

# Package: Polytect (via r-universe)

June 15, 2026

**Title** An R package for digital data clustering

**Version** 1.4.0

**Description** Polytect is an advanced computational tool designed for the analysis of multi-color digital PCR data. It provides automatic clustering and labeling of partitions into distinct groups based on clusters first identified by the flowPeaks algorithm. Polytect is particularly useful for researchers in molecular biology and bioinformatics, enabling them to gain deeper insights into their experimental results through precise partition classification and data visualization.

**biocViews** ddPCR, Clustering, MultiChannel, Classification

**License** Artistic-2.0

**URL** <https://github.com/emmachenlingo/Polytect>

**BugReports** <https://github.com/emmachenlingo/Polytect/issues>

**Encoding** UTF-8

**LazyData** false

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.2

**Depends** R (>= 4.4.0)

**Imports** stats, utils, grDevices, mvtnorm, sn, dplyr, flowPeaks, ggplot2, tidyverse, cowplot, mlrMBO, DiceKriging, smooof, ParamHelpers, lhs, rgenoud, BiocManager

**Suggests** testthat (>= 3.0.0), knitr, rmarkdown, ddPCRclust

**VignetteBuilder** knitr

**Config/testthat/edition** 3

**Config/pak/sysreqs** cmake libfontconfig1-dev libfreetype6-dev libfribidi-dev libgdal-dev gdal-bin libgeos-dev libglu1-mesa-dev libgmp3-dev make libgs10-dev libharfbuzz-dev jags libicu-dev libjpeg-dev libpng-dev libtiff-dev libuv1-dev libwebp-dev libxml2-dev libmpfr-dev libopenmpi-dev libssl-dev libproj-dev libx11-dev zlib1g-dev

**Repository** <https://bioc-release.r-universe.dev>

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BPV

*BPV data*

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### Description

A 3-color dPCR data of bovine papilloma virus assay

### Usage

`data(BPV)`

### Format

A data frame of fluorescence intensities in each channel. Each row represents each partitions, and each column each channel.

**channel1** fluorescence intensities of color 1

**channel2** fluorescence intensities of color 2

**channel3** fluorescence intensities of color 3

### Examples

`data(BPV)`

`head(BPV)`

---

|    |                |
|----|----------------|
| CA | <i>CA data</i> |
|----|----------------|

---

**Description**

2-color competitive assay of competition BRAF V600E assay with 1% mutant

**Usage**

```
data(CA)
```

**Format**

A data frame of fluorescence intensities in each channel. Each row represents each partitions, and each column each channel. data is not orthogonal.

**channel1** fluorescence intensities of color 1

**channel2** fluorescence intensities of color 2

**Examples**

```
data(CA)
head(CA)
```

---

|          |                        |
|----------|------------------------|
| CNV5plex | <i>CNV 5-plex data</i> |
|----------|------------------------|

---

**Description**

CNV 5-plex universal probes

**Usage**

```
data(CNV5plex)
```

**Format**

A data frame of fluorescence intensities in each channel. Each row represents each partitions, and each column each channel.

**channel1** fluorescence intensities of color 1

**channel2** fluorescence intensities of color 2

**channel3** fluorescence intensities of color 3

**channel4** fluorescence intensities of color 4

**channel5** fluorescence intensities of color 5

**Examples**

```
data(CNV5plex)
head(CNV5plex)
```

---

|          |                        |
|----------|------------------------|
| CNV6plex | <i>CNV 6-plex data</i> |
|----------|------------------------|

---

**Description**

CNV 6-plex universal probes

**Usage**

```
data(CNV6plex)
```

**Format**

A data frame of fluorescence intensities in each channel. Each row represents each partitions, and each column each channel.

**channel1** fluorescence intensities of color 1

**channel2** fluorescence intensities of color 2

**channel3** fluorescence intensities of color 3

**channel4** fluorescence intensities of color 4

**channel5** fluorescence intensities of color 5

**channel6** fluorescence intensities of color 6

**Examples**

```
data(CNV6plex)
head(CNV6plex)
```

---

|          |   |
|----------|---|
| conc_cal | <i>concentration calculation function</i> |
|----------|---|

---

**Description**

This function takes a data frame of fluorescence intensities and partition clusters as input. It can be results from polytect\_clust or polytect\_merge. It will give the target concentration as output.

**Usage**

```
conc_cal(df_data, cluster_num, sampvol = 0.91, volmix = 20, voltemp = 20)
```

**Arguments**

|                          |   |
|--------------------------|---|
| <code>df_data</code>     | A data frame containing partition fluorescence intensities and corresponding cluster label. This can be the output of <code>polytect_merge</code> or any data frame containing the above information. |
| <code>cluster_num</code> | the expected number of clusters   |
| <code>sampvol</code>     | The sample volume in microliters ( $\mu\text{L}$ )  |
| <code>volmix</code>      | The volume of the mixture   |
| <code>voltemp</code>     | The volume of the template  |

**Value**

a data frame of target concentration.

**Examples**

```
data(HR)
df_data<-polytect_clust(HR,4)
conc_cal(df_data,4)
```

---

HIV

*HIV data*

---

**Description**

A 4-color dPCR data of intact HIV-1 proviruses

**Usage**

```
data(HIV)
```

**Format**

A data frame of fluorescence intensities in each channel. Each row represents each partitions, and each column each channel.

**channel1** fluorescence intensities of color 1

**channel2** fluorescence intensities of color 2

**channel3** fluorescence intensities of color 3

**channel4** fluorescence intensities of color 4

**Source**

<https://www.biorxiv.org/content/10.1101/2023.08.18.553846v1>

**Examples**

```
data(HIV)
head(HIV)
```

---

|    |                |
|----|----------------|
| HR | <i>HR data</i> |
|----|----------------|

---

**Description**

A high-resolution 2-color dPCR data of RPP30 genomic DNA assay

**Usage**

```
data(HR)
```

**Format**

A data frame of fluorescence intensities in each channel. Each row represents each partitions, and each column each channel. good separation but some crosstalk.

**channel1** fluorescence intensities of color 1

**channel2** fluorescence intensities of color 2

**Source**

<https://pubmed.ncbi.nlm.nih.gov/33992770/>

**Examples**

```
data(HR)
head(HR)
```

---

|    |                |
|----|----------------|
| LR | <i>LR data</i> |
|----|----------------|

---

**Description**

A low-resolution 2-color dPCR data of development of genotyping assays for plants various

**Usage**

```
data(LR)
```

**Format**

A data frame of fluorescence intensities in each channel. Each row represents each partitions, and each column each channel. barely separable on x-axis.

**channel1** fluorescence intensities of color 1

**channel2** fluorescence intensities of color 2

**Examples**

```
data(LR)
head(LR)
```

---

|    |                |
|----|----------------|
| MM | <i>MM data</i> |
|----|----------------|

---

**Description**

A multi-mode 2-color dPCR data of HIV gBlock sequences

**Usage**

```
data(MM)
```

**Format**

A data frame of fluorescence intensities in each channel. Each row represents each partitions, and each column each channel. obvious multimodality.

**channel1** fluorescence intensities of color 1

**channel2** fluorescence intensities of color 2

**Source**

<https://pubmed.ncbi.nlm.nih.gov/37827643/>

**Examples**

```
data(MM)
head(MM)
```

---

|                |                                     |
|----------------|-------------------------------------|
| polytect_clust | <i>Main function for clustering</i> |
|----------------|-------------------------------------|

---

**Description**

This is the main function for clustering. The function will start with flowPeaks, then merge the excess clusters. It will return a data frame of fluorescence intensities and partition labels.

**Usage**

```
polytect_clust(
  data,
  cluster_num,
  fp_par = "default",
  fp_optim = c(0.1, 1, 1.5),
  lambdas = rep(2, 64 - log2(64)),
  coefs = rep(1, 6)
)
```

**Arguments**

|             |  |
|-------------|--|
| data        | A matrix of fluorescence intensities in each channel. Each row represents each partitions, and each column each channel.   |
| cluster_num | The expected maximum number of clusters.   |
| fp_par      | The parameters for flowPeaks. fp_par=c("default","manual","auto"). When "default" is chosen, the default parameters of flowPeaks will be used. With "manual", you have to fill in fp_optim.  |
| fp_optim    | The paramters for flowPeaks that users have to fill in manually when fp_par is set at "manual".  |
| lambdas     | The penalty terms for the deviation from the expected cluster centers. Higher lambdas penalizes the deviation more.  |
| coefs       | The coefficients to adjust for the expected cluster centers. The default is 1 which can be used for common assay designs and has to be modified for special assays such as competing assays. |

**Value**

A data frame containing the original fluorescence intensity and the cluster labels.

**Examples**

```
data(HR)
head(polytect_clust(HR, 4))
```

---

polytect\_merge      *Function for merging*

---

**Description**

This function takes the clustering result as input. Users can first perform any clustering algorithm, then use this function. It will return a data frame of fluorescence intensities and partition labels.

**Usage**

```
polytect_merge(
  data,
  cluster_num,
  base_clust,
  lambdas = rep(2, 64 - log2(64)),
  coefs = rep(1, 6)
)
```

**Arguments**

|             |  |
|-------------|--|
| data        | A matrix of fluorescence intensities in each channel. Each row represents each partitions, and each column each channel.   |
| cluster_num | The expected maximum number of clusters.   |
| base_clust  | A list that contains partition labels given by initial clustering.   |
| lambdas     | The penalty terms for the deviation from the expected cluster centers. Higher lambdas penalizes the deviation more.  |
| coefs       | The coefficients to adjust for the expected cluster centers. The default is 1 which can be used for common assay designs and has to be modified for special assays such as competing assays. |

**Value**

A data frame containing the original fluorescence intensity and the cluster labels.

**Examples**

```
data(HR)
dist_matrix <- dist(HR)
hc <- hclust(dist_matrix, method = "ward.D2")
hc_clusters <- cutree(hc, k = 6)
base_clust <- list()
base_clust$cluster <- hc_clusters
head(polytect_merge(HR, 4, base_clust))
```

---

polytect\_plot

*Plotting function for clustering results*

---

**Description**

This function takes results from `polytect_clust` and `polytect_merge`, or a data frame containing fluorescence intensities and partition labels. It will output all combination of 2-color plots.

**Usage**

```
polytect_plot(df_data, cluster_num, cluster_selected = TRUE)
```

**Arguments**

`df_data` A data frame containing partition fluorescence intensities and corresponding cluster label. This can be the output of `polytect_clust` and `polytect_merge` or any data frame containing the above information.

`cluster_num` the expected number of clusters

`cluster_selected` Indicator of whether all the clusters are present in the plots. If TRUE, then only selected ones (the ones only positive in the selected 2 dimensions) are shown. The default value is "TRUE".

**Value**

2-color plots.

**Examples**

```
data(HR)
df_data<-polytect_clust(HR,4)
polytect_plot(df_data,4)
```

---

`polytect_summary`      *Summary function*

---

**Description**

This function takes results from `polytect_clust` and `polytect_merge`, or a data frame containing fluorescence intensities and partition labels. It will summarise cluster centers, cluster sizes and cluster silhouette coefficients.

**Usage**

```
polytect_summary(df_data)
```

**Arguments**

`df_data` A data frame containing partition fluorescence intensities and corresponding cluster label. This can be the output of `polytect_clust` and `polytect_merge` or any data frame containing the above information.

**Value**

a data frame of the summary of cluster centers, cluster sizes and cluster silhouette coefficients.

**Examples**

```
data(HR)
df_data<-polytect_clust(HR,4)
polytect_summary(df_data)
```

---

`sil_plot`*Plotting function for silhouette coefficients*

---

**Description**

This function takes results from `polytect_clust` and `polytect_merge`, or a data frame containing fluorescence intensities and partition labels. It will output the silhouette coefficients of each cluster.

**Usage**

```
sil_plot(df_data)
```

**Arguments**

`df_data` A data frame containing partition fluorescence intensities and corresponding cluster label. This can be the output of `polytect_clust` and `polytect_merge` or any data frame containing the above information.

**Value**

plot of silhouette coefficients for each cluster.

**Examples**

```
data(HR)
df_data<-polytect_clust(HR,4)
sil_plot(df_data)
```

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