

Package	Repository	Number of strong dependency packages	Number of all dependency packages	Number of parent packages	Max heaviness from parent packages	Max co- heaviness from parent packages	Heaviness on child packages	Number of child packages	Heaviness on downstream packages	Number of downstream packages
Rcmdr	CRAN	135	157	14	38	32	101.2	45	100.8	46
Seurat	CRAN	145	266	50	reducible 8	11	85.3	38	86.1	40
lumi	Bioconductor	162	170	19	53	47	114.2	13	83.8	18
RTCGA	Bioconductor	127	180	15	60	5	128.0	9	128.0	9
minfi	Bioconductor	141	165	34	24	16	62.4	38	68.7	60
tidyverse	CRAN	107	120	29	reducible 17	5	48.4	89	48.0	94
survminer	CRAN	115	139	18	40	4	58.2	27	58.6	36
taxize	CRAN	127	145	24	55	8	77.4	12	76.7	13
devtools	CRAN	76	119	23	12	5	47.0	80	45.3	95
GenomicScores	Bioconductor	98	154	17	26	40	56.0	26	56.3	27
WGCNA	CRAN	108	113	17	reducible 47	28	52.3	33	50.7	35
caret	CRAN	81	200	16	reducible 27	15	41.0	180	40.0	209
car	CRAN	87	125	14	26	39	40.6	183	36.5	618
brms	CRAN	123	187	24	reducible 37	12	65.1	13	65.1	13
AER	CRAN	92	170	7	reducible 78	4	52.6	22	54.3	22
ecospat	CRAN	232	255	24	reducible 117	49	151.0	3	151.0	3

Upstream package	Dependency path	Dependency depth	Heaviness on car
pbkrtest	pbkrtest → car 26	2	26
lme4	lme4 → car 20	2	20
nloptr	nloptr → lme4 → car 33      20	3	15
testthat	testthat → nloptr → lme4 → car 37      33      20	4	14
scales	scales → ggplot2 → broom → pbkrtest → car 8      20      15      26	5	7

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graph LR
    scales((scales)) -- 8 --> ggplot2((ggplot2))
    ggplot2 -- 20 --> broom((broom))
    broom -- 15 --> pbkrtest((pbkrtest))
    pbkrtest -- 26 --> car((car))
    testthat((testthat)) -- 37 --> nloptr((nloptr))
    nloptr -- 33 --> lme4((lme4))
    lme4 -- 20 --> car
  
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Depth	Number of Paths
Depth = 1	166 paths
Depth = 2	221 paths
Depth = 3	144 paths
Depth = 4	37 paths
Depth = 5	12 paths

Downstream package	Dependency path	Dependency depth	Heaviness of car on downstream package
DJL	car → DJL 88	2	88
DistatisR	car → DistatisR 88	2	88
GEWIST	car → GEWIST 88	2	88

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The diagram illustrates a network of bioinformatics tools. The central node is 'car' (orange). Red arrows highlight a path from 'car' to 'RTCGA' and '9 leaves'. Blue arrows show other connections, such as from 'car' to 'FactoMineR' and 'CytoGLMM'. Nodes are labeled with names like 'car', 'FactoMineR', 'CytoGLMM', 'RTCGA', and '9 leaves'.