

# GitHub issues overview

- Issues open discussion threads related to a repo
  - Bugs, requested features, intended next steps
- Anyone can **open an issue** related to a GitHub repo
  - Collaborators
  - External users
  - Reviewers
- Issues are tracked until they are resolved
- Many project management features

weecology / **portalr**

Watch 5

Star 4

Fork 9

Code

Issues 11

Pull requests 1

Actions

Projects 0

Wiki

Insights

A collection of functions to summarize the Portal Data <https://weecology.github.io/portalr/>

ecology

community-ecology

small-mammal-trapping

553 commits

11 branches

4 releases

1 environment

10 contributors

View license

Branch: master

New pull request

Create new file

Upload files

Find file

Clone or download



ha0ye Fix error message.

Latest commit 9496956 21 hours ago



R

Fix error message.

21 hours ago



man

add check function for default data path

23 hours ago



paper

added doi to references in paper.md; updated R ref

2 months ago



tests

add check function for default data path

23 hours ago



vignettes

use alternate method to check if running vignettes as part of R CMD C...

3 days ago

&lt;&gt; Code

! Issues 11

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Wiki

Insights

Filters ▾

is:issue

Labels

Milestones

New issue

✕ Clear current search query, filters, and sorts

<input type="checkbox"/>	! 11 Open ✓ 77 Closed	Author ▾	Projects ▾	Labels ▾	Milestones ▾	Assignee ▾	Sort ▾
<input type="checkbox"/>	<b>Add startup message about setting the data path</b> #194 opened 2 days ago by ha0ye						
<input type="checkbox"/>	<b>upcoming CRAN release of dplyr (Feb 8)</b> #192 by gmyenni was closed 3 days ago						1
<input type="checkbox"/>	<b>error catching github pat issue</b> #188 by juniperlsimonis was closed on Jan 13						
<input type="checkbox"/>	<b>Check that treatment is returned with plant data summarized at the plot level</b> #186 opened on Jan 10 by ha0ye  Release ver 0.3						
<input type="checkbox"/>	<b>Use a system variable to store the default data path</b> <b>enhancement</b> #185 by ha0ye was closed 3 days ago  Release ver 0.3						
<input type="checkbox"/>	<b>Add more badges?</b> #181 by Pakillo was closed on Dec 28, 2018						
<input type="checkbox"/>	<b>JOSS review: Consider renaming/restructuring load_ functions?</b> #180 by Pakillo was closed on Jan 11						7
<input type="checkbox"/>	<b>JOSS review: add DOI for papers, and revise R citation</b> #179 by Pakillo was closed on Jan 7						1

Filters ▾

🔍 is:issue

Labels

Milestones

New issue

✕ Clear current search query, filters, and sorts



🔔 11 Open ✓ 77 Closed

Author ▾

Projects ▾

Labels ▾

Milestones ▾

Assignee ▾

Sort ▾



🔔 Add startup message about setting the data path

#194 opened 2 days ago by ha0ye



🔔 upcoming CRAN release of dplyr (Feb 8)

#192 by gmyenni was closed 3 days ago



🔔 error catching github pat issue

#188 by juniperlsimonis was closed on Jan 13



🔔 Check that treatment is returned with plant data summarized at the plot

#186 opened on Jan 10 by ha0ye 🚧 Release ver 0.3



🔔 Use a system variable to store the default data path enhancement

#185 by ha0ye was closed 3 days ago 🚧 Release ver 0.3



🔔 Add more badges?

#181 by Pakillo was closed on Dec 28, 2018



🔔 JOSS review: Consider renaming/restructuring load\_functions?

#180 by Pakillo was closed on Jan 11



🔔 JOSS review: add DOI for papers, and revise R citation

#179 by Pakillo was closed on Jan 7

Filter by who's assigned

Filter users

Assigned to nobody



diazrenata Renata Diaz



breds22e Ellen Bledsoe



emchristensen Erica Christensen



ethanwhite Ethan White



gmyenni Glenda



ha0ye Hao Ye



henrykironde henry senyondo



juniperlsimonis Juniper Simonis



sarahsupp Sarah Supp

&lt;&gt; Code

🔔 Issues 11

🔗 Pull requests 1

▶ Actions

📁 Projects 0

📖 Wiki

📊 Insights

Filters ▾

🔍 is:issue assignee:diazrenata

Labels

Milestones

New issue

✕ Clear current search query, filters, and sorts

☐ 1 Open ✓ 3 Closed Author ▾ Projects ▾ Labels ▾ Milestones ▾ Assignee ▾ Sort ▾☐ 🚫 **metabolic energy equation**  
#160 by emchristensen was closed on Sep 17, 2018☐ 🟢 **Add vignettes to demonstrate usage of the package**  
#123 opened on Apr 25, 2018 by ha0ye☐ 🚫 **Standardizing abundances according to how many plots were trapped**  
#47 by diazrenata was closed on Apr 24, 2018 🏷️ Release ver 0.1☐ 🚫 **Write biomass function**  
#1 by gmyenni was closed on Jan 18, 2018 🏷️ Release ver 0.1

Filter by who's assigned

Filter users

Assigned to nobody

✓  **diazrenata** Renata Diaz **bleds22e** Ellen Bledsoe **emchristensen** Erica Christensen **ethanwhite** Ethan White **gmyenni** Glenda💡 ProTip! Type `g` `p` on any issue or pull request to go back to 1

## metabolic energy equation #160

Edit

New issue

 Closed

emchristensen opened this issue on Aug 20, 2018 · 1 comment



emchristensen commented on Aug 20, 2018

Member

+ 😊 ...

Right now the energy() function calculates energy as  $(\text{mass})^{0.75}$ . White et al 2004 (in Am Nat) used:  $5.69 * (\text{mass})^{0.75}$  which was based on field metabolic data -- we should probably use this version instead (and maybe do a vignette if there isn't one on energy already).

 ha0ye assigned gmyenni and diazrenata on Aug 29, 2018 diazrenata closed this on Sep 17, 2018

diazrenata commented on Sep 17, 2018

Member

+ 😊 ...

Just updated this.

Assignees

 gmyenni diazrenata

Labels



None yet

Projects



None yet

Milestone



No milestone

Notifications

🔊 Unsubscribe

&lt;&gt; Code

🔔 Issues 11

🔗 Pull requests 1

🎮 Actions

📁 Projects 0

📖 Wiki

📊 Insights

Filters ▾

🔍 is:issue

Labels

Milestones

New issue

✕ Clear current search query, filters, and sorts

☐ 🔔 11 Open ✓ 77 Closed

Author ▾

Projects ▾

Labels ▾

Milestones ▾

Assignee ▾

Sort ▾

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#194 opened 2 days ago by ha0ye

☐ 🛑 upcoming CRAN release of dplyr (Feb 8)

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💬 1

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💬 7

☐ 🛑 JOSS review: add DOI for papers, and revise R citation

#179 by Pakillo was closed on Jan 7



💬 1



# JOSS review: Consider renaming/restructuring load\_ functions? #180

Edit

New issue

 Closed

Pakillo opened this issue on Dec 26, 2018 · 7 comments



Pakillo commented on Dec 26, 2018

Contributor



Hi,

Another comment related to my JOSS review ([openjournals/joss-reviews#1098](https://openjournals/joss-reviews#1098)).

As my first encounter with the package, I got a bit confused at first with the `load_*` functions ([https://weecology.github.io/portalr/reference/load\\_data.html](https://weecology.github.io/portalr/reference/load_data.html)). It isn't obvious from their names what particular data these functions are loading. As there is `load_plant_data` and `load_ant_data`, maybe `load_data` could be renamed as `load_rodent_data` for consistency, or `load_trapping_data` to account for the fact that not only rodents fall in traps, but also reptiles, birds, etc?

I note there is already a `load_trapping_data` function, but this one does not seem to load any abundance or catch data like the others, but rather the data on when and where trappings took place? Then this function role would be different from the other three (i.e. loading data from rodents (mostly), plants, and ants), and could be perhaps renamed as an independent function? (e.g. as the others you have to get weather data, NDVI, etc).

Just a suggestion... Because it took me a couple of minutes to learn what each function would do. But up to you of course!

Assignees

 ha0ye

Labels



None yet

Projects




None yet

Milestone



No milestone

Notifications

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ha0ye commented on Jan 10

Member



@diazrenata Did you have thoughts on renaming `get_stake_data()` ?



diazrenata commented on Jan 10

Member



It seems more intuitive to me to refer to it as `get_individual_data()` , but I can see the rationale for `get_stake_data()` .



ha0ye commented on Jan 10

Member



@diazrenata Well, since we're renaming `get_rodent_data()` to `summarize_rodent_data()` , are you in favor of `summarize_individual_data()` ? I was wondering if `summarize_individual_rodents()` would be clearer about it being the rodent data.



gmyenni commented on Jan 10

Member



The initial idea was that `stake_data` was the more or less 'raw' individual data, and `individual_data` would be the 'cleaned' individual data (where unique tags actually refer to distinct individuals), which is still on the to-do list. But we could also call this the `individual_data` , and call the cleaned data `tag_data` . That's probably more intuitive all the way around, yeah? ie `summarize_individual_rodents()` and `summarize_rodent_tags()`



gmyenni commented on Jan 10 • edited

Member



Note though that `get_stake_data()` doesn't (at the moment) actually summarize. It just cleans a bit. So while that would be consistent with the 'type' of function it is, it isn't technically true.



ha0ye referenced this issue on Jan 10

Rename load functions #187

Merged



ha0ye closed this in #187 on Jan 11



ha0ye commented on Jan 10

Member



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diazrenata commented on Jan 10

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ha0ye commented on Jan 10

Member



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ha0ye referenced this issue on Jan 10

Rename load functions #187

Merged



ha0ye closed this in #187 on Jan 11

# Rename load functions #187

[Edit](#)**Merged** ha0ye merged 3 commits into master from rename-load-functions on Jan 11

💬 Conversation 4

🔗 Commits 3

🔧 Checks 0

📄 Files changed 35

+743 -655



ha0ye commented on Jan 10

Member

+ 👤 ...

closes #180



ha0ye added some commits on Jan 10



rename functions: ...

Verified

1622863



finish renaming/refactoring and update version #

Verified

✓ 8646f23



ha0ye requested review from gmyenni , bleds22e , diazrenata and juniperlsimonis on Jan 10



diazrenata reviewed on Jan 10

[View changes](#)

diazrenata left a comment

Member

+ 👤 ...

Thanks for implementing this! That was so fast, and I really appreciate all of the scruffy data-wrangling that has happened here.

I think keeping the naming conventions consistent (load\_X\_data and summarize\_X\_data) is helpful, even if there's relatively little processing done in some of the summarize\_ functions. As far as stakes vs individuals vs tags goes, I made my suggestions earlier without the context that the stakes/individual distinction was named with the idea of using individuals to track unique tags, and I think any answer + documentation will be fine and won't be a barrier to using the function appropriately!

Reviewers



diazrenata



gmyenni



bleds22e



juniperlsimonis



Assignees



No one—assign yourself

Labels



None yet

Projects



None yet

Milestone



No milestone

Notifications

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## Rename load functions #187

Edit

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Conversation 4

Commits 3

Checks 0

Files changed 35

+743 -655



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Member

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Verified 1622863

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Verified ✓ 8646f23

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View changes

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Reviewers



diazrenata



gmyenni



bleds22e



juniperlsimonis



Assignees



No one—assign yourself

Labels



None yet

Projects



None yet

Milestone



No milestone

Notifications

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# Rename load functions #187

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💬 Conversation 4

🔗 Commits 3

🔔 Checks 0

📁 Files changed 35

+743 -655



ha0ye commented on Jan 10

Member

+ 👤 ...

closes #180

📁 ha0ye added some commits on Jan 10

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Verified 162263

📁 finish renaming/refactoring and update version #

Verified ✓ 8646f23

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Reviewers

⚙

diazrenata

💬

gmyenni

✓

bleds22e

●

juniperlsimonis

●

Assignees

⚙

No one—assign yourself

Labels

⚙

None yet

Projects

⚙

None yet

Milestone

⚙

No milestone

Notifications

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# In summary (and beyond!)

- Communication
  - Collaborators
  - Users of open source software packages
  - Reviewers
- Project management
  - Issue tracking and resolution
  - Assignees
  - Labels and milestones
  - Project boards