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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.

Stat	istics
For all	ctaticti

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
The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
A statement on 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 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)
For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted Give <i>P</i> 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 <i>d</i> , Pearson's <i>r</i>), indicating how they were calculated
Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.
Software and code
Policy information about <u>availability of computer code</u>
Data collection Matlab 2020b, Java Script

Custom MATLAB (R2020b) code, SPM12, MarsBaR toolbox (V0.45) Data analysis

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 and code used for this manuscript can be accessed here: https://github.com/caromc03/Smoker-s-Forward-Thinking

Research involving human participants, their data, or biological material

Policy information about studies with <u>human participants or human data</u>. See also policy information about <u>sex, gender (identity/presentation)</u>, <u>and sexual orientation</u> and <u>race, ethnicity and racism</u>.

Reporting on sex and gender

Sex was considered in the study designed and determined based on self-reporting. Consent has been obtained for sharing of individual-level data. Data collected on sex was collected in Prolific for the online sample and in the University of Texas at Dallas and the University of the Texas Southwestern Medical Center for the in-person sample. Online Sample Reporting on sex: 41 male and 31 female smokers, 93 male and 54 female non-smokers. In-person Reporting on sex 14 male and 3 female smokers, 14 male and 11 female non-smokers.

Reporting on race, ethnicity, or other socially relevant groupings

Participants self-reported race and ethnicity. The following races where reported:

- Asian: A person having origins in any of the original peoples of the Far East, Southeast Asia, or the Indian subcontinent, including, for example, Cambodia, China, India, Japan, Korea, Malaysia, Pakistan, the Philippine Island, Thailand, and Vietnam. (Note: Individuals from the Philippine Islands have been recorded as pacific islanders in previous data collection strategies.)
- Black or African American: A person having origins in any of the black racial groups of Africa.

White: A person having origins in any of the original peoples of Europe, the Middle East or North Africa.

Ethnicity was reported as yes/no to the following question:

- Do you consider yourself to be Hispanic or Latino? Hispanic or Latino: A person of Mexican, Puerto Rican, Cuban, South or Central American or other Spanish culture or origin, regardless of race.

Confounding variables related to race and ethnicity were controlled by matching these demographics across smoker and non-smoker samples.

Population characteristics

Demographics were controlled across smoker and non-smoker samples. Samples were matched based on sex handedness, education, and age.

Recruitment

For in-person recruitment, we distributed flyers across the Dallas-Fort Worth (DFW) metropolitan area targeting diverse locations such as bars, convenience stores and coffee shops. While efforts were made to promote study participation across various local communities, it is important to acknowledge the potential for selection bias towards individuals interested in science and research. Additionally, the in-person sample had a low representation of women smokers.

We consequently expanded our recruitment efforts by obtaining a larger online sample through Prolific. Here, the male-to-female ratio displayed less bias, and a broader range of nicotine users was included to investigate the generalizability of the from the in-person sample. Again, it is crucial to note a selection bias in this online sample, as Prolific users are likely to be motivated to support research and science.

To reduce selection biases of the present study, future research should explore the influence of motivation for science among both nicotine users a non-users on the outcomes related to forwarding thinking and downstream effects of current actions. Additionally, larger-scale studies are warranted to address the potential sex differences in nicotine addiction-related neural mechanisms.

Ethics oversight

The fMRI study was approved by the Institutional Review Board of the University of Texas at Dallas and the University of the Texas Southwestern Medical Center. The online study was approved by the Institutional Review Board at the Icahn School of Medicine at Mount Sinai. All participants signed informed consent before participating in the study.

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 bel	ow that is the best fit for your research. It	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 <u>nature.com/documents/nr-reporting-summary-flat.pdf</u>

Behavioural & social sciences study design

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

Study description

The study was designed to collect quantitative data by having participants play a two-party exchange task in a Phillips 3T MRI (inperson sample) or play the same economic exchange task in Prolific (online sample).

Research sample

In-person: non-nicotine users were chosen from a previously published sample (Na et al., 2021). Participants are individuals from the Dallas-Forth Worth metropolitan area. We provide tables with the complete demographics in Table 1. Mean age for nicotine users is 36.88(10.44) & 31.16(11.08) for non-users. Please see above for sex reporting.

Sampling strategy

We utilized a combined snowballing and randomized sampling approach for the in-person study. Flyers were distributed around the Dallas-Fort Worth (DFW) metropolitan area, including venues like bars, convenience stores, and coffee shops. This strategy aimed to

encourage participation through both word of mouth (snowball effect) and random encounters with flyers. Meanwhile, the online sampling method was randomized within a pool of Prolific users.

A previous study conducted by our lab (Na et al., 2020) focused on forward thinking in healthy participants (N = 48) employed the same fMRI task paradigm. This earlier study revealed a Cohen's d of 0.63 for the main effect of offer size. Based on this finding, we estimated a minimum sample size of n = 17 in each condition to acheive 80% power in detecting an effect at alpha = 0.05 (two-tailed).

Data collection

No individuals were present during data collection aside from participant and researcher. Devices used: Phillips 3T MRI

Timing

Data for the in-person samples was collected in 2017-2018. Data for the online samples were collected in 2020. Data analysis was conducted from 2021-2022.

Data exclusions

Recruitment exclusion criteria: The exclusion criteria were any major medical, neurological, or psychiatric conditions; any incompatibility with MRI safety (e.g. metal implants); and any dependence on substances other than nicotine and alcohol (nicotine users) or any substance dependence (non-nicotine users).

Participant exclusions: Non-nicotine in person users were chosen from a previously published sample (Na et al., 2021) to match with nicotine users based on sex, handedness, education, and age. Participants that did not match with the non-smoker sample in this previous study were excluded. Similarly, the online-sample smokers and non-smokers were matched based on demographics and remaining non-matched participants were excluded.

Task exclusions: The first 5 trials were excluded from all participants' data to allow behavior to stabilize after participants explored the contingencies of the task in these initial trials. The last 5 trials from the nicotine users' responses were excluded given that there was less incentive to reject offers closer to the end of the game.

Non-participation

There are no dropouts in the study given that the task was completed in one session. No follow up studies were needed.

Randomization

Experimental groups were determined based on nicotine use (not randomized). The criteria for in-person nicotine-smoker recruitment included participants who smoked more than 10 cigarettes daily for at least a year and were fluent in English. In addition to assessing smoking habits, participants are categorized based on nicotine dependence using the Structured Clinical Interview for DSM Disorders. The criteria for online nicotine smokers recruitment included participants that smoked at least one cigarette per week (wider range of nicotine users). Covariates for both in-person and online participants were controlled by matching across nicotine users and non-users based on sex, age, education, and handedness

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.

Ma	iterials & experimental systems	Me	thods
n/a	Involved in the study	n/a	Involved in the study
\times	Antibodies	\boxtimes	ChIP-seq
\boxtimes	Eukaryotic cell lines	\boxtimes	Flow cytometry
\times	Palaeontology and archaeology		MRI-based neuroimaging
\boxtimes	Animals and other organisms		
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\times	Dual use research of concern		
\boxtimes	Plants		
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Plants

Seed stocks

Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.

Novel plant genotypes

Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor

Authentication

Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.

Magnetic resonance imaging

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Design type

Design is task and event related

Design specifications

The task consisted of two blocks with two experimental conditions ('Controllable' vs. 'Uncontrollable'). The original task with healthy controls included 40 trials per condition and nicotine users played a slightly shorter version of 30 trials that were shown to generate similar results (Na et al., 2021). Nevertheless, to match the task length between nicotine users and non-nicotine users, only the first 30 trials from healthy control data were included in the analyses.

Behavioral performance measures

Behavioral performance measures were taken from our economic exchange task: 1) Rejection rate of offers (total and divided by offer size), 2) offer sizes (mean and trial to trial), 3) self-reported perceived influence over their partners' offers in each condition using a scale from 0 to 100 ("perceived controllability).

Acquisition

Imaging type(s)

Functional and anatomical (used only for coregistration)

Field strength

3T

Sequence & imaging parameters

High-resolution T1-weighted scans $(1.0 \times 1.0 \times 1.0 \text{ mm})$ were acquired using a 3D magnetization prepared rapid gradient-echo (MPRAGE) sequence. Functional images were acquired using echo-planar imaging (EPI) and tilted 30° from AC-PC axis. The detailed settings for the functional imaging were repetition time (TR) = 2,000 ms, echo time (TE) = 25 ms, flip angle = 90°, voxel size = $3.4 \times 3.4 \times 4.0$ mm, 38 slices.

Area of acquisition

Both whole brain and regions of interest where used. Coordinates were chosen from an independent studies (see below for coordinates)

Diffusion MRI

Used

Not used

Preprocessing

Preprocessing software

Scans were preprocessed using standard statistical parametric mapping (SPM12, Wellcome Department of Imaging Neuroscience; https://www.fil.ion.ucl.ac.uk/spm/) algorithms, including slice timing correction, co-registration, and smoothing with an 8 mm Gaussian kernel.

Normalization

The mean functional images for each subject were co-registered to the subject's high-resolution T1 structural scan, using a 12-parameter affine transformation. The participant's T1 image was segmented into gray and white matter and then normalized using nonlinear basis functions to the Montreal Neurological Institute (MNI) space with the functional images normalized to the template and resampled into 2 mm×2 mm functional voxels.

Normalization template

Images were normalized into group-space using the Montreal Neurological Institute (MNI) template.

Noise and artifact removal

To account for large head movements, we used the ArtRepair toolbox52 to examine and repair volumes with large motion artifacts. We used the art_motionregress and art_global modules of the single subject pipeline. The ArtRepair algorithm was further used to generate the motion parameters to be included in the GLM design matrix. Volumes were examined for fast head movements using the automated defaults such that volumes with movement of >0.5 mm/TR were tagged and interpolated with the nearest usable volumes. A temporal high-pass filter of 128 Hz was applied to the fMRI data, and temporal autocorrelation was modeled using a first-order autoregressive function.

Volume censoring

No volumes were censored

Statistical modeling & inference

Model type and settings

We conducted general linear modeling (GLM) of the functional scans to examine the neural correlates of forward thinking value as well as norm prediction errors (PEs). The following event regressors were included: 1) offer onset, 2) choice submission, 3) outcome onset, and 4) perceived controllability rating. Importantly, we specified a parametric modulator of the forward projected choice value from the 2-step model, normalized at the individual level, at the onset of choice submission. A separate GLM was conducted in which norm PE replaced the total choice values as the parametric regressor to examine the neural representation of norm PEs. In both GLMs, six motion parameters were included as covariates.

Contrast images representing either total choice value or norm prediction error at the individual level were entered into a one-way between-subject ANOVA test for the whole-brain map to compare neural differences between nicotine users and non-nicotine users (PFDR < 0.05 and k > 50).

Effect(s) tested

One-way between-subject ANOVA test for the whole-brain map

Specify type of analysis:

Whole brain

ROI-based

⊠ Both

Anatomical location(s)

Beta values representing choice value-related activations were extracted using the MarsBar toolbox from an 8-mm radius sphere of the vmPFC using coordinates [-2, 50, -2] from an independent study (D'Argembeau et al., 2011). Beta values representing norm PE were extracted at a coordinate of the midbrain [-4, -26, -11] on an 8-mm radius sphere, from an independent study (Murty et al., 2011).

Statistic type for inference

(See Eklund et al. 2016)

In the fMRI GLM analyses statistical inference was made based on the F statistics derived from whole-brain ANOVA statistical maps. Significant effects were identified at P < 0.05 family-wise error cluster-corrected at a cluster-defining threshold of P < 0.005, uncorrected with a cluster size threshold of P < 0.005, uncorrected with a cluster size threshold of P < 0.005, uncorrected with a cluster size threshold of P < 0.005, where P < 0.005 is a cluster size threshold of P < 0.005. We relied in cluster-extend thresholding in our statistical inference in order to allow sufficient sensitivity to detect effects given the experimental sample size.

Correction

Significant effects were identified at P < 0.05 family-wise error cluster-corrected at a cluster-defining threshold of P < 0.005, uncorrected with a cluster size threshold of k = 50.

Models & analysis

n/a	Involved in the study
\boxtimes	Functional and/or effective connectivity
\boxtimes	Graph analysis
\boxtimes	Multivariate modeling or predictive analysis