductor Repository** - we will be doing that - This document is sent out only to get your suggestions/feedback and notify you of our on-going work

### 3 Suggested Changes

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To see the suggested biocView tree structure, please look at:

```
system.file("inst", "dot", "biocViewsVocab.dot", package = "biocViews")
```

#### 3.1 Renamed or Discontinued biocViews

The following biocViews terms will be renamed or discontinued:

```
##                suggested biocViews
## AssayDomains          <NA>
## AssayTechnologies     Technology
## Bioinformatics         <NA>
## BiologicalDomains     <NA>
## ConnectTools          ThirdPartyClient
## Enrichment            <NA>
## GraphsAndNetworks     GraphAndNetwork
## HighThroughputSequencing Sequencing
## MethyIseq             MethylSeq
## MultipleComparisons   MultipleComparison
## NetworkAnalysis       <NA>
## Networks              Network
## NetworkVisualization  <NA>
## Regulation            <NA>
## RNAseq                RNASeq
## Sequences             <NA>
## Signaling             <NA>
```

#### 3.2 Discontinued User-defined biocViews

We also found that a couple of package contributors had defined their own biocViews in order to best represent their package.

Please note that hence forth the Package contributors will not be allowed to add biocViews terms which do not exist in biocViews Vocabulary.

A number of packages had user defined biocViews which will be corrected as shown below to reflect the new changes:

```
##                corrected biocViews
## AffymetrixChip     OneChannel
## Affymetrix         OneChannel
## BatchEffectAssessment BatchEffect
## ChiPseq            ChIPSeq
## ChIPseq            ChIPSeq
## ClusterValidation  Clustering
## CopyNumberVariants CopyNumberVariation
## CNV                CopyNumberVariation
## DataPreprocessing  Preprocessing
## Design             ExperimentalDesign
## DNAmethylation     DifferentialMethylation
## DualChannel        TwoChannel
```

```

## Flowcytometry                FlowCytometry
## FlowCytData                  FlowCytometry
## Flow cytometry                FlowCytometry
## High Throughput Sequencing    Sequencing
## HighThroughputSequencingData Sequencing
## HighThroughputSequencingData Sequencing
## Microarrays                   Microarray
## MicroArray                   Microarray
## microRNA                       miRNA
## MRNAMicroarray                mRNAMicroarray
## Multiple Comparisons          MultipleComparison
## RIPseq                        RIPSeq
## RNAExpressionData             DifferentialExpression
## SequenceAnnotation            GenomeAnnotation
## SequencingMatching            SequenceMatching
## SNP.                          SNP
## Statistics                    StatisticalMethod
## Technology                    <NA>
## Visualisation                 Visualization
## visualization                 Visualization

```

The following is a list of packages and their biocviews which will be discontinued.

```

##          Package      discontinued biocViews
## 976      clippda       SampleSize
## 978      AgiMicroRna   AgilentChip
## 1062     iChip         NimbleGen
## 1064     iChip         Agilent
## 1071     rGADEM        GenomicSequence
## 1095     SamSPECTRAL   Cancer
## 1097     SamSPECTRAL   StemCells
## 1098     SamSPECTRAL   HIV
## 1112     MotIV         GenomicSequence
## 1145     flowMeans     Cancer
## 1147     flowMeans     StemCells
## 1148     flowMeans     HIV
## 1206     RDRTtoolbox   Dimension
## 1252     LVSmiRNA      AgilentChip
## 1371     chopsticks    SNPsAndGeneticVariability
## 1415     AnnotationFuncs AnnotationData
## 1559     VariantAnnotation Homo_sapiens
## 1618     CNAnorm       Cancer
## 1619     CNAnorm       Lung
## 1623     cummeRbund    RNAseqData
## 1657     stepwiseCM    Integration
## 1707     cn.mops       Homo_sapiens
## 1710     cn.mops       HapMap
## 1790     gwascat       genetics
## 1884     cancerclass   Cancer
## 1896     MiRaGE        RNAseqData
## 1914     flowPeaks     Gating
## 1928     PWMEnrich     GenomicSequence
## 1975     MotifDb       GenomicSequence
## 2001     lmdme         ExperimentData
## 2002     lmdme         Cancer

```

```

## 2013      hapFabia      Homo_sapiens
## 2017      hpar          Homo_sapiens
## 2028      motifStack   GenomicsSequence
## 2031      DeconRNASeq   ExperimentData
## 2221      dexus        Mus_musculus
## 2222      dexus        Homo_sapiens
## 2223      dexus        Zea_Mays
## 2224      dexus        Macaca_mulatta
## 2225      dexus        Pan_troglodytes
## 2231      dexus        HapMap
## 2233      dexus        RNAseqData
## 2308      geNetClassifier Leukemia
## 2309      geNetClassifier Cancer
## 2359      plethy       biocViews
## 2360      plethy       Infastructure
## 2388      spliceR      RNAseqData
## 2389      spliceR      software
## 2394      mitoODE      ExperimentData
## 2406      RDAVIDWebService ExperimentData
## 2407      RDAVIDWebService Cancer
## 2462      rfPred       Homo-sapiens
## 2545      AllelicImbalance Allelic Imbalance
## 2546      AllelicImbalance AI
## 2547      AllelicImbalance ASE
## 2569      dagLogo      GenomicsSequence
## 2628      ChAMP        IlluminaChip
## 2647      interactiveDisplay AnnotationData
## 2718      iClusterPlus Genomic data
## 2738      trackViewer   GenomicsSequence

```

### 3.3 New additions to *biocViews* Vocab

The following new *biocViews* will be available:

```

##                               Count
## Software -> AssayDomain        0
## Sequencing -> DNaseq           0
## Sequencing -> ExomeSeq         0
## Sequencing -> SmallRNA         0
## Sequencing -> Microbiome       0
## Sequencing -> WholeGenome      0
## Sequencing -> DenovoGenome     0
## Sequencing -> TargetedResequencing 0
## Sequencing -> DenovoTranscriptome 0
## Sequencing -> MicrobialStrain  0
## Microarray -> MethylationArray  0
## Microarray -> GenotypingArray  0
## Microarray -> MicroRNAArray    0
## Microarray -> ChipOnChip       0
## Microarray -> ReversePhaseProteinArray 0
## Software -> ResearchField      0
## ResearchField -> Pharmacogenomics 0
## ResearchField -> Pharmacogenetics 0

```

```
## ResearchField -> Cheminformatics 0
## ResearchField -> StructuralGenomics 0
## ResearchField -> Biophysics 0
## ResearchField -> MathematicalBiology 0
## ResearchField -> BiomedicalInformatics 0
## ResearchField -> ComparativeGenomics 0
## ResearchField -> FunctionalGenomics 0
## ResearchField -> SystemsBiology 0
## ResearchField -> ComputationalChemistry 0
## ResearchField -> Agroinformatics 0
## Software -> BiologicalQuestion 0
## BiologicalQuestion -> AlternativeSplicing 0
## BiologicalQuestion -> Coverage 0
## BiologicalQuestion -> DemethylateRegionDetection 0
## BiologicalQuestion -> DenovoAssembler 0
## BiologicalQuestion -> DifferentialPeakCalling 0
## BiologicalQuestion -> DifferentialSplicing 0
## BiologicalQuestion -> DriverMutation 0
## BiologicalQuestion -> FunctionalPrediction 0
## BiologicalQuestion -> GeneFusionDetection 0
## BiologicalQuestion -> GenePrediction 0
## BiologicalQuestion -> GeneSignaling 0
## BiologicalQuestion -> GeneTarget 0
## BiologicalQuestion -> GenomeAssembly 0
## BiologicalQuestion -> GenomeWideAssocaition 0
## BiologicalQuestion -> GenomicVariation 0
## BiologicalQuestion -> GermlineMutation 0
## BiologicalQuestion -> HistoneModification 0
## BiologicalQuestion -> IndelDetection 0
## BiologicalQuestion -> LinkageDisequilibrium 0
## BiologicalQuestion -> MetagenomeAssembly 0
## BiologicalQuestion -> MicrosatelliteDetection 0
## BiologicalQuestion -> NucleosomePositioning 0
## BiologicalQuestion -> PeakDetection 0
## BiologicalQuestion -> QuantitativeTrailLocus 0
## BiologicalQuestion -> Scaffolding 0
## BiologicalQuestion -> SomaticMutation 0
## BiologicalQuestion -> SplicedAlignment 0
## BiologicalQuestion -> StructuralVariation 0
## BiologicalQuestion -> TranscriptomeVariant 0
## BiologicalQuestion -> VariantDetection 0
## Software -> WorkflowStep 0
## WorkflowStep -> Alignment 0
## WorkflowStep -> Normalization 0
## WorkflowStep -> GenomeBrowsers 0
## StatisticalMethod -> Bayesian 0
## StatisticalMethod -> DecisionTree 0
## StatisticalMethod -> HiddenMarkovModel 0
## StatisticalMethod -> MultidimensionalScaling 0
## StatisticalMethod -> PatternLogic 0
## StatisticalMethod -> PrinicipalComponent 0
## StatisticalMethod -> Regression 0
## StatisticalMethod -> SupportVectorMachine 0
## StatisticalMethod -> Survival 0
```

### 3.4 count of existing biocViews

Here is a count of the number of packages that use the existing biocViews terms:

##	Count
## BiocViews -> Software	46
## AssayDomain -> aCGH	12
## AssayDomain -> CellBasedAssays	34
## AssayDomain -> ChIPchip	7
## AssayDomain -> CopyNumberVariation	40
## AssayDomain -> CpGIsland	5
## AssayDomain -> DNAMethylation	25
## AssayDomain -> ExonArray	4
## AssayDomain -> GeneExpression	82
## AssayDomain -> GeneticVariability	17
## AssayDomain -> SNP	33
## AssayDomain -> Transcription	36
## Software -> Technology	2
## Technology -> Sequencing	154
## Sequencing -> RNASeq	47
## Sequencing -> ChIPSeq	32
## Sequencing -> RIPSeq	1
## Sequencing -> MethylSeq	8
## Sequencing -> miRNA	3
## Technology -> Microarray	284
## Microarray -> MultiChannel	3
## Microarray -> OneChannel	67
## Microarray -> TwoChannel	49
## Microarray -> mRNAArray	284
## Microarray -> TissueMicroarray	284
## Microarray -> ProprietaryPlatforms	1
## Technology -> FlowCytometry	32
## Technology -> MassSpectrometry	27
## Technology -> qPCR	6
## Technology -> MicrotitrePlateAssay	12
## Technology -> SAGE	9
## ResearchField -> CellBiology	16
## ResearchField -> Genetics	71
## ResearchField -> Metabolomics	7
## ResearchField -> Metagenomics	2
## ResearchField -> Proteomics	48
## ResearchField -> Epigenetics	4
## BiologicalQuestion -> DifferentialExpression	131
## BiologicalQuestion -> DifferentialMethylation	2
## BiologicalQuestion -> FunctionalAnnotation	59
## BiologicalQuestion -> GeneRegulation	12
## BiologicalQuestion -> GeneSetEnrichment	16
## BiologicalQuestion -> GenomeAnnotation	60
## BiologicalQuestion -> MotifAnnotation	61
## BiologicalQuestion -> MotifDiscovery	4
## BiologicalQuestion -> NetworkEnrichment	6
## BiologicalQuestion -> NetworkInference	13
## BiologicalQuestion -> SequenceMatching	17
## BiologicalQuestion -> VariantAnnotation	58

```
## WorkflowStep -> ExperimentalDesign      1
## WorkflowStep -> Annotation              58
## WorkflowStep -> BatchEffect             1
## WorkflowStep -> MultipleComparison      58
## WorkflowStep -> Pathways                37
## Pathways -> GO                          25
## WorkflowStep -> Preprocessing           116
## WorkflowStep -> QualityControl          74
## WorkflowStep -> ReportWriting           16
## WorkflowStep -> Visualization          129
## Visualization -> Network                3
## Software -> StatisticalMethod           15
## StatisticalMethod -> Classification     47
## StatisticalMethod -> Clustering         70
## StatisticalMethod -> DimensionReduction  1
## StatisticalMethod -> FeatureExtraction  1
## StatisticalMethod -> GraphAndNetwork    62
## StatisticalMethod -> NeuralNetwork      3
## StatisticalMethod -> TimeCourse         22
## Software -> Infrastructure              89
## Infrastructure -> ThirdPartyClient      8
## Infrastructure -> DataImport            69
## Infrastructure -> DataRepresentation    22
## Infrastructure -> GUI                   13
```

### 3.5 Session Info

Here is the output of sessionInfo on the system on which this document was compiled:

```
sessionInfo()

## R Under development (unstable) (2014-02-06 r64933)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
##
## locale:
## [1] LC_COLLATE=English_United States.1252 LC_CTYPE=English_United States.1252
## [3] LC_MONETARY=English_United States.1252 LC_NUMERIC=C
## [5] LC_TIME=English_United States.1252
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] knitr_1.5
##
## loaded via a namespace (and not attached):
## [1] BiocStyle_1.1.16 evaluate_0.5.1  formatR_0.10   highr_0.3      stringr_0.6.2
## [6] tools_3.1.0
```