

Reporting Summary

Nature Portfolio 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 Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

- | n/a | Confirmed |
|-------------------------------------|--|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> The statistical test(s) used AND whether they are one- or two-sided
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A description of all covariates tested |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A full description of the statistical parameters 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) |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
<i>Give P values as exact values whenever suitable.</i> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated |

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

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

- | | |
|-----------------|--|
| Data collection | No software was used for data collection |
| Data analysis | Open-source software used in analysis of terrestrial laser scan data (optQSM and TreeQSM) ver. 2.4.1) is described in the Methods. Tree rings were analyzed with TSAPO-Win software (Rinntech, Inc.) |

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 and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

All data will be publicly available without restriction at Dryad (10.5061/dryad.z612jm6jw)

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender	<i>Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design whether sex and/or gender was determined based on self-reporting or assigned and methods used. Provide in the source data disaggregated sex and gender data where this information has been collected, and consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.</i>
Population characteristics	<i>Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."</i>
Recruitment	<i>Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.</i>
Ethics oversight	<i>Identify the organization(s) that approved the study protocol.</i>

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is 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/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Ecological, evolutionary & environmental sciences study design

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

Study description	The FACE facility comprises six experimental arrays surrounding plots of approximately 30 m diameter. CO ₂ -enriched air (1-2% by volume) is released from vertical vent pipes in three of the arrays to attain a target CO ₂ concentration at plot center that is 150 ppm above ambient CO ₂ .
Research sample	The study site is a deciduous forest dominated by 180-year old <i>Quercus robur</i> L. trees, which represent 92% of the forest's basal area. The forest canopy is 24-26 m high with a leaf area index of the overstory of about 6. The forest understory comprises <i>Corylus avellana</i> L. coppice, <i>Acer pseudoplatanus</i> L., <i>Crataegus monogyna</i> Jacq., and a few individuals of other broadleaf species.
Sampling strategy	All trees with dbh>10 cm within the defined plts were measured. Leaf litter was collected in 2 or 3 traps per plot (201-2020) and 6 traps per plot (2020-2022). Fine-root production was measured in 5 in-growth cores per plot.
Data collection	Dendrobands were measured by MEC and AGJ (2016-2018), RJN and CM (2019) and RTG (2020-2023). TLS data were collected by KVV. Tree rings were collected by NJL and CM and analyzed by NJL. Exudation was measured by MKR. Litter was collected by DB. Fine root were measured by ARS and AK
Timing and spatial scale	Dendrobands were measured approximately monthly between April and December. TLS scan was done in in January and February 2022. Tree rings were collected in June 2021 and August 2022. Litter was collected monthly from March-October and weekly from mid-October to mid-December. Exudation was measured in August and November 2020 and March and June 2021. Fine root in-growth cores were processed on 4/27/21, 9/7/21, 1/18/22, 5/9/22, 9/12/22, and 1/23/23.
Data exclusions	No data were excluded
Reproducibility	The experiment cannot be repeated.
Randomization	CO ₂ treatments were randomly assigned to the experimental plots, which were laid out without bias. Tree growth per plot after CO ₂ treatment was initiated was normalized to pretreatment differences based on average basal area increment from 2011-2015 from tree ring analysis.
Blinding	Blinding was not possible because the data were collected in the plots with defined treatments.
Did the study involve field work?	<input checked="" type="checkbox"/> Yes <input type="checkbox"/> No

Field work, collection and transport

Field conditions	The site is accessible by road, PPE is required for all researchers, and buildings on site provide protection from adverse weather. Mean annual maximum and minimum temperatures (1991 – 2020) were 13.5 and 6.0 °C with 676 mm precipitation.
Location	central England: 52.801°N, 2.301°W
Access & import/export	Leaf, root, and soil samples are maintained on site or at the University of Birmingham.
Disturbance	FACE facility construction was engineered to minimize tree removal. No vegetation is removed from the experimental plots and soil sampling is confined to defined locations.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involvement in the study
<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 and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

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