

## Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

### Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. figure legend, table legend, main text, or Methods section).

n/a Confirmed

- ☐ ☒ The exact sample size ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement
- ☐ ☒ An indication of whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☐ ☒ The statistical test(s) used AND whether they are one- or two-sided  
*Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
- ☐ ☒ A description of all covariates tested
- ☐ ☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- ☐ ☒ A full description of the statistics including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- ☐ ☒ For null hypothesis testing, the test statistic (e.g.  $F$ ,  $t$ ,  $r$ ) with confidence intervals, effect sizes, degrees of freedom and  $P$  value noted  
*Give  $P$  values as exact values whenever suitable.*
- ☒ ☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- ☐ ☒ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- ☐ ☒ Estimates of effect sizes (e.g. Cohen's  $d$ , Pearson's  $r$ ), indicating how they were calculated
- ☐ ☒ Clearly defined error bars  
*State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on [statistics for biologists](#) may be useful.

### Software and code

Policy information about [availability of computer code](#)

Data collection

No software was used for data collection

Data analysis

We used R (version 3.5.0). The R code used in the analysis presented in this paper is available online and can be accessed at [https://github.com/cesarterrer/CO2\\_Upscaling](https://github.com/cesarterrer/CO2_Upscaling).

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [guidelines for submitting code & software](#) for further information.

### Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

A data availability statement was presented in the manuscript. The data of all the analyses are publicly accessible.

## Field-specific reporting

Please select the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☐ Behavioural & social sciences ☒ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/authors/policies/ReportingSummary-flat.pdf](https://www.nature.com/authors/policies/ReportingSummary-flat.pdf)

## Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

|                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|-----------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Study description                 | Synthesis study based on a meta-analysis of data from CO <sub>2</sub> experiments. We identify the best descriptors ("moderators") of the CO <sub>2</sub> effect on biomass in the dataset based on random-forest meta-analysis. We design a nonlinear mixed-effects meta-regression with selected moderators, including "site" as a random factor, and use this statistical model to project the CO <sub>2</sub> fertilization effect on biomass globally.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| Research sample                   | Published data from CO <sub>2</sub> experiments, excluding pot studies and plants grown in soils of unknown properties.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| Sampling strategy                 | We compiled data from as many studies as possible, as long as they met the criteria specified in methods. We prioritized studies using natural soils.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| Data collection                   | We used previously compiled datasets, such as those by INTERFACE ( <a href="https://www.bio.purdue.edu/INTERFACE/experiments.php">https://www.bio.purdue.edu/INTERFACE/experiments.php</a> ), the Global List of FACE Experiments from the Oak Ridge National Laboratory ( <a href="http://facedata.ornl.gov/global_face.html">http://facedata.ornl.gov/global_face.html</a> ), the ClimMani database on manipulation experiments ( <a href="http://www.climmani.org">www.climmani.org</a> ), and the databases described by Dieleman et al. (2012), Baig et al. (2015), and Terrer et al. (2016, 2017, 2018). We used Google Scholar to locate the most recent publications for each of the previously listed experiments, as well as soil data for as many experiments as possible. If no soil data were found, the experiment was excluded from the main analysis, but included in a sensitivity analysis with inferred data from proxies. |
| Timing and spatial scale          | The most recent data were sampled in the field in 2015 and published in 2018; we thus collected data until the date of submission. Experiments were not excluded based on date of publication, as long as they met the criteria specified in methods and data about soil properties were reported.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| Data exclusions                   | We included as many observations as possible for our analysis. Criteria for exclusion from the main analysis were: i) Soil C:N and N content data for the specific soils in which the plants were grown were not reported. For example, studies that included a N fertilization treatment were only included when C:N was measured in situ, and not in unfertilized plots. ii) species did not form associations with either AM or ECM. Only species in two studies were non-mycorrhizal, insufficient to identify the drivers of the eCO <sub>2</sub> response in this group; and iii) the duration of the experiment was less than 2 months.                                                                                                                                                                                                                                                                                                |
| Reproducibility                   | Our analyses were based on published data (included in Supplementary Fig. 2) and public satellite products and global datasets (Supplementary Table 2), and the results can be reproduced using the R code in <a href="https://github.com/cesartrerrer/CO2_Upscaling">https://github.com/cesartrerrer/CO2_Upscaling</a>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| Randomization                     | Grouping was based on a machine-learning model selection approach                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| Blinding                          | Our study is based on existing data, therefore blinding is not relevant.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| Did the study involve field work? | <input type="checkbox"/> Yes <input checked="" type="checkbox"/> No                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |

## Reporting for specific materials, systems and methods

### Materials & experimental systems

|                                     |                                                      |
|-------------------------------------|------------------------------------------------------|
| n/a                                 | Involvement in the study                             |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Unique biological materials |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Antibodies                  |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Eukaryotic cell lines       |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology               |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Animals and other organisms |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Human research participants |

### Methods

|                                     |                                                 |
|-------------------------------------|-------------------------------------------------|
| n/a                                 | Involvement in the study                        |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> ChIP-seq               |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Flow cytometry         |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> MRI-based neuroimaging |