Universiteit Leiden
The Netherlands

Eating disorder psychopathology dimensions based on individual co-occurrence patterns of symptoms over time: a dynamic time warp analysis in a large naturalistic patient cohort

Landt, M.C.T.S.O.; Dingemans, A.E.; Giltay, E.J.

ORIGINAL ARTICLE

Eating disorder psychopathology dimensions based on individual co-occurrence patterns of symptoms over time: a dynamic time warp analysis in a large naturalistic patient cohort

Margarita C. T. Slof-Op 't Landt[1,2] · Alexandra E. Dingemans[1,2] · Erik J. Giltay[2]

Abstract

Purpose Most of the network approaches in eating disorders found the highest degree of centrality for symptoms related to weight and shape concerns. However, longitudinal analyses are scarce and may increase our insight of the complex characteristics and dynamics over time. In the current study, an alternative non-linear method to perform longitudinal network analyses, the dynamic time warp approach, was used to examine whether robust dimensions of eating disorder psychopathology symptoms could be found based on the individual dynamic interplay of eating disorder symptoms co-occurrence patterns in time.

Methods The study sample included a naturalistic cohort of patients ($N = 255$) with all eating disorder subtypes who were assessed with the eating disorder examination questionnaire (EDE-Q) at a minimum of four times during treatment. Dynamic time warp analyses yielded distance matrices within each individual patient, which were subsequently aggregated into symptom networks and dimensions at the group level.

Results Aggregation of the individual distance matrices at the group level yielded four robust symptom dimensions: 1. restraint/rules, 2. secret eating/fasting, 3. worries/preoccupation, and 4. weight and shape concern. The items 'fear of weight gain' and 'guilt' were bridge symptoms between the dimensions 1, 3 and 4.

Conclusion Dynamic time warp could capture the within-person dynamics of eating disorder symptoms. Sumscores of the four dimensions could be used to follow patients over time. This approach could be applied in the future to visualize eating disorder symptom dynamics and signal the central symptoms within an individual and groups of patients.

Level of evidence Level III: evidence obtained from well-designed cohort or case–control analytic studies.
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Introduction

The increasingly applied network approach in psychopathology conceptualizes symptoms as mutually interacting, often reciprocally reinforcing, elements of a complex network [1, 2]. According to this theory, symptoms are not merely observable indicators of an underlying disorder, rather they should be viewed as components that constitute the disorder through their relationships with one another. In a psychopathology network, the symptoms are represented as nodes which are connected through a set of edges representing the associations between these symptoms [1]. In weighted networks, the thickness of the edge signifies the strength of the association and hence the probability that activation of one symptom will be associated with activation of symptoms connected to it [2]. Depending on their position within a network, some symptoms seem to be more important or central than others. These central symptoms have strong connections to other symptoms in the network, and because of

✉ Margarita C. T. Slof-Op 't Landt
r.slof@rivierduinen.nl

1   Rivierduinen Eating Disorders Ursula, PO Box 405, 2300 AK Leiden, The Netherlands

2   Department of Psychiatry, Leiden University Medical Center, Leiden, The Netherlands

these strong connections, it is hypothesized that they could be maintaining the network [1, 3].

Within the eating disorder field, the application of network theory is thought to lead to new knowledge regarding the development and maintenance of eating disorders, and ultimately may enable improvement of both classification and treatment approaches [4]. The majority of the cross-sectional network approaches performed so far found the highest degree of centrality for symptoms related to weight and shape concerns [4–8]. This seems to indicate that weight and shape concerns are the most important symptoms in maintaining an eating disorder [1, 3]. A finding consistent with the transdiagnostic model, which posits that overvaluation of weight and shape forms the core psychopathology for all eating disorders' subtypes [9].

Longitudinal network analyses in eating disorders, which may increase our insight of the complex dynamics over time, are scarce. Such studies enable the disentanglement of the complex temporal dynamics of interacting eating disorder symptoms both at the group and individual level. Levinson and colleagues conducted four of these longitudinal network studies [10–13]. At the group level, again, symptoms related to weight and shape concerns were found to be central across most network types and time [10, 11, 13]. However, intra-individual network analyses showed a large heterogeneity between patients in the centrality of specific eating disorder cognitions and behaviours [10–13] translating in diverse symptom trajectories. In other words, symptoms may follow markedly different paths between patients [14]. This latter finding stresses the importance of investigating individual networks further, since these may foster precision medicine in eating disorders, because specific (subgroups of) patients may need a different focus in their treatment.

Most longitudinal network research to date has used vector autoregressive models. Despite various strengths, these traditional models need many assessments (intensive time-series data), and rely on several assumptions including linearity of associations and fixed time intervals between successive assessments [15]. Furthermore, if changes in symptoms occur over longer periods of time than the preceding assessment point, they cannot always be recognized as being associated within these traditional models. This could lead to difficulties when working with data from clinical practice, which are rarely intensive times series data, and many of the assumptions are difficult to be met. An alternative non-linear method to perform longitudinal network analyses is the dynamic time warp approach in which 'elastic' distance measures are used [14, 16]. The dynamic time warp method calculates the distance for each pair of symptoms (between each symptom and all the other symptoms) in the model across several time points (time series). In Fig. 1a, b, 2 examples of such a time series are presented (the scores of 2 symptoms across 27 time

points). The distance between the two time series can be calculated to determine the similarity between them. This distance could be calculated by summing up the differences between the two symptoms at the same time point, the so-called Euclidian distance (represented in Fig. 1c, d). However, this will yield a rather poor similarity metric, since two symptoms will not always change at the same pace in time. The dynamic time warp looks for the best alignment between the two times series (Fig. 1e, f), allowing similar scores to match even if they are not measured at the exact same time point. This can lead to a better similarity score, as can be seen when comparing the distance measures between Fig. 1c, e. The method therefore takes into account that causal associations between symptoms may exist over a range of time intervals. An advantage of the dynamic time warp approach when using naturalistic clinical data is that it is also a robust method when having sparse panel data. In daily clinical practice, it is not always feasible for patients to complete many assessments in a short period of time, but based on the standard recurring assessments during treatment the dynamic time warp could be used to examine longitudinal relationships over a longer period of time. Another advantage of the dynamic time warp method is that it first identifies co-occurrence patterns on an individual level and then aggregates these to identify symptom dimensions on the group level. In this way, the relationships within each individual patient are taken into account to identify clusters of symptoms which are consistent on the group level.

The main aim of the present study was to investigate which eating disorder symptoms dynamically cluster together in individuals over the course of treatment, and whether temporal dimensions of eating disorder symptoms could be identified at the group level. To our knowledge, this is the first study to examine the temporal dynamics of interacting eating disorder symptoms and to identify bridge symptoms over time between eating disorder symptom dimensions. For these analyses, we used longitudinal data, assessed during Routine Outcome Monitoring (ROM), from the Eating Disorder Examination Questionnaire (EDE-Q [17]) in a naturalistic cohort of treatment seeking individuals with all eating disorder subtypes ($N = 255$). The first research question was whether robust dimensions of eating disorder psychopathology symptoms could be found based on the individual dynamic interplay of eating disorder symptoms co-occurrence patterns in time. It was expected, despite the heterogeneity between individuals, that the dynamic time warp analyses would yield several robust eating disorder psychopathology dimensions at the group level. Based on the results of previous cross-sectional and longitudinal network analyses in eating disorders, we expected that one of the dimensions would exist of symptoms related to shape and weight concerns. In addition, we expected that items
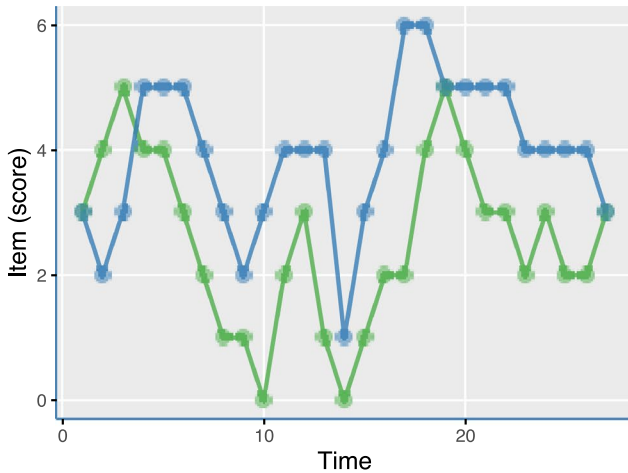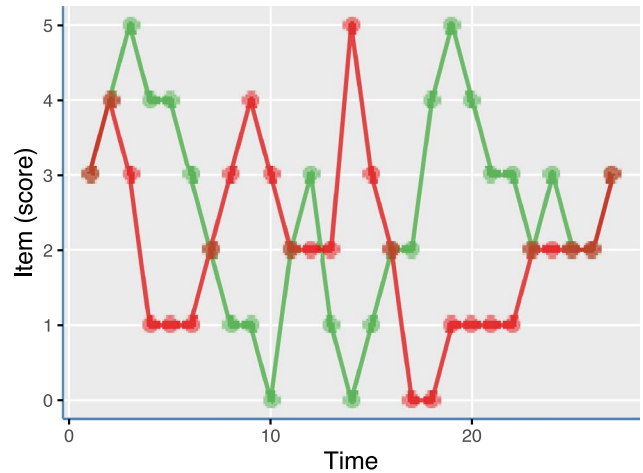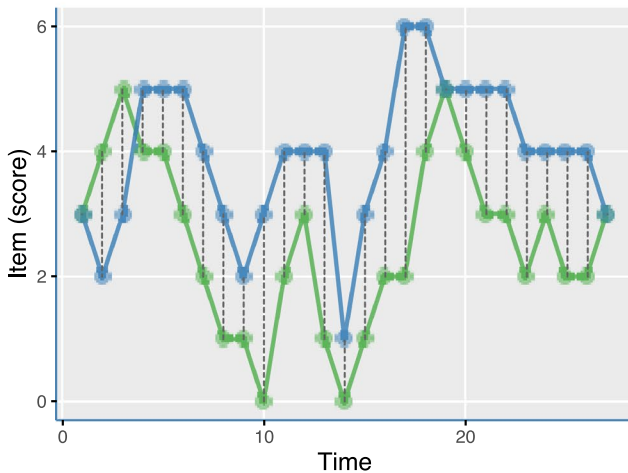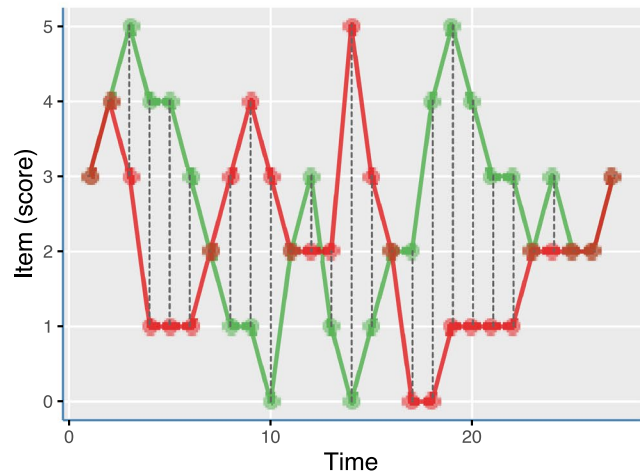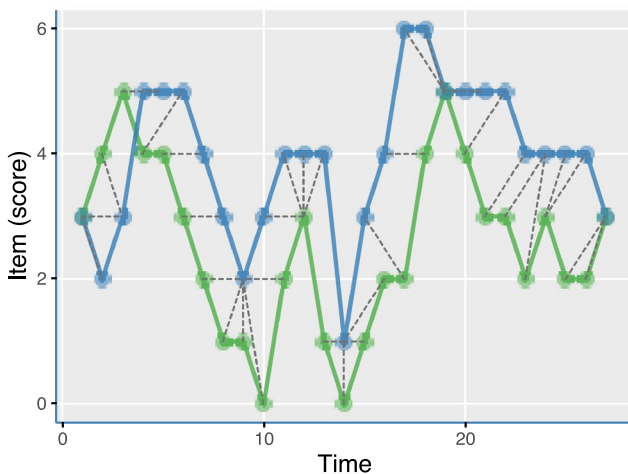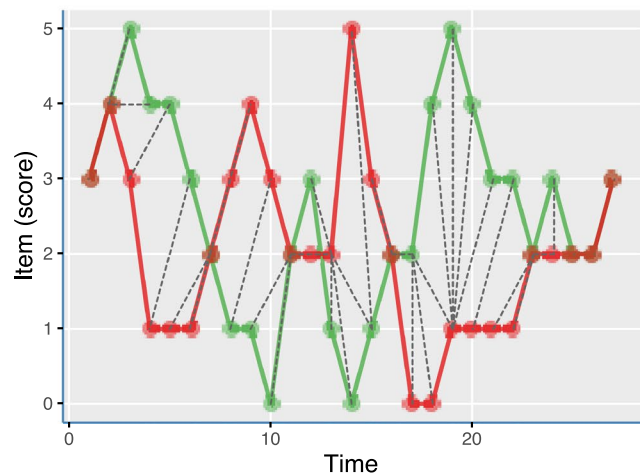
Fig. 1 Explanation of the dynamic time warp method. **a**, **b** Times series comprised of raw scores on two symptoms assessed at 27 time points are depicted. **c**, **d** The Euclidian distance between the two times series is calculated, meaning the summed distance scores between the symptoms that were assessed at the same time point. **d**, **e** the dynamic time warp method is shown to calculated the distance between the two time series. The dynamic time warp looks for the best alignment between the two times series allowing similar scores to match even if they are not measured at the exact same time point

belonging to the restraint and the eating concerns subscales of the original EDE-Q would also form separate dimensions. The second research question was whether bridge symptoms could be identified among the eating disorder psychopathology dimensions using these dynamic network analyses. None of network analyses that were previously performed identified eating disorder symptom dimensions, and bridge symptoms were only examined if another trait or disorder was investigated in addition to the eating disorder. Because of the high degree of centrality of the symptoms related to weight and shape in previous studies, we expected that some of these would also act as important bridge symptoms between the found dimensions. The third research question was whether these dimensions could be used to characterize the trajectories of (specific subgroups of) patients with an eating disorder. We expected that the changes on the dimensions in time could be used to distinguish patients from each other.

Methods

Participants

All patients with an eating disorder [18] who sought treatment (residential, day, or outpatient) at GGZ Rivierduinen Eating Disorders Ursula between 2003 and 2014, and who were assessed, as part of the ROM, by means of the EDE-Q [17] at a minimum of four times during treatment, were selected for the present study. Before 2012, the ROM assessments took place at the beginning and end of treatment and when treatment setting changed (e.g., from outpatient to inpatient). From 2012 onward, ROM assessments were scheduled every 6 months during treatment. Patients with insufficient mastery of the Dutch language, and patients who were unable to complete assessments due to poor physical condition were ineligible for ROM. Diagnoses were made by a multidisciplinary team of experienced clinicians (psychologists and psychiatrists) specialized in eating disorders, according to the DSM-IV criteria [18], using questions of two standardized semi-structured interviews: the Eating Disorder Examination [19] and the Longitudinal Interval Follow-up Evaluation [20, 21]. The Medical Ethics Committee of the Leiden University Medical Center approved the general study protocol on ROM, in which ROM is considered integral to the treatment process (written informed consent is not institutionally required). All participants gave permission for the anonymized use of their data for scientific purposes [22]. Patient-identifiable data were removed from the database in order anonymize the data and the study was undertaken in accordance with

ethical principles stated in the Helsinki Declaration, and did not lead to extra burden for the patients.

Measures

The EDE-Q is a self-report questionnaire for the assessment of eating disorder-specific psychopathologies. The original 36-item version was used [17]. Twenty-two items assess the core attitudinal features of eating disorder pathology and 14 items assess the frequency of core eating disorder behaviors (e.g. binge eating and extreme methods of weight control) occurring in the preceding 28 days. The 22 items assessing psychopathology are rated on 7-point forced-choice scales (0–6), with higher scores reflecting greater severity or frequency, and were used in the current analyses. The EDE-Q was shown to be reliable and valid in assessing eating disorders [23]. The present study used a Dutch translation of the EDE-Q, which was made with permission of the developers of the questionnaire [17]. The internal Cronbach's alpha in this study was 0.95 [24].

Statistical analyses

To investigate which eating disorder symptoms dynamically cluster together in individuals over the course of treatment, and whether temporal dimensions of eating disorder symptoms could be identified at the group level, several statistical analyses were performed. An overview of the different statistical steps both at the individual and the group level is given in Fig. 2. For further reading, two studies have previously used the dynamic time warp approach in patients with depression [14, 16]. First at the individual level, co-occurrence patterns of the 22 EDE-Q psychopathology items were assessed for each of the 255 patients using dynamic time warp analyses in R [25]. The dynamic time warp was used to calculate distances between each pair of symptoms within each patient, leading to 231 ((22*21)/2) distances per individual. For the two time-series to become optimally aligned, the dynamic time warp uses a dynamic (i.e., stretching and compressing) programming approach to minimize a predefined distance measure [16, 26, 27]. Since the dynamic time warp analysis is a complex and technical topic, we give an example for this specific study. This is illustrated in Fig. 3, in which three exemplar EDE-Q item (item 12 "fear of weight gain", item 15 "guilt", and item 36 "exposure discomfort") time-series are shown for a single patient (no. 128). The trajectories of the raw scores over time (assessment every 6 months) on the three items are presented in Fig. 3a. In Fig. 3c, d, e, the trajectories of each of the possible item pairs (12 vs 15, 12 vs 36 and 15 vs 36) were plotted, to enable calculation of the shortest distance between them. The dotted lines illustrate the warped (i.e. elastic) modification of one item to get an optimal alignment with the scores of
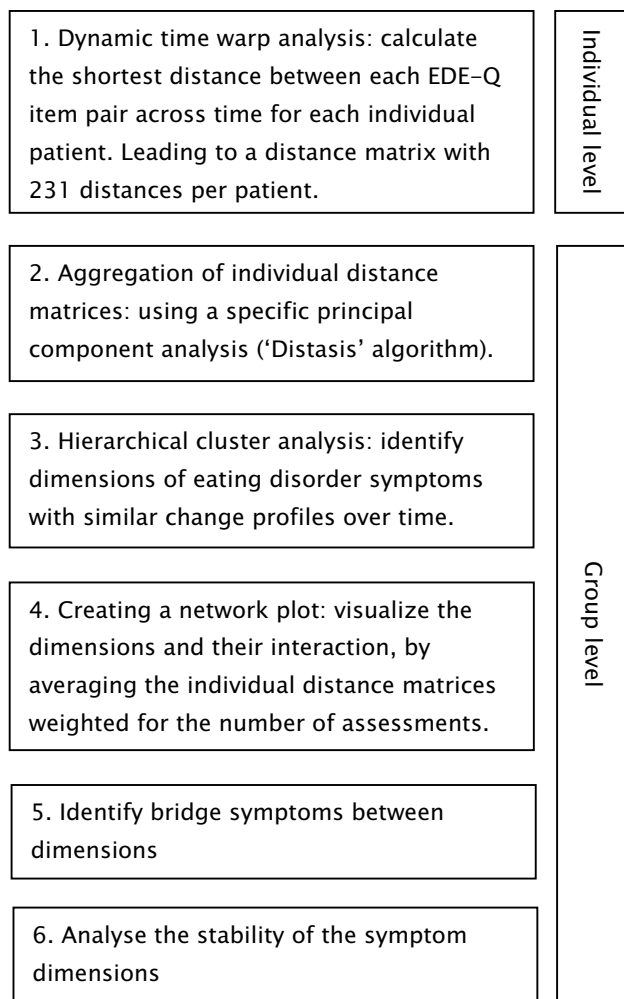
1. Dynamic time warp analysis: calculate the shortest distance between each EDE–Q item pair across time for each individual patient. Leading to a distance matrix with 231 distances per patient.

Individual level

2. Aggregation of individual distance matrices: using a specific principal component analysis ('Distasis' algorithm).

3. Hierarchical cluster analysis: identify dimensions of eating disorder symptoms with similar change profiles over time.

4. Creating a network plot: visualize the dimensions and their interaction, by averaging the individual distance matrices weighted for the number of assessments.

5. Identify bridge symptoms between dimensions

6. Analyse the stability of the symptom dimensions

Group level

Fig. 2 Overview of the statistical analyses that were performed in the current study, starting with the analyses at the individual level (dynamic time warp), and the subsequent statistical steps at the group level to identify the symptom dimensions

the other item. To calculate the dynamic time warp distance (shortest path), a cost matrix was constructed in which the scores of the two items of a pair on the seven time points were plotted; one item on the x-axis, and the other on the y-axis (as presented in the lower part of Fig. 3c, d, e). The timeframe (or step pattern) for matching the two sequences in these analyses was constrained, the eating disorder symptom scores could be matched to a maximum of one time point before $(t - 1)$ or one time point after the current assessment $(t + 1)$. The use of this so-called 'symmetric1' step pattern, with a 'Sakoe-Chiba' window band of 1 (shown in the right part of Fig. 3a), was visualized in the cost matrices (Fig. 3c, d, e) as the orange distance scores, and resulted in the shortest red "warping path". This warping path leads to a distance measure: items with the best alignment, having a more similar slope and changes over time, resulted in the smallest distance. In Fig. 3b, the distances between items

12, 15 and 36, as calculated in the cost matrices (Fig. 3c, d, e) are represented in a distance matrix. It is clear for this particular patient that items 12 and 15 have a more similar trajectory over time (distance score of 9), than the other item pairs (distance score of 16 and 19, respectively). For the dynamic time warp analysis in the current study, all EDE-Q psychopathology items were standardized, in order for distances to be based on the dynamics over time of each pair of items within one individual patient. Similar to the example, the dynamic time warp distances between each symptom pair in each patient were grouped in a distance matrix containing 231 distinct distances per patient. Which, in the total group led to 231 * 255 = 58,905 calculated 'dynamic time warp distances'.

At the group level, the second and third statistical steps (Fig. 2) were performed to investigate whether temporal dimensions of eating disorder symptoms could be identified. A specific type of principal component analysis, the 'Distatis' algorithm [28], was performed to aggregate the 255 distance matrices of the individuals (step 2 in Fig. 2). Distasis is based on a three-way principal component analysis. To compare all 255 distance matrices, it combined them into a common structure called a compromise and then projected the original distance matrices onto this compromise. Compromise factors (i.e., principal components) were estimated. Since the first three compromise factors explain the highest amount of variance, each of the 22 EDE-Q symptoms were plotted on two X–Y planes; one according to the first and second compromise factor and one according to the first and third compromise factor. The coordinates of the observations on the compromise factors were used to plot the items such that the positions in the map best reflect the similarities between the change profiles of the items. Those items that are close together, tend to go up and down together in time within patients. An interactive three-dimensional plot was also calculated [29]. These plots gave a first visualisation of the symptom dimensions at the group level.

The results of the Distasis approach were subsequently analysed in a hierarchical cluster analysis, to identify dimensions of symptoms with similar change profiles (step 3 Fig. 2). We first estimated the optimal number of dimensions by use of the elbow method, based on the percentage of variance explained as a function of the number of clusters. Furthermore, the silhouette method [30] calculates the average distance of each item to all the items in the same dimension as well as the average distance to all the items in the nearest dimension, with a plot of the average scores over all items against different number of dimensions. The number of dimensions yielding the highest average silhouette score is the best number of dimensions [31]. Using the hierarchical 'Ward.D2' cluster analysis, the total within cluster variance was minimized, and dissimilarities were squared before cluster updating. The hierarchical clustering was visualized
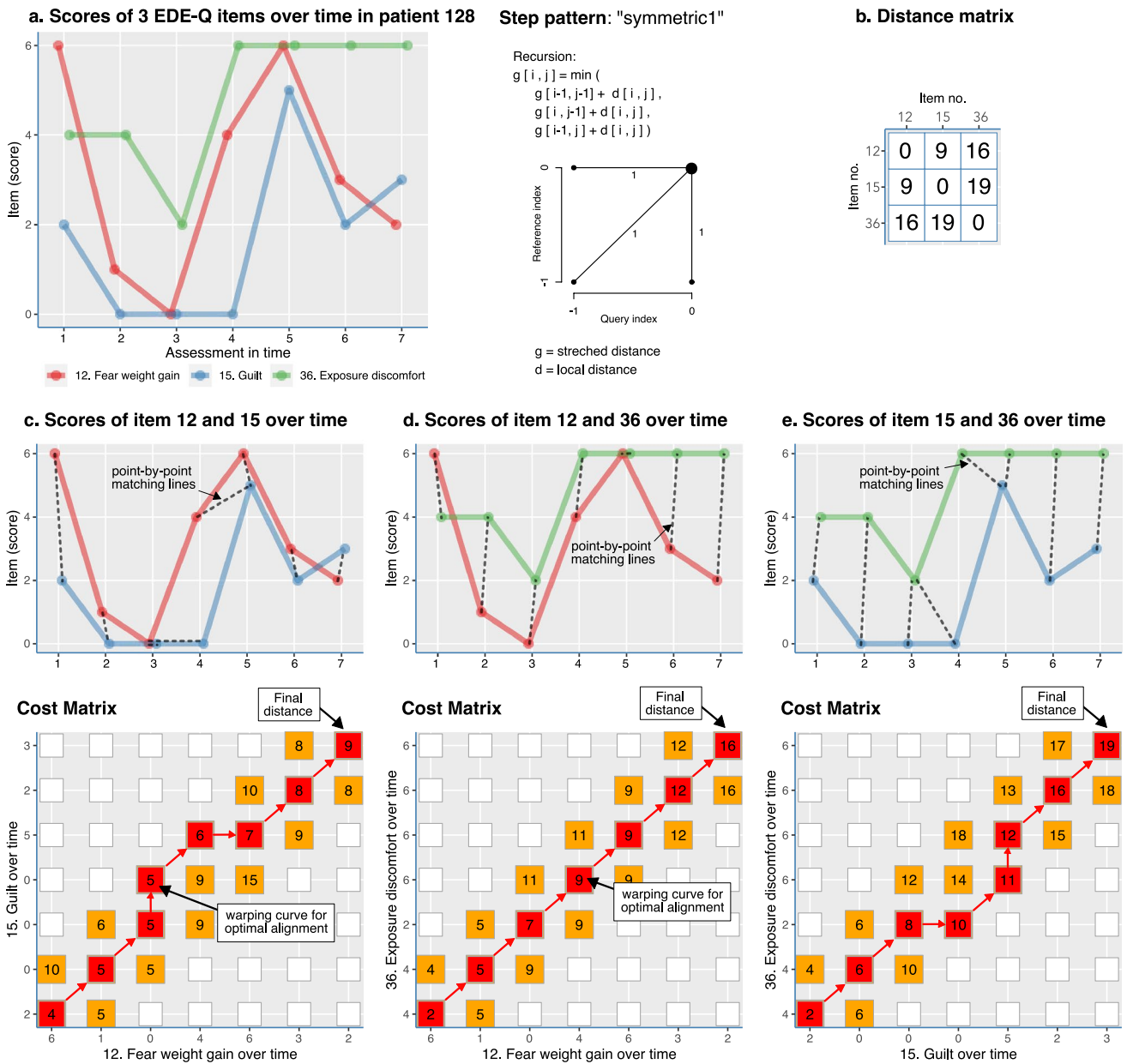
Fig. 3 Explanation of the dynamic time warp analysis, a shape-based algorithm for measuring similarity between two temporal sequences. Dynamic time warp is based on the concept of a warping curve, that stretches the two given time series so that they will overlap. We analyzed three EDE-Q symptom scores over time from patient no. 128. **a** The (unstandardized) scores of these individual items 12, 15, and 36 are given over time, with timepoint "1" being baseline. The first step in dynamic time warp involves creating a local cost matrix which has 7 × 7 dimensions (as we had 7 assessments in time). In the second step, the dynamic time warp algorithm finds the path that minimizes the alignment between the two item scores by iteratively stepping through the cost matrix, starting at the lower left corner and finishing at the upper right corner, while aggregating the total distance (i.e., 'cost'). At each step, the algorithm takes the step in the direction in which the cost increases the least under the chosen constraint. The constraint was the Sakoe-Chiba window of size one, with one timepoint before and after the current assessment. The way in which the algorithm traverses through the cost matrix is dictated by the chosen step pattern, in our case the default "symmetric1" step pattern. **c**, **d**, **e** Explain the calculations of dynamic time warp distances for the three symptom pairs with their respective cost matrices. The grey dotted lines illustrate how each potential misalignment at every timepoint separately is overcome. These lines represent the warped (i.e., stretching) modification of one item to get an optimal alignment, yielding 9, 16, and 19 as for their respective distances, which are included in the distance matrix [b]. The red and blue lines show a more similar route over time than that of the green line, which is represented by the smaller distance compared to each distance with the green line

in a dendrogram, which represents the dimensions and the general distance between the dynamics of the 22 symptoms.

To visualize the dimensions and their interaction a network plot was created (step 4 Fig. 2), by averaging the distance matrices over the 255 patients, weighted for the number of assessments per patient (ranging from 4 through 12). Using the R package 'qgraph' [32], the structure of the average distance matrix was visualized into a symptom network. A network with 22 nodes, representing 22 EDE-Q items, was obtained and connected with edges, representing the inverse of distances between symptom trajectories (i.e., 1/distance, thus thicker edges represent shorter distances). Thus, the thickness of the edges indicated the similarity of the changes over time in item scores.

We expected that some of the symptoms in one dimension would be more strongly connected to symptoms of all different dimensions than other symptoms, which could be considered bridge symptoms [33]. To identify these bridge symptoms (step 5 Fig. 2), the mean differences of all 22 symptoms with all symptoms that were not part of their own dimension were calculated. The items that were most strongly connected were thus identified as bridge symptom.

To analyse the stability of the symptom network (step 6 Fig. 2), we divided the patients into two groups using a random split. In both groups, a dynamic time warp and network analysis were done, and the two resulting networks were compared in a Procrustes analysis, to yield the congruence factor [34]. The congruence coefficients (with the 2.5th and 97.5th percentiles) were estimated, through bootstrapping of 200 random splits of the 255 participants. A value below 0.85 is indicates poor similarity, a value in the range of 0.85 to 0.94 indicates fair similarity, and a value of 0.95 can be considered as being equal [35].

Finally, to explore the potential use of the identified symptom dimensions in the characterisation of the trajectories of unique patients, we plotted the scores on these dimensions of eight exemplar patients (four with anorexia nervosa, and four with bulimia nervosa) during follow-up.

The baseline table was constructed using SPSS version 25 (IBM Corp Released 2017, IBM SPSS Statistics for Windows, Version 25). For all other calculations, we used RStudio (R version 3.6.0; R Foundation for Statistical Computing, Vienna, Austria, 2016. URL: https://www.R-project.org/), with main packages 'dtw' (version 1.20.1), 'parallelDist' (version 0.2.4), 'DistatisR' (version 1.0.1), 'qgraph' (version 1.6.2), and 'smacof' (version 2.1–1) for the Procrustes analysis.

Results

The sample was comprised mainly of women (n = 251, 98.4%) with a mean age of 26.9 years (range 12–61). The majority had a Dutch ethnic background (87.9%), and an intermediate education level (54.5%; 20.7% low educational level, and 23.9% high educational level). For the socio-economic status the majority was employed (39.6%), 22% was on sick leave/disabled, 16.7% was unemployed/homemaker, and 15.5% were in school/study. Eating disorder diagnoses (DSM-IV [18]) were anorexia nervosa (n = 100), bulimia nervosa (n = 37), eating disorder not otherwise specified (n = 110), or binge-eating disorder (n = 8). The mean BMI was 22.1(SD = 9.9), with the highest BMI in the binge-eating disorder group (M = 36.7, SD = 9.1) and the lowest BMI in the anorexia nervosa group (M = 13.1, SD = 6.8). The mean total EDE-Q score was 4.1 (SD = 1.1), with no significant differences between eating disorder subtypes. The average number of assessments was 4.7 (range 4–12) and the time between two subsequent assessments was on average 8 months (range 2–18). All patients were treated according to the Dutch multidisciplinary guideline for eating disorders. The vast majority of patients were treated as outpatients and treatment was tailored to the needs of the individual patient (for more information; [36]).

Dynamic time warp and network analysis

After standardization of the 22 EDE-Q item scores, dynamic time warp distance was used to assess the 231 distances between each symptom pair, which were calculated for each of the 255 patients. These 255 distance matrices were subsequently analysed using Distasis, which is comparable to a principle component analysis and combines the distance matrices into a common structure called a compromise and plots the 22 EDE-Q items according to the compromise factors (i.e. principal components). The first three compromise factors explained 18.7%, 12.8% and 7.6% of the inertia of the 255 distance matrices (in total 39.1%). In the compromise plots, the position of the 22 EDE-Q items was given plotted, respectively, against their first and second compromise factor values (Fig. 4a), and against their first and third compromise factor values (Fig. 4b). Supplementary file 1 presents the 3D-plot in which each EDE-Q item is plotted according to all three compromise factors.

After hierarchical cluster analysis of the three compromise factors, both the elbow and silhouette plots indicated an optimum of four dimensions (Fig. 4c). In the dendrogram (Fig. 4d), these four dimensions, identified due to their similar dynamics over time, are presented: 1. "restraint/rules" (with three EDE-Q items); 2. "secret eating/fasting" (with two items); 3. "worries/preoccupation" (with seven items); and 4. "weight and shape concern" (with ten items).

The 255 distance matrices were also aggregated into one average distance matrix. Figure 5 visually presents the average distance matrix in a network plot, which shows us how the symptoms are connected within and between the four dimensions. The items 'fear of weight gain' (part
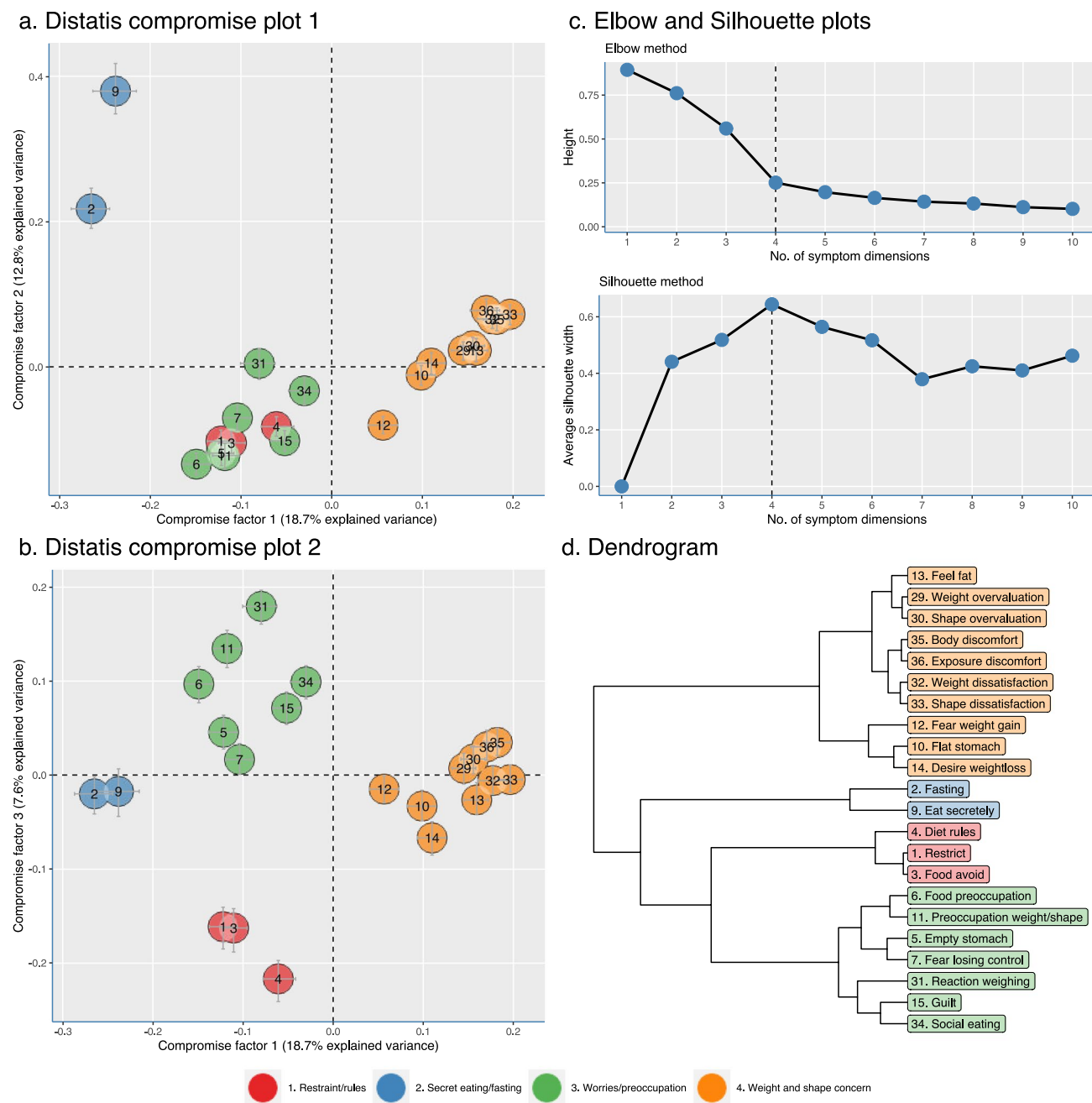
Fig. 4 Nomothetic analyses based on all distance matrices from 255 patients with an eating disorder. **a**, **b** Compromise plot based on distatis analysis (three-way principal component analysis) that shows the position of the objects in the compromise space using the first 2 compromise factors (**a**) and the first and the third compromise factor (**b**). **c** The scree plot displays the eigenvalues in a downward curve based on the distatis analysis. The number of dimensions was determined using the elbow method (i.e., point were the slope of the curve is levelling of, in our example this is four; after this point the slope of the curve becomes more stable) and silhouette plot (i.e., 4 dimensions also yielded the highest average silhouette score). **d** Dendrogram based on Ward's (D2, i.e., general agglomerative hierarchical clustering procedure) clustering criterion on the weighted mean distance matrix from all patients

of the dimension "weight and shape concern") and 'guilt' (part of the dimension "worries/preoccupation") were bridge symptoms between the dimensions 1, 3 and 4, since they were more strongly connected to symptoms of the different dimensions than the rest of the items. The second dimension "Secret eating/fasting" was not connected with the other dimensions.

Fig. 5 Network plot the average distances of each symptom pair, which shows how the symptoms are connected within and between the four dimensions. The thickness of the edges indicate the strength of the similarity of the changes over time in item scores. The bridge symptoms were 'Fear of weight gain' and 'Guilt'
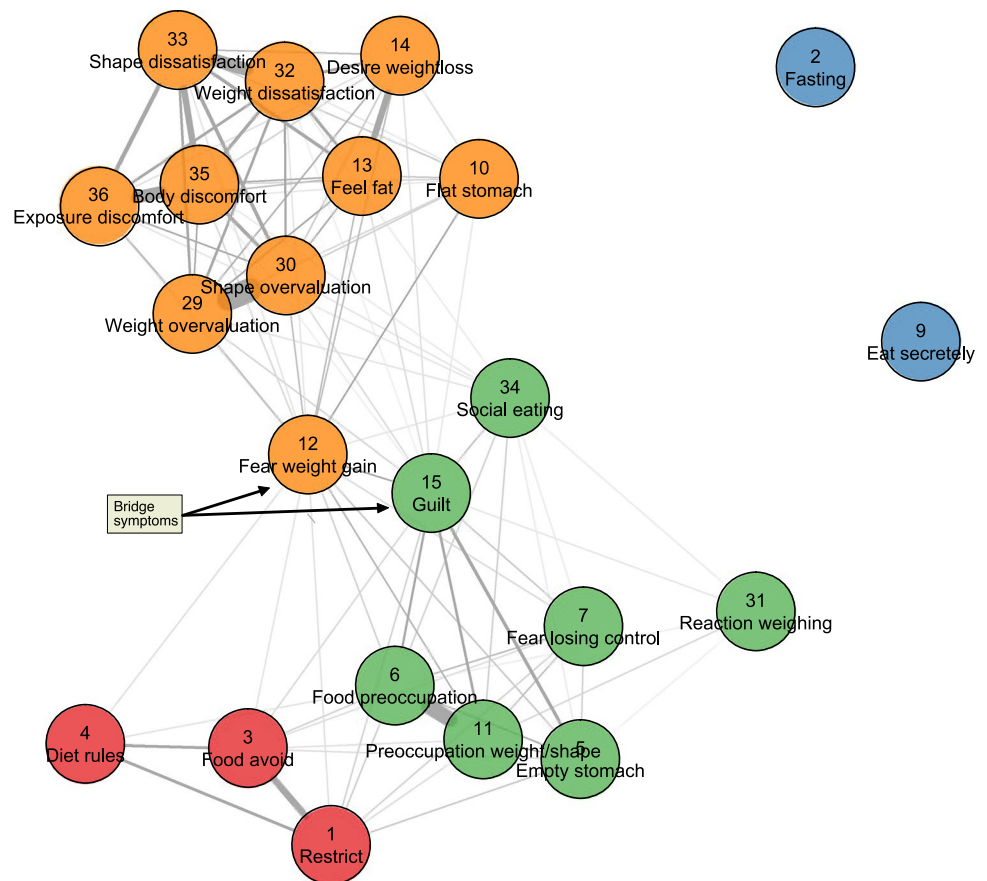

To test the robustness and to further validate our finding of 4 symptom dimensions, we randomly split our sample into 2 groups of which one comprised 127 patients and the other 128 patients. Subsequently, dynamic time warp and network analyses were performed in both groups after which the results were compared. The identified symptom network appeared to be highly stable, as the same network structure was found in both samples (Fig. 6). The median congruence coefficient was very high at 0.993.

Finally, Fig. 7 shows the scores on the four symptom dimensions in eight exemplar patients (four with anorexia nervosa and four with bulimia nervosa). The scores on these symptom dimensions over time seem to be unique for each patient, and these could potentially be used to inform treatment. For patient 83 for example, the dimensions "restraint/rules", "worries/preoccupation", and "weight and shape concern" seem to be very stable and present during the follow-up, whereas the dimension "secret eating/fasting" seems to become gradually worse. The dimension "restraint/rules" seems to be the dominant aspect of the eating disorder in patient 146, and may be an important focus for treatment. For patient 40, dimension "weight and shape concern" shows the slightest change in time, and may be important in maintaining the eating disorder.
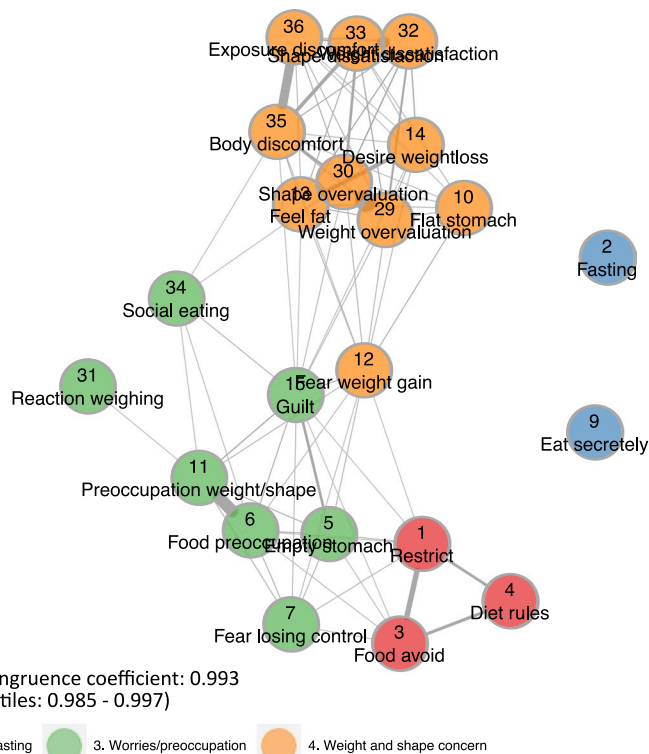
Discussion

The aim of the current study was to investigate whether temporal dimensions of eating disorder symptoms could be identified in a sample of individuals seeking treatment for an eating disorder, using the dynamic time warp approach. Four robust dimensions of eating disorder psychopathology symptoms were found which appeared to change together over time. In other words, each of the four clusters was comprised of eating disorder symptoms that covaried together, with changes in one symptom being accompanied by changes in other symptoms within the same cluster. As expected, symptoms related to shape and weight concerns showed similar co-occurrence patterns in time and formed one dimension together. For example, if one is more satisfied about one's weight and shape, the fear of gaining weight and the desire to lose weight will also become less or vice versa. Somewhat comparable to the original EDE-Q restraint subscale, we also found a "Restraint/rules" dimension comprised of three of the five original items; 'restraint', 'food avoidance' and 'diet rules'. The items 'fasting' (originally belonging to the restraint subscale) and 'secret eating' (originally belonging to the

a. Network plot in 127 patients with an eating disorder (random split)
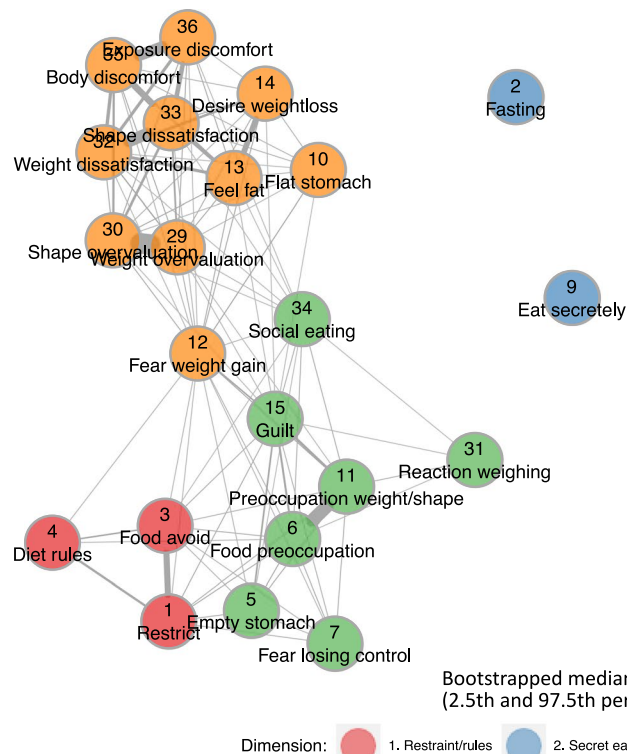
b. Network plot in 128 patients with an eating disorder (random split)

Bootstrapped median congruence coefficient: 0.993
(2.5th and 97.5th percentiles: 0.985 - 0.997)

Dimension: ● 1. Restraint/rules ● 2. Secret eating/fasting ● 3. Worries/preoccupation ● 4. Weight and shape concern

Fig. 6 Network plots of two subsamples (**a**, **b**) of the 255 patients. We used an automated split with a subset of 127 and 128 patients, in which we conducted separate dynamic time warp analyses. Network configurations for both are shown. Using Procrustes analysis the two networks were brought into a similar space in which statistically meaningless differences were removed without changing the fit. The median congruence coefficient was very high at 0.993 (2.5th and 97.5th percentiles of values) when we bootstrapped the random split procedure 200 times), indicating stability of the 4 symptom dimensions across participants

eating concern subscale), showed similar co-occurrence patterns and together formed a distinct dimension "Secret eating/fasting" in the current study. The final dimension we found was "Worries/preoccupation", and comprised of most original eating concern subscale items ('food preoccupation', 'fear losing control', 'guilt' and 'social eating') complemented with the items 'empty stomach', 'preoccupation weight/shape', and 'reaction weighing'.

Three of the four dimensions appeared to be connected with each other, while the dimension "Secret eating/fasting" seemed to be independent from the rest. The items 'fear of weight gain' and 'guilt' acted as bridge symptoms, which was not completely in line with our hypothesis. Given the importance of symptoms related to weight and shape concerns shown in previous network analyses [4–8], we expected that the bridge symptoms would be exclusively found among these symptoms. However, the bridge symptoms identified in previous network studies in eating disorders [4] were never the symptoms with the highest centrality. Feeling guilty after eating was previously found to be a bridge symptom in bulimia nervosa with anxiety [37] and in

eating disorders with negative affect [38]. Furthermore, guilt also seems to play a driving role in binge eating [39, 40]. From a complex dynamic system perspective [41], aiming treatment on fear of gaining weight and guilt would theoretically help to collapse both the symptom dimensions and the maintaining network, with as a result that symptoms would no longer reinforce each other.

As a first exploration, we finally examined whether the scores on these four symptom dimensions could be used to distinguish the specific trajectories of individual patients. The individual trajectories of exemplar patients indeed showed (see Fig. 7) the potential applicability of the symptom dimensions in clinical practice, these dimensions could be useful in treatment and thus setting new steps towards personalized treatment approaches. For this, not only the symptom dimensions identified at the group level could be suitable. Individual longitudinal networks can also be estimated based on the dynamic time warp distance matrix calculated for a single patient [16].

It is important to keep in mind that, as with all statistical analyses, the results of the current dynamic time warp

a. Patients with anorexia nervosa
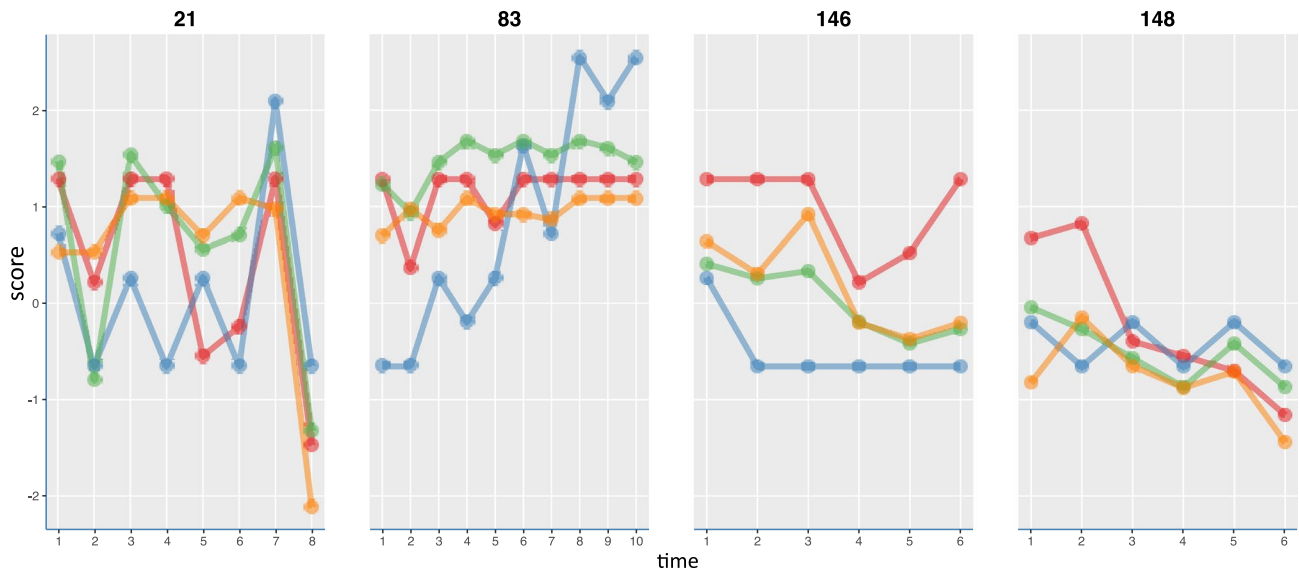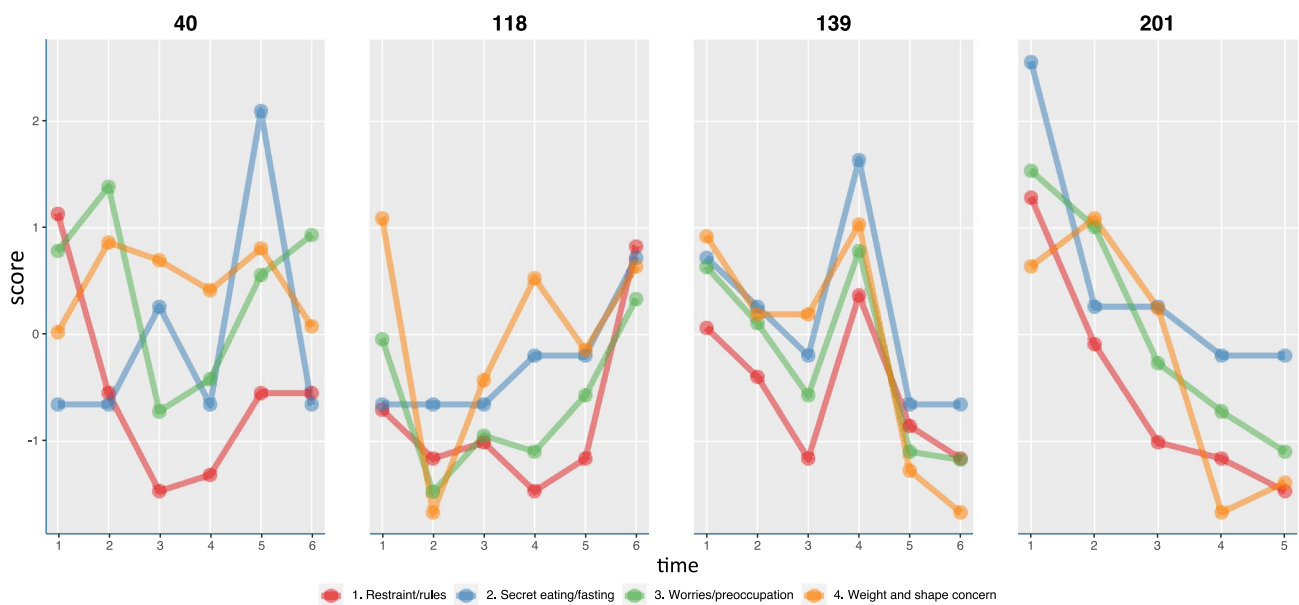

b. Patients with bulimia nervosa

Fig. 7 The scores on the four eating disorder symptom dimensions over time for eight exemplar patients. **a** Four with anorexia nervosa (no. 21, 83, 146, and 148) and **b** four with bulimia nervosa (no. 40, 118, 139, and 201)

analyses are dependent of the variables that are entered into the model, i.e., the EDE-Q psychopathology item scores. The validated EDE-Q was selected because of its widespread use and good psychometric quality [23, 24], making our findings more easily replicable for future studies. The present study focussed solely on the EDE-Q psychopathology symptoms, to prevent excessive influence of the scaling difference between the EDE-Q psychopathology (ordinal) and behaviour items (continuous). Previous cross-sectional

network analyses that included other eating disorder scales (e.g. Eating Disorder Inventory, or Eating Pathology Symptoms Inventory) also led to the identification of other central features [5, 8, 42–47]. Since co-occurrence patterns and mutual influence will probably not be limited to eating disorder psychopathology symptoms alone, future studies should include broader measurement instruments, more assessments per patient (changes may occur in shorter time frames), and not be limited to eating disorder psychopathology (e.g., also

include lifestyle, behavioural, and therapeutic elements), to gain more insight in the development, maintenance, and treatment of these disorders.

Strength and limits

Although dynamic time warp analyses are not new and have been used in diverse fields of research (e.g., speech recognition, data mining, machine learning), this approach has only recently been applied in the field of psychiatry [14, 16]. One of the strengths of this dynamic longitudinal approach is that it takes into account the possibility that two symptoms may not rise and fall exactly at the same two subsequent time points (the so-called lag-1-time vector autoregression analyses) as is hypothesized in more traditional longitudinal network analyses. Another strength of this method is that contrary to other techniques, dynamic time warp is also applicable if only sparse panel data are available [48]. Furthermore, it can visualise how symptom dynamics unfold over time for a single patient. Finally, in contrast to other techniques, a fixed time interval of two successive measurement moments and the stationarity assumption of data (indicating that the mean, variance and autocorrelation structure does not change over time) are not required for dynamic time warp analysis. Dynamic time warp will function better when there are relatively larger changes in scores over time within patients. When such changes occur, then this algorithm will more easily detect which symptom changes go up and down together in time.

The study must be seen in the light of a few limitations. The first limitation is that although the sample size was large, there was a steep decrease in the number of patients for each additional assessment (100% with four assessments, 39.6% with five, 17.6% with six). Second, the time interval between the ROM assessments varied widely within patients. Although this is not a violation of the assumptions of the dynamic time warp approach, the reliability and robustness of the identified symptom dimensions were not affected, it is possible that with shorter time intervals between assessments the group level analyses might yield different dimensions and bridge symptoms. There is also a clinical advantage of using shorter time intervals, since the subsequent dynamic idiographic patterns in patients could be used to adapt and intervene earlier and more effectively on central symptoms. A third limitation comprises the variety in treatments of our participants. Since we included a naturalistic cohort of treatment seeking individuals, the majority of our sample was receiving treatment during the ROM assessments. However, part of our sample also ended their treatment and started again several months later during the follow-up, a common phenomenon in clinical practice given the substantive rates of relapse in patients with eating disorders [49]. Both treatment and time could, therefore,

have influenced the identified symptom dynamics. Another limitation is that our data were collected a longer time ago, patients enrolled between 2003 and 2014, therefore, the diagnoses were based on DSM-IV criteria [18]. A fifth limitation was that data were collected as part of Routine Outcome Monitoring, and no extensive data on comorbidity, psychotherapy and pharmacotherapy had been collected. Finally, the clustering of symptoms within a network may not always be due to the true relationships among the symptoms but can for example be artificially in- or decreased when certain items partly overlap (i.e., are too similar in content or response categories) [50]. This may also be the case for the 22 psychopathology items of the EDE-Q. Several of these items, for example 'weight overvaluation' and 'shape overvaluation', have previously been shown to measure quite similar underlying constructs [51]. However, strong content overlap between some of the items did not affect the membership of the four symptom dimensions.

Conclusion

The present study showed that dynamic time warp could capture the within-person dynamics of eating disorder symptoms. The longitudinal patterns of the individual patients could be aggregated at a group-level to identify robust eating disorder symptom dimensions over time. Subscores of the four dimensions could give a better indication of progression or regression of severity of eating disorder in time than overall sum EDE-Q scores can. This approach could be applied in the future to visualize eating disorder symptom dynamics and signal the central symptoms within an individual and groups of patients. From a clinical perspective, these trajectories could help to enhance personalized treatment strategies for these disorders. For dynamic time warp to be of clinical value for the individual patient more extensive assessments are needed. It could be explored in future studies whether daily assessments for 2 or 3 weeks, may yield idiographic symptom networks and centrality measures which insights could serve as feedback to both the clinician and patient, and aid clinical decision making. Further exploration is necessary to find out whether the dynamic time warp analysis will lead to actionable insights for personalized medicine.

What is already known on this subject?

Longitudinal network approaches which may increase our insight of the complex dynamics over time are scarce in the eating disorder field. The traditional longitudinal network analyses are bound by a number of assumptions, which limits its applicability in clinical practice.

What does this study add?

An alternative non-linear method to perform longitudinal network analyses, dynamic time warp analysis, could capture the within-person dynamics of eating disorder symptoms over time. With this method, the longitudinal patterns of the individual patients could subsequently be aggregated at a group-level to identify four robust eating disorder symptom psychopathology dimensions. From a clinical perspective, this approach could help to enhance personalized treatment strategies.

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1007/s40519-022-01504-5.

Data availability The data that support the findings of this study are available from the corresponding author upon reasonable request.

Declarations

Conflict of interest The authors have no relevant financial or non-financial interests to disclose.

Ethics approval The Medical Ethics Committee of the Leiden University Medical Center approved the general study protocol on Routine Outcome Monitoring (ROM), in which ROM is considered integral to the treatment process (written informed consent is not institutionally required). The study was undertaken in accordance with ethical principles stated in the Helsinki Declaration.

Informed consent All participants gave permission for the anonymized use of their data for scientific purposes.

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