

# Package ‘cmmr’

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**Title** CEU Mass Mediator RESTful API

**Version** 1.0.3

**Depends** R (>= 4.4.0)

**Imports** httr, progress, RJSONIO, cli

## Description

CEU (CEU San Pablo University) Mass Mediator is an on-line tool for aiding researchers in performing metabolite annotation. 'cmmr' (CEU Mass Mediator RESTful API) allows for programmatic access in R: batch search, batch advanced search, MS/MS (tandem mass spectrometry) search, etc.

For more information about the API Endpoint please go to <<https://github.com/YaoxiangLi/cmmr>>.

**License** GPL-3

**Encoding** UTF-8

**URL** <https://github.com/YaoxiangLi/cmmr>

**RoxygenNote** 7.3.2

**Suggests** testthat

**NeedsCompilation** no

**Author** Yaoxiang Li [aut, cre] (ORCID: <<https://orcid.org/0000-0001-9200-1016>>),  
Alberto Gil de la Fuente [aut],  
Charles Hinzman [aut],  
Amrita Cheema [aut]

**Maintainer** Yaoxiang Li <[liyaoxiang@outlook.com](mailto:liyaoxiang@outlook.com)>

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advanced\_batch\_search *Advanced Batch Search using CEU Mass Mediator API*

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## Description

advanced\_batch\_search performs an advanced batch search on the CEU Mass Mediator API and returns a dataframe of search results.

## Usage

```
advanced_batch_search(
  cmm_url = "https://ceumass.eps.uspceu.es/api/v3/advancedbatch",
  chemical_alphabet = "ALL",
  modifiers_type = "none",
  metabolites_type = "all-except-peptides",
  databases = "[\"HMDB\"]",
  masses_mode = "mz",
  ion_mode = "positive",
  adducts = "[\"all\"]",
  deuterium = FALSE,
  tolerance = 7.5,
  tolerance_mode = "ppm",
  masses = NULL,
  all_masses = "[]",
  retention_times = NULL,
  all_retention_times = "[]",
  composite_spectra = NULL
)
```

## Arguments

cmm_url	A character string specifying the CEU Mass Mediator API endpoint. Default is "https://ceumass.eps.uspceu.es/api/v3/advancedbatch".
chemical_alphabet	A character string specifying the chemical alphabet to use. Options are "CHNOPS", "CHNOPSCL", or "ALL".
modifiers_type	A character string specifying the modifier type. Options are "none", "NH3", "HCOO", "CH3COO", "HCOONH3", or "CH3COONH3".
metabolites_type	A character string specifying the metabolites type. Options are "all-except-peptides", "only-lipids", or "all-including-peptides".
databases	A JSON-formatted character string specifying the databases to search. Examples include "["all"]", "["HMDB"]", "["LipidMaps"]".

masses_mode	A character string specifying the masses mode. Options are "neutral" or "mz".
ion_mode	A character string specifying the ionization mode. Options are "positive", "negative", or "neutral".
adducts	A JSON-formatted character string specifying the adducts to include in the search. Examples include '['"M+H", "M+Na"]' for positive mode.
deuterium	A logical value indicating whether to consider deuterium substitutions. TRUE or FALSE.
tolerance	A numeric value specifying the mass tolerance (Range: 0 to 100).
tolerance_mode	A character string specifying the tolerance mode. Options are "ppm" or "mDa".
masses	A numeric vector of masses to search.
all_masses	A JSON-formatted character string representing an array of mass arrays.
retention_times	A numeric vector of retention times corresponding to the masses.
all_retention_times	A JSON-formatted character string representing an array of retention time arrays.
composite_spectra	A JSON-formatted character string representing composite spectra.

### Value

A dataframe containing the search results from the CEU Mass Mediator API.

### Examples

```
## Not run:
df <- advanced_batch_search(
  cmm_url = "https://ceumass.eps.uspceu.es/api/v3/advancedbatch",
  chemical_alphabet = "ALL",
  modifiers_type = "none",
  metabolites_type = "all-except-peptides",
  databases = '['"HMDB"]',
  masses_mode = "mz",
  ion_mode = "positive",
  adducts = '['"all"]',
  deuterium = FALSE,
  tolerance = 7.5,
  tolerance_mode = "ppm",
  masses = c(400.3432, 288.2174),
  all_masses = "[]",
  retention_times = c(18.842525, 4.021555),
  all_retention_times = "[]",
  composite_spectra = paste0(
    '[' [ { "mz": 400.3, "intensity": 307034.9 },',
    ' { "mz": 311.2, "intensity": 400.1 } ] ]'
  )
)
## End(Not run)
```

---

`batch_search`*Encapsulation of CEU Mass Mediator batch search API*

---

## Description

`batch_search` returns a dataframe with the results from the database search.

## Usage

```
batch_search(  
  cmm_url = "https://ceumass.eps.uspceu.es/api/v3/batch",  
  metabolites_type = "all-except-peptides",  
  databases = "[\"all-except-mine\"]",  
  masses_mode = "mz",  
  ion_mode = "positive",  
  adducts = "[\"M+H\", \"M+Na\"]",  
  tolerance = 10,  
  tolerance_mode = "ppm",  
  unique_mz  
)
```

## Arguments

<code>cmm_url</code>	A URL string for the CEU Mass Mediator or a local API endpoint.
<code>metabolites_type</code>	Search metabolites type: "all-except-peptides", "only-lipids", or "all-including-peptides".
<code>databases</code>	A JSON array of databases to search: e.g., "all", "HMDB", "LipidMaps", etc.
<code>masses_mode</code>	Masses mode: "neutral" or "mz".
<code>ion_mode</code>	Ionization mode: "positive" or "negative".
<code>adducts</code>	A JSON array of adducts to include in the search, e.g., '["M+H", "M+Na"]'.
<code>tolerance</code>	A numeric tolerance value (range: 0-100).
<code>tolerance_mode</code>	Tolerance mode: "ppm" or "mDa".
<code>unique_mz</code>	A numeric vector of unique m/z values for the search.

## Value

A dataframe containing search results.

## Examples

```
## Not run:  
df_pos <- batch_search(  
  "https://ceumass.eps.uspceu.es/api/v3/batch",  
  "all-except-peptides",
```

```

    ["all-except-mine"],
    "mz",
    "positive",
    ["M+H", "M+Na"],
    10,
    "ppm",
    c(670.4623, 1125.2555, 602.6180)
)

## End(Not run)

```

---

```
create_advanced_batch_body
```

*Create POST request Body for batch search*

---

## Description

create\_advanced\_batch\_body returns a string of advanced search POST request body.

## Usage

```

create_advanced_batch_body(
  chemical_alphabet = "all",
  modifiers_type = "none",
  metabolites_type = "all-except-peptides",
  databases = "[\`hmdb\`]",
  masses_mode = "mz",
  ion_mode = "positive",
  adducts = "[\`all\`]",
  deuterium = "false",
  tolerance = "7.5",
  tolerance_mode = "ppm",
  masses = "[400.3432, 288.2174]",
  all_masses = "[]",
  retention_times = "[18.842525, 4.021555]",
  all_retention_times = "[]",
  composite_spectra = paste0("[[{\`mz\`: 400.3432, \`intensity\`: 307034.88 }, ",
    "{ \`mz\`: 311.20145, \`intensity\`: 400.03336 }]]")
)

```

## Arguments

```

chemical_alphabet      "CHNOPS", "CHNOPSCL", "ALL"
modifiers_type         "none", "NH3", "HCOO", "CH3COO", "HCOONH3", "CH3COONH3"
metabolites_type       "all-except-peptides", "only-lipids", "all-including-peptides"

```

databases	"all", "all-except-mine", "HMDB", "LipidMaps", "Metlin", "Kegg", "in-house", "mine"
masses_mode	"neutral", "mz"
ion_mode	"positive", "negative"
adducts	for positive mode ["M+H", "M+2H", "M+Na", "M+K", "M+NH4", "M+H-H2O"] for negative mode ["M-H", "M+Cl", "M+FA-H", "M-H-H2O"], for neutral ["M"]
deuterium	boolean 'true' 'false'
tolerance	double (Range: [0..100])
tolerance_mode	"ppm", "mDa"
masses	double
all_masses	array of doubles
retention_times	double
all_retention_times	array of doubles
composite_spectra	array of arrays of spectra_object

**Value**

If all inputs are all correctly formatted, a dataframe will be returned for the result.

---

create\_batch\_body      *Create POST request Body for batch search*

---

**Description**

create\_batch\_body returns a string of a POST request body.

**Usage**

```
create_batch_body(
  metabolites_type = "all-except-peptides",
  databases = "[\"all-except-mine\"]",
  masses_mode = "mz",
  ion_mode = "positive",
  adducts = "[\"M+H\", \"M+Na\"]",
  tolerance = 10,
  tolerance_mode = "ppm",
  unique_mz
)
```

**Arguments**

metabolites_type	"all-except-peptides", "only-lipids", "all-including-peptides"
databases	"all", "all-except-mine", "HMDB", "LipidMaps", "Metlin", "Kegg", "in-house", "mine"
masses_mode	"neutral", "mz"
ion_mode	"positive", "negative"
adducts	for positive mode [M+H, M+2H, M+Na, M+K, M+NH4, M+H-H2O]
tolerance	double (Range: [0..100])
tolerance_mode	"ppm", "mDa"
unique_mz	An array of unique m/zs

**Value**

If all inputs are all correctly formatted, a string of a POST request will be returned for the result.

**Examples**

```
batch_body <- create_batch_body(
  "all-except-peptides",
  ["all-except-mine"],
  "mz",
  "positive",
  ["M+H", "M+Na"],
  10,
  "ppm",
  c(670.4623, 1125.2555, 602.6180)
)

batch_body <- create_batch_body(
  "all-except-peptides",
  ["all-except-mine"],
  "mz",
  "negative",
  ["M-H", "M+Cl"],
  10,
  "ppm",
  c(670.4623, 1125.2555, 602.6180)
)

## Not run:
create_batch_body(c(670.4623, 1125.2555, 602.6180))

## End(Not run)
```

---

create_msms_body	<i>Create MS/MS search POST request body</i>
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---

### Description

create\_msms\_body returns a string of a POST request body.

### Usage

```
create_msms_body(  
    ion_mass,  
    ms_ms_peaks,  
    precursor_ion_tolerance = 500,  
    precursor_ion_tolerance_mode = "mDa",  
    precursor_mz_tolerance = 1000,  
    precursor_mz_tolerance_mode = "mDa",  
    ion_mode = "positive",  
    ionization_voltage = "all",  
    spectra_types = "experimental"  
)
```

### Arguments

ion_mass	ion_mass
ms_ms_peaks	ms_ms_peaks
precursor_ion_tolerance	precursor_ion_tolerance
precursor_ion_tolerance_mode	precursor_ion_tolerance_mode
precursor_mz_tolerance	precursor_mz_tolerance
precursor_mz_tolerance_mode	precursor_mz_tolerance_mode
ion_mode	ion_mode
ionization_voltage	ionization_voltage
spectra_types	spectra_types

### Value

If all inputs are all correctly formatted, a string of a POST request will be returned for the result.

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msms\_search

*MS/MS Search using CEU Mass Mediator API*


---

## Description

msms\_search performs an MS/MS search on the CEU Mass Mediator API and returns a dataframe with the search results.

## Usage

```
msms_search(
  ion_mass,
  ms_ms_peaks,
  precursor_ion_tolerance = 100,
  precursor_ion_tolerance_mode = "mDa",
  precursor_mz_tolerance = 500,
  precursor_mz_tolerance_mode = "mDa",
  ion_mode,
  ionization_voltage = "all",
  spectra_types = "experimental",
  cmm_url = "https://ceumass.eps.uspceu.es/api/msmssearch"
)
```

## Arguments

ion_mass	Numeric. Mass of the ion to search for.
ms_ms_peaks	Matrix. The MS/MS peaks, with two columns representing mass and intensity.
precursor_ion_tolerance	Numeric. Tolerance for the precursor ion (default: 100.0).
precursor_ion_tolerance_mode	Character. Tolerance mode for precursor ion: "ppm" or "mDa" (default: "mDa").
precursor_mz_tolerance	Numeric. Tolerance for the m/z (default: 500.0).
precursor_mz_tolerance_mode	Character. Tolerance mode for precursor m/z: "ppm" or "mDa" (default: "mDa").
ion_mode	Character. Ionization mode: "positive" or "negative".
ionization_voltage	Character. Ionization voltage to use (default: "all").
spectra_types	Character. Spectra types: "experimental" or other supported types.
cmm_url	Character. URL for the CEU Mass Mediator API (default: "https://ceumass.eps.uspceu.es/api/msmssearch").

## Value

A dataframe containing the search results from the CEU Mass Mediator API.

**Examples**

```
## Not run:
ms_ms_peaks <- matrix(
  c(
    40.948, 0.174,
    56.022, 0.424,
    84.370, 53.488,
    101.500, 8.285,
    102.401, 0.775,
    129.670, 100.000,
    146.966, 20.070
  ),
  ncol = 2,
  byrow = TRUE
)

df <- msms_search(
  ion_mass = 147,
  ms_ms_peaks = ms_ms_peaks,
  ion_mode = "positive"
)

## End(Not run)
```

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