SUPPLEMENTARY MATERIAL

The architecture of abnormal reward processing in dementia: multimodal hedonic phenotypes and brain substrate, by A Chokesuwattanaskul et al

Multiple correspondence analysis: background and rationale

Multiple correspondence analysis (MCA) is a type of exploratory factor analysis specifically designed for categorical datasets, analogous to principal component analysis on continuous datasets. One distinct advantage of MCA is that it does not assume any particular distribution of the data. MCA projects the data onto a lower dimensional space that maximally retains the information of the initial data, and allows simultaneous examination of all potentially relevant variables (a further advantage over conventional pair-wise associations). Because MCA is conducted at the level of response categories rather than variables, it allows the relationship between each response category and variable to be characterised. For example, if there are three types of responses (increased, decreased, no change) for a particular reward behaviour, MCA will generate three variables to represent these response categories, represented in an 'indicator matrix', where each row corresponds to a participant and each column represents a response category.

After the indicator matrix is derived, it is transformed into a probability matrix where each element is divided by the grand sum of the matrix, hence the name. The final step is to apply singular vector decomposition on the "standardised" probability matrix, to generate the eigenvectors of rows and columns and a matrix of eigenvalues. Intuitively, eigenvectors of this standardised probability represent the explained variance (information) in different, orthogonal dimensions. We reduce the dimension to match the desired number of factors: the eigenvectors and eigenvalues, standardised by the magnitude of the sum of the row and column values in the probability matrix, are used to generate row and column factor scores.

Each factor acts as a 'latent variable' that explains a portion of the variance in the data. The first factor accounts for the largest portion of explained variance; each subsequent factor is orthogonal to the former factors and describes a portion of the remaining variance. In general, the 'elbow' on the scree plot of explained variance is used to determine the number of factors to retain. Additionally, it is recommended that all retained factors together explain > 70% of the total variance ('inertia'). Here, the principal factors 1 and 2 are column factors: they represent a portion of variance in the column dimension of the data. The correlation (squared cosine) of a feature on a particular factor quantifies the strength of association

between them - a measure of the quality of representation of the feature by that factor, or how well the feature (presence vs. absence) is discriminated by the factor. Higher squared cosine values correspond to greater discriminatory power. The sum of squared cosine values across all retained factors denotes how well each feature is represented by the retained factors (normalised between 0 and 1, a value closer to 1 signifying that the feature is well represented).

Another useful property of MCA is that it allows additional data not included explicitly in the original analysis to be mapped as "supplementary data" onto the same dimensions as the original model. In other words, MCA allows us to map new data points, whether a new observation or a new feature (here, diagnostic groups), into the common, derived factor space. We can derive the factor values for the supplementary feature by exploiting the information derived from singular vector decomposition. If the original features are represented in the matrix $f(COL)$ x $f(ROW)$, a supplementary feature, c_1, is mapped into the column factor space as: $f(COL + c_1)$ x $f(ROW)$; the additional information will be f(c_1) x f(ROW)). Such supplementary features do not affect the factor analysis of the original data, however, this process allows them to be assessed (and visualised) in a common space with the original features.

Cluster stability analysis: background

Cluster stability analysis¹ is a form of sensitivity analysis used for evaluating the performance of clustering algorithms. Here, we employed a bootstrapping technique that subsamples a designated proportion (here, 80%) of data from the whole dataset, with replacement after each iteration. The kmeans clustering algorithm was applied on all subsampled data. In each iteration, the similarity of the clustering result on the subsample with the entire original dataset was determined by calculating the mean percentage of participants in each cluster who belonged to the same cluster in the original analysis, across all clusters (see Supplementary Figure 3). A similarity of 100% would signify all participants in each cluster in the subsample were included in the same clusters in the original analysis on the entire dataset. A cluster stability index was derived by averaging the percentage similarity of every subsample over the assigned number of iterations.

Brain imaging acquisition and pre-processing

For each patient, a sagittal 3D magnetization-prepared rapid-gradient echo T1-weighted volumetric brain MRI sequence (TE/TR/TI 2.9/2200/900ms, dimensions $256 \times 256 \times 208$, voxel volume of 1.1 \times 1.1×1.1 mm) was acquired on a Siemens Prisma 3T MRI scanner using a 32- channel phased-array head-coil and pre-processed using standard procedures in SPM12 (www.fil.ion.ucl.ac.uk/spm, details in

Supplementary material). Ninety-six volumetric brain MRI scans from the patient cohort (22 bvFTD, 23 AD, 20 nfvPPA, 20 svPPA, 11 lvPPA) were included in the VBM analysis. Twenty-three patients were excluded either because their scan was unavailable or of inadequate quality. Pre-processing of brain images was performed using the New Segment and Diffeomorphic Anatomical Registration Through Exponentiated Lie Algebra (DARTEL) toolboxes on SPM12, following an optimised protocol. Normalisation, segmentation, and modulation of grey and white matter images were performed using default parameter settings. Grey matter images were smoothed using a 6 mm full-width-at-halfmaximum Gaussian kernel. A study-specific template brain image was created by warping all biascorrected native space brain images to the final DARTEL template and calculating the average of the warped brain images. Total intracranial volume for each participant was calculated by summing grey matter, white matter and cerebrospinal fluid volumes.

Supplementary Table 1. Neuropsychological and general behavioural characteristics of participant

groups

Counts (percentage of group) are shown for behavioural change data; and mean (standard deviation) or median (interquartile range) scores are shown for neuropsychological tests (with maximum scores in parentheses). Differences between diagnostic groups were assessed using ANOVA, Kruskal-Wallis test and chi-square test with post-hoc correction. Significant differences between patient groups and healthy controls are in bold; significant differences between patient groups are coded as follows: ¹significantly different from AD, 2 significantly different from lvPPA, 3 significantly different from bvFTD, 4 significantly different from svPPA, 5 significantly different from nfvPPA (all p_{FDR} < 0.05). AD, patient group with typical Alzheimer's disease; BPVS, British Picture Vocabulary Scale (Dunn, Dunn and Whetton, 1982); bvFTD, patient group with behavioural variant frontotemporal dementia; Controls, healthy control group ; D-KEFS, Delis Kaplan Executive System (Delis et al., 2001); DS, Digit Span; GDA, Graded Difficulty Arithmetic test (Jackson and Warrington, 1986); GNT, Graded Naming Test (McKenna and Warrington, 1983); lvPPA, patient group with logopenic variant primary progressive aphasia; nfvPPA, patient group with nonfluent/agrammatic variant primary progressive aphasia; PIQ, performance IQ; RMT, Recognition Memory Test (Warrington, 1984); svPPA, patient group with semantic variant primary progressive aphasia; TMT, trail making test; VIQ, verbal IQ; VOSP, Visual Object and Space Perception Battery – Object Decision test (Warrington, McKenna and Orpwood, 1998); WASI, Wechsler Abbreviated Scale of Intelligence (Wechsler, 1997). A reduced number of participants completed certain tests, as follows: ^an-1, ^bn-2, ^cn-3, ^dn-4, ^en-5, ^fn-6, ^gn-7, ^hn-8, ^mn-13.

Respondents were patients' primary caregivers or healthy control participants. Prior to completing the survey, caregivers were instructed that a relevant behavioural 'change' in a particular reward domain might comprise an evident alteration in liking, enjoyment and/or interest (e.g., seeking or avoidance of the relevant item) that the caregiver had observed in the person with dementia.

Supplementary Table 3. Caregiver comments extracted from the reward behavioural symptom survey

Representative comments from primary caregivers completing the symptom survey about patients' reward behaviours are presented here. AD, patients with typical Alzheimer's disease; bvFTD, patients with behavioural variant frontotemporal dementia; lvPPA, patients with logopenic aphasia; nfvPPA, patients with progressive non-fluent aphasia; svPPA, patients with semantic dementia.

Supplementary Table 4. Correlations of reward features with principal factors

This table displays the squared cosine value for each reward feature with the two principal factors (factor 1 and factor 2) identified from the multiple correspondence analysis. The sum of the squared cosines from factor 1 and factor 2 for each feature is shown in the column 'Sum'. Features with a high sum of squared cosine values (sum close to 1) are well-represented by the two principal factors. Dec, decreased; Inc, increased.

Supplementary Table 5. Associations of principal reward factors with general disease characteristics and socio-emotional behaviours

The table summarises the association of principal factors 1 and 2 with MMSE score and general socioemotional behaviours across the combined patient cohort. Spearman's rho correlation coefficients and associated p values are shown for MMSE score; median (interquartile range) values are shown for patient subgroups reporting presence vs absence of each socio-emotional behaviour, together with p values of each subgroup comparison (assessed using Mann-Whitney U tests). MMSE, Mini-Mental State Examination score.

Supplementary Table 6. Demographic, clinical and neuropsychological characteristics of patients in each reward behavioural cluster

Counts (standard deviation) are shown for general demographic and clinical data; counts (percentage of group) are shown for diagnostic syndromes and behavioural change data; and mean (standard deviation) or median (interquartile range) scores are shown for neuropsychological tests (with maximum scores in parentheses). Differences between reward behavioural clusters were assessed using ANOVA, Kruskal-Wallis test and chisquare test with post-hoc correction. Significant differences (p_{FDR} < 0.05) compared with the 'control-like' cluster are in bold; significant differences compared with other reward clusters are coded as follows: ¹significantly different from 'reward-seeking' cluster, ²significantly different from 'reward-restricted' cluster, ³significantly different from 'eating-predominant' cluster (all p_{FDR}<0.05). AD, patient group with typical Alzheimer's disease; BPVS, British Picture Vocabulary Scale (Dunn, Dunn and Whetton, 1982); bvFTD, patient group with behavioural variant frontotemporal dementia; Controls, healthy control group; D-KEFS, Delis Kaplan Executive System (Delis et al., 2001); DS, Digit Span; f, female; GDA, Graded Difficulty Arithmetic test (Jackson and Warrington, 1986); GNT, Graded Naming Test (McKenna and Warrington, 1983); Handed, handedness; Illness, estimated symptom duration; L, left; lvPPA, patient group with logopenic variant primary progressive aphasia; m, male; MMSE, Mini-Mental State Examination score (Folstein, Folstein and McHugh, 1975); nfvPPA, patient group with nonfluent/agrammatic variant primary progressive aphasia; no., number; PIQ, performance IQ; R, right; RMT, Recognition Memory Test (Warrington, 1984); svPPA, patient group with semantic variant primary progressive aphasia; TMT, trail making test; VIQ, verbal IQ; VOSP, Visual Object and Space Perception Battery – Object Decision test (Warrington, McKenna and Orpwood, 1998); WASI, Wechsler Abbreviated Scale of Intelligence (Wechsler, 1997); y, years. A reduced number of participants completed certain tests, as follows: a_n-1 , b_n-2 , c_n-3 , d_n-4 , e_n-5 , f_n-6 , g_n-7 , h_n-8 , i_n-9 , j_n-10 , k_n-11 , l_n-12 .

Supplementary Table 7. Prevalence of reward behavioural changes in all reward behavioural clusters

This table summarises the prevalence of altered reward behaviours in each hedonic domain for each reward cluster, as determined from the symptom survey (see text and Supplementary Table 2); raw counts and percentage of group are indicated. Significant differences (chi-square test with post-hoc $p_{FDR} < 0.05$) compared with the 'control-like' cluster are in bold; significant differences compared with other reward clusters are coded as follows: ¹significantly different from 'reward-seeking' cluster, ²significantly different from 'reward-restricted' cluster, 3significantly different from 'eating-predominant' cluster. Change, overall frequency and dominant direction of behavioural alteration (see main text, Supplementary Tables 2 and 3).

Supplementary Figure 1. A scree plot showing the eigenvalue (y-axis) of each principal factor from the multiple correspondence analysis of all reward features, after applying the Greenacre correction method. The proportion of explained variance (%) is shown for each principal factor. The 'elbow' in the plot trajectory indicates that most variance is accounted for by the first two principal factors.

Supplementary Figure 2. A scree plot showing the value of the sum of squared errors at each number of clusters, derived from a k-means clustering algorithm on the first and second principal factors representing reward features. The 'elbow' in the plot trajectory indicates that most variability is accounted for by cluster $n = 4$.

Supplementary Figure 3. A histogram showing the output of the cluster stability analysis. The x-axis shows the average percentage similarity between clusters in each subsample and the original clusters; the y-axis displays the count of the subsamples. The cluster stability analysis was performed by iteratively sampling 80% of the original data and applying the k-means clustering algorithm on the resampled dataset with replacement after each of 5000 iterations. From the graph, most iterations resulted in an average cluster similarity percentage >95%. The cluster stability index (average subsampled cluster similarity) over all 5000 iterations was 97.5%.

References

1. Ben-Hur A, Elisseeff A, Guyon I. A stability based method for discovering structure in clustered data. *Pac Symp Biocomput*. 2002:6-17.