

THE TATTVAYOGABINDU OF RĀMACANDRA

Critical Edition and Annotated Translation of an Early
Modern Text on Rājayoga, with a Comparative Analysis of
the Complex Yoga Taxonomies from the Same Period



त्रिमूर्तियनम्॥ शुभ्रवेनसंक्षेपादयोगज्ञात्वा लिख्या ॥ गत्योगस्य द्विरूपान्तरात्मा गतेषु नक्षत्राणां गत
वरदोषनक्षयाधिविजादयुक्तसमयवाचकूपत्रकाले प्राचीनतिर्थविकासवद्वद्वयाग्राहक स्वत्वं रुद्राभिर्यात्मानः
नयोगश्चवर्योगश्चरुद्योगश्चक्षमयोगश्चलययोगश्च धानयोगश्च मनुष्याग्राहनक्षयाग्राहननायाग्राहनवयोगश्च वृद्धयोगश्च ॥
अष्टव्याग्राहनद्योगश्च योगश्च उपर्यवद्वयाग्राहनामध्यानीक्षियाग्राहनक्षयाग्राहनक्षयाग्राहन ॥ कृष्णमूर्कित्वयोगश्चलिपि
असंख्यकृद्यकृद्य ॥ यीक्षणात्कालीकार्यान्तरमन्तरम् ॥ १॥ गत्युद्विरूपान्तरात्मायाग्राहन गात्रव ॥ क्रमाविधकवृत्तमात्रा
ग्राहनस्मिन्द्युत्तमा ॥ २॥ एव ग्राहकियुग्मापासीक्षियाग्राहनां निर्द्वया ॥ मात्रायमेवामायादित्यामासद्वयवा ॥ ३॥ क्रान्त
व्याप्तिरुद्योगात्मानादीन्द्रथाऽसेविश्वाग्रहश्चाद्यत्वालयस्त्रियोग्यनिर्द्वयाग्रहस्त्रियोग्यनिर्द्वयाग्रह ॥ यस्त्रियोग्यनिर्द्वयाग्रहस्त्रियोग्यनिर्द्वयाग्रह ॥ (यस्त्रियोग्यनिर्द्वय)

Figure I: Folio iv of Ms. N₁.

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Chapter I

Introduction

I.I Stemmatic analysis

THE stemmatic analysis of the *Tattvayogabindu* for the creation of a *stemma codicum* that represents the relationships between the collated manuscripts is based on philological observations and supplemented by various computational methods from the field of phylogenetics to support these observations empirically.¹ The following pages of this section will explain how I construe the *stemma codicum*.

I.I.I Philological observations

Before collating the manuscripts, I transcribed every single available witness of the *Tattvayogabindu* and arranged the transcriptions synoptically. This approach proved helpful for the critical editing of the *Tattvayogabindu*. The text comprises a mixture of prose and verse. Many prose passages are structurally very similar, with identical beginnings and sentence endings, resulting in virtually no manuscript that does not omit words, sentences, or entire sections due to eye skips caused by the text's arrangement. Additionally, there are frequent instances across the manuscripts where words, phrases, or even whole passages are transposed. No manuscript exists without substantial *lacunae*. Creating a synoptic comparison of the transcriptions was crucial to maintaining an overview in these cases and reconstructing a text closest to the original. The synoptic comparison reveals the structural differences and provides a clear overview. See the following example:

This one example (Figure 2) of one sentence illustrates the broad structural differences as they recur consistently. It became apparent during the

¹Certainly, in the case of the *Tattvayogabindu*, reconstructing the *stemma codicum* would have been feasible even manually, given the relatively manageable textual tradition, without yielding fundamentally different results. However, precisely in light of the text's well-preserved and uncontaminated transmission — easily comprehensible to the human mind — the stemmatic analysis of the *Tattvayogabindu*'s textual witnesses conducted here can, in my view, serve as a valuable exemplar. It demonstrates both the utility and the limitations of computer-assisted stemmatics and provides data that can benefit future users of this technology.

%	tasya cakrasya pūrnagiri	etādrśam nāma / \D
%	tasya cakrasya pūrnagiri	etādrśam nāma / \N1
%	tasya cakrasya pūrnagiri	etādrśam nāma / \N2
%	tasya cakrasya pūrnagire	etādrśam nāmāḥ \U1
%	tasya pūrnagiripīṭham iti	etādrśam nāma \P
%madhye	tasya pūrnagiripīṭham iti	ekādaśam nāma // \U2
%	tasya pūrnagiripīṭham iti samjñā	etādrśam nāma \B
%	tasya pūrnagiripīṭham iti samjñā	etādrśam nāma \L
%	tasya pūrnagiripīṭha	etādrśam nāma / \E

Figure 2: Example: Synoptic transcription of the *Tattvayogabindu*'s witnesses.

transcription of the textual witnesses that the transmission of the Urtext or archetype divides into two main branches, each traceable to a hyparchetype.² Both hyparchetypes not only differ structurally but also share most of their readings and key errors.

I refer to the first hyparchetype as β (D, N₁, N₂, and U₁) for the simple reason that the manuscripts of this group contain the oldest dated witness and in all likelihood a structural arrangement that is closer to the original than the γ -group, which contains additional material in some places. Although this group frequently contains errors, in many cases, there are one or more manuscripts where the reading is entirely convincing. The oldest dated manuscript N₁ (1716 CE) is from Nepal, of which N₂ is a direct copy. I also collated N₂ as it provided two significant benefits. Firstly, the hand of N₁ is partially difficult to read and, in some places, almost illegible, so N₂, being very readable, was extremely helpful. Secondly, there are occasional minor discrepancies between the manuscripts, likely corrections by the scribe of N₂. This scribe had an excellent understanding of the text, and his corrections proved to be helpful. Unfortunately, the transmission of the β -group has significant gaps, some of which overlap, resulting in extended text passages where only one witness of the β -group can be relied upon.

I refer to the second hyparchetype as γ (B, E, L, P and U₂). This group is significant due to the abovementioned circumstances, as its transmission

² Paolo Trovato and others explain the very high rate of lost archetypes and two-branched stemmata by “the high (90%) rate of extinction of individual copies”, cf. Trovato, 2017: 86.

contains almost the entire text with only a few isolated gaps. Among the five available textual witnesses of the γ -group is the printed edition E, based on a hitherto unknown manuscript. The Pandit editor attempted to correct poorly transmitted text passages by his *divinatio*. Unfortunately, apart from some grammatical emendations, he often failed in this endeavour.

A further branching of manuscripts splits from the γ -group, comprising B and L. These contain the worst and most erroneous transmission of the text by far. Surprisingly, in some rare cases, they provided the decisive and only convincing reading, making their inclusion in the collation indispensable. Overall, the γ -group is noted for containing additional material in some passages, usually verse insertions that elaborate on a specific term. These were critically edited with the available witnesses and included in the grayscale.

There is no detectable contamination between the β and γ groups, making editorial practice easier and using computerised stemmatics more reliable. In editorial practice, both groups of manuscripts proved to be equally useful, despite the tendency to favour the β group, which is closer to the original due to its structural characteristics, since both groups contain numerous errors. In most cases, these errors could be explained and corrected by contrasting them with the other group.

I.I.2 Computer Stemmatatics applied to the *Tattvayogabindu*

For the final constitution of the *stemma codicum*, all transcriptions of the entire *Tattvayogabindu* were analyzed using common algorithms from phylogenetic software tools for stemmatic analysis. The dataset was stored in the Nexus format. The numerous gaps in the transmission were coded as non-significant sites in the data to prevent the results from being distorted by the large *lacunae* or the interpolations of the γ -group, particularly manuscript U₂. The results were compared with my philological observations, and the findings of both approaches were combined. Here, I present three phylogenetic trees which support and complement my philological considerations. This work serves as an example of how such computer-assisted methods can

be applied to stemmatic analysis in a less complex transmission like that of the *Tattvayogabindu*, to create a *stemma codicum* based on empirical data, harmonizing the empiricism of phylogenetic analysis with the expertise of the philologist. No computer-generated tree can automatically provide an optimal representation of a text's transmission.³ In the case of cladistic analysis with Maximum Parsimony, Maas explains that this arises because the strict bifurcating structure of that type of computer-generated tree, in which every existing textual witness is connected by exactly one line to a single inferred witness, cannot account for the contamination in the tradition. In the special case of *Tattvayogabindu*, however, there is no contamination between the β and γ groups, which makes the application of such phylogenetic algorithms to the tradition much less susceptible to errors. Furthermore, the bifurcating structure cannot represent cases where some copies were made more than once and more than one copy has survived. In the computer-generated tree of the cladistic method, every existing manuscript is represented as a copy of an inferred witness, which is inaccurate; in most text transmissions, numerous manuscripts are copies of other existing manuscripts.⁴ If the editor is aware of these issues, knows his text's transmission well, and understands the mechanisms of the algorithms and their results, the wrongly assumed bifurcations and contamination of certain computer-generated models can be detected. Only then can computer-generated models, like cladistic analysis, inform and thus improve the editor's decisions to manually draw a plausible and data-based *stemma codicum* that reflects the underlying transmission of the text as well as possible.

³Cf. Guillaumin (2020: 339–356) for an overview of the criticism digital methods have faced since their inception.

⁴See Maas, 2009: 80.

I.I.2.1 Tree I: Maximum Parsimony

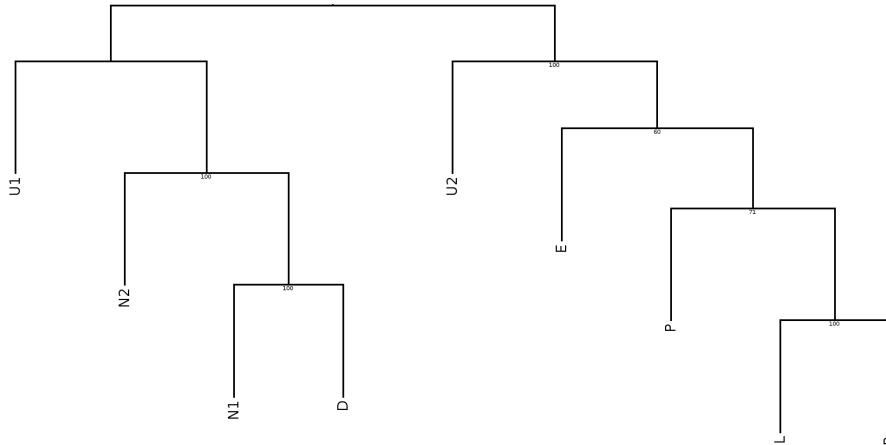


Figure 3: Generated with Mesquite Version 3.81 (build 955). **Algorithm:** *Parsimony Tree Analysis* with PAUP 4.0a168. **Dataset:** Full collation of the *Tattvayogabindu*.

The phylogenetic analysis method based on the *Maximum Parsimony* algorithm is one of the most widely used methods for stemmatic analysis in philology.⁵ The tree (Figure 3) has an excellent CI (Consistency Index) of 0.869. This means that the proposed tree structure can explain about 87% of the phylogenetic tree's trait changes. My earlier observation that the manuscripts divide into two main groups was an explicit criterion for placing the tree's root precisely between these two groups, a division also supported by the *Maximum Parsimony* algorithm. However, this tree has two apparent weaknesses. It does not recognize that N₂ is a direct copy of N₁. That is

⁵*Maximum Parsimony* calculates all possible bifurcating trees and searches for the most parsimonious tree (the one requiring the fewest changes) among them. *Maximum Parsimony* groups manuscripts according to their shared derived characters. Only parsimony informative sites in the data are used for the *Maximum Parsimony* analysis. A site within the data is considered informative if it consists of more than one variant and at least two variants are recorded at least twice. All other sites are excluded, cf. Windram, Shaw, Robinson, and Howe (2008: 445-446).

because of the above-mentioned strict bifurcating assumptions of the algorithm mentioned above, and the scribe of N_2 corrected some passages, making the character states closer to those of U_1 . The second weakness, indicated by the relatively low bootstrap score⁶ of only 60 at the branching where E is located, and the bootstrap score of 71 at the branching where P is located. That is because the character states resulting from the editorial interventions of the Pandit of the printed edition cannot be smoothly explained by the computer in light of the remaining transmission. Therefore, the positions of E and P must be carefully considered. The position of U_2 was also surprising. With many interpolations, this manuscript might easily have been underestimated for its stemmatic relevance to the γ -group. However, its base text (excluding the interpolations) conserves an important transmission stage of the γ -group.

⁶Bootstrapping is a method to detect statistical support of phylogenetic trees, see Felsenstein (1985). Bootstrapping is a test to determine whether the whole dataset supports the tree or if the tree is a marginal choice among several almost equal alternatives. That is accomplished by testing the tree with randomized subsamples of the dataset, then building trees from each of these and finally calculating the frequency with which the different parts of the tree are reproduced in each of these random subsamples. The bootstrap support is assigned according to the frequency of a specific group of manuscripts occurring in the subsample trees. If the specific group is found in every subsample tree, then the bootstrap support will be 100%; if it is found in only half of the subsamples, it will have a bootstrap support of 50%. Values of 70% or higher are considered to indicate reliable groupings, cf. Baldauf (2003: 250).

I.I.2.2 Tree 2: Neighbour-joining

These are two unrooted Neighbor-joining trees (Figure 4).⁷ They are based on the same dataset. The only difference lies in the distance measures used to quantify the evolutionary distance between sequences of *akṣaras*.

These distances are then used to construct phylogenetic trees. The left tree uses the Gene Content Distance,⁸ while the right tree uses the standard p-distance, a simple measure of sequence divergence.⁹ The results differ only

⁷ *Neighbor-joining* is a particular approach to phylogenetic analysis that SplitsTree can execute. The primary mechanism behind this is a hierarchical clustering technique, see Naruya and Nei, 1987. A concise explanation by the authors is as follows: “The principle of this method is to find pairs of operational taxonomic units (OTUs [= neighbours]) that minimize the total branch length at each level of clustering of OTUs starting from a star-shaped tree. The branch lengths and topology of a parsimonious tree can be quickly determined using this method.” In this case, it can be visualized as follows: The algorithm is fed with a diverse set of texts in the form of manuscript transcripts, which act as operational taxonomic units. *Neighbor-joining* divides them into smaller groups with shared features. First, the algorithm measures the distance of each possible pair of manuscripts. This distance indicates how different or similar they are regarding specific features. Then, the algorithm finds the two manuscripts with the smallest distance between them. These are the “closest neighbours” in terms of similarity. These two individual manuscripts are then joined together to form a node. This node represents an assumed common ancestor. The algorithm then recalculates the distances between this newly created node and all other manuscripts. These distances reflect each manuscript’s overall similarity or dissimilarity to the new node. The process repeats and identifies the next pair of nearest manuscripts or groups of manuscripts, creates the next node, and adjusts the distances. In this way, a phylogenetic tree is created. The function repeats these steps until all manuscripts and groups of manuscripts are connected in an undirected tree-like structure in which the length of the branches and the distance between the nodes represent the relationships of the manuscripts based on their similarities. Neighbour-joining assumes a constant rate of evolution across all lineages, and branch lengths correspond to evolutionary distances. The resulting trees can vary considerably depending on how the data are coded and how gaps are treated. The application of *neighbor-joining* to support philological work is discussed by Hoenen, Manafzadeh, Stadler, Roos, Hoenen, and Guillaumin (2020: 319).

⁸ The Gene Content Distance is a measure used to compare the presence or absence of genes across different genomes. The distance between two genomes is calculated based on the differences in their gene content, cf. Huson and Steel, 2004. Instead of gene content, in our case, the presence or absence of *akṣaras* is compared.

⁹ The “Uncorrected P” or p-distance calculates the proportion of nucleotide or amino acid sites at which two sequences differ. The calculation of Uncorrected P is simple. The number of differing sites is divided by the total number of sites compared; see Huson and Bryant, 2022: 46.

slightly, but in my assessment, the trees of both distances correspond with key philological observations, particularly regarding the β -group. While the tree using the Gene Content Distance reflects the close relationship between N_1 and N_2 , it does not show that N_1 is the manuscript closest to the archetype β . Conversely, this relationship is correctly depicted in the tree using p-distance (Uncorrected P).

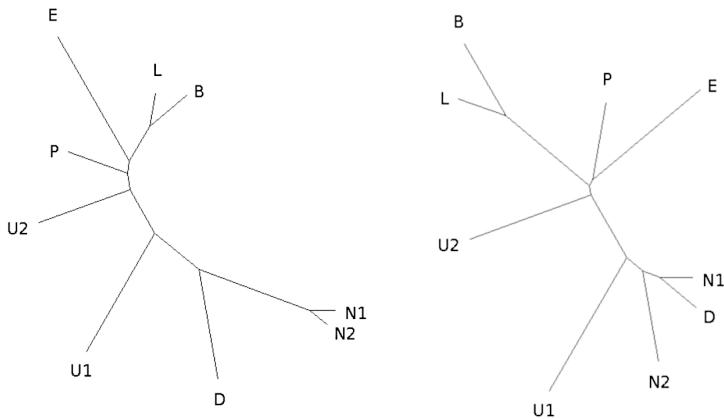


Figure 4: Generated with SplitsTree 4 version 4.19.2. **Algorithm:** *Neighbor-joining* (unrooted). Two trees with identical algorithms and datasets but different distance measures. **Distance** (left): Gene Content Distance. **Distance** (right): Uncorrected P. **Dataset:** Full collation of the *Tattvayogabindu*.

I.I.2.3 Tree 3: Minimum Spanning Tree

Another vital aspect is illustrated by the *Minimum Spanning Tree* (Figure 5).¹⁰ A *Minimum Spanning Tree* can help to confirm important manuscripts due to its algorithmic properties. In our case, it highlights the central manuscripts of the two groups, namely N₁ for the β -group and P for the γ -group, which perfectly aligns with the philological observation. The *Minimum Spanning Tree* algorithm has only been used rarely in philology. Further experiments with different text traditions with known stemma would be necessary to determine whether these valid results occur repeatedly.

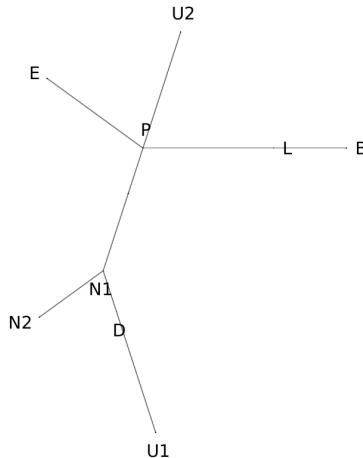


Figure 5: Generated with SplitsTree App 6.3.12. Algorithm: *Minimum Spanning Tree*. Distance: Uncorrected P. Dataset: Full collation of the *Tattvayogabindu*.

¹⁰The algorithm underlying the *Minimum Spanning Tree* calculates an undirected and unrooted tree-shaped graph representing the simplest way to connect all the manuscripts by minimizing the corresponding nodes based on their pairwise distances, see e.g. Hoenen, Manafzadeh, Stadler, Roos, Hoenen, and Guillaumin (2020: 317). Also see Cormen, Leierson, Rivest, and Stein (2009). Furthermore, see Huson and Bryant (2022: 43). The goal of the *Minimum Spanning Tree* is to calculate the connections between the manuscripts so that the total length to connect all manuscripts settles on the minimum. The *Minimum Spanning Tree* thus, in our use case, represents the simplest and most efficient way to connect a set of manuscripts while minimizing the total distance (based on their differences) of the connections. The resulting tree is far from a stemma and does not include hypothetical ancestral nodes at branching points; any shown branching point corresponds to a manuscript in every case.

I.I.2.4 Stemma codicum

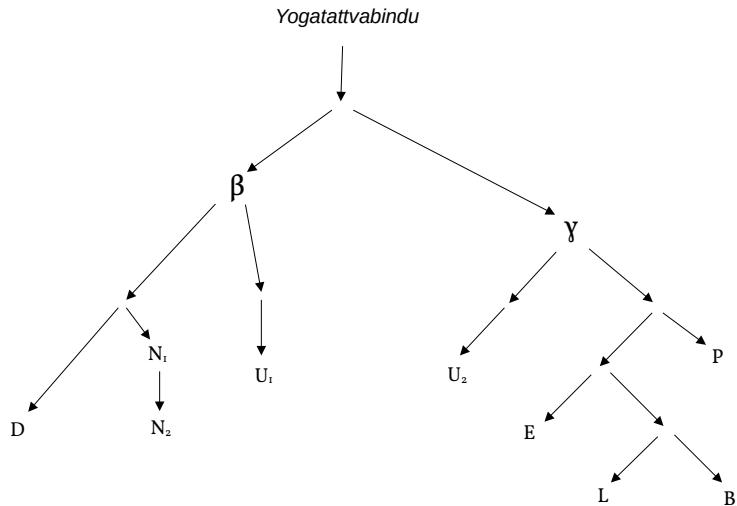


Figure 6: Stemmatic hypothesis of the *Tattvayogabindu*.

The cumulative evidence from the phylogenetic algorithms, combined with my philological observations and considerations, leads to the following *stemma codicum* (Figure 6) of the *Tattvayogabindu*. This graph represents a plausible hypothesis of the relationships between the textual witnesses based on the current state of knowledge, forming the foundation upon which the critical edition presented in this dissertation was prepared.

Chapter 2

The *Tattvayogabindu* of Rāmacandra Critical Edition & Annotated Translation

Chapter 3

Appendix

3.1 Figures



Figure 7: The *dehasvarūpa* of *ajapāgāyatri*. The image, reminiscent of a hipogriff, is part of an illustrated Sanskrit manuscript written in the Śāradā script. Preserved as a single large scroll under Acc. No. 1334 at the Oriental Institute in Srinagar (Kashmir), it is entitled *Nādīcakra*. The manuscript contains a depiction of the yogic body's *cakras* and *nāḍis*. The text surrounding the figure closely corresponds to the additional material found in manuscript U₂ of the *Tattvayogabindu*. The manuscript reads (diplomatic transcription): *om daśame pūrṇagiripiṭhe lalāṭamāṇḍale candro devatā amṛtaśaktih paramātmā ṛṣih dvāviṁśaddalāni amṛtavāsinikalā 4: ambikā 1 lambikā 2 gha(m)ṭkā 3 tālikā 4 dehasvarūpam kākamukham 1 naranetram 2 gośrṅgam 3 lalāṭabrahmapara 4 hayagrīvā 5 mayūramuśchaṁ 6 hamsacārītani 7 sthāna.*



Figure 8: Viṣṇu Viśvarūpa, India, Rajasthan, Jaipur, ca. 1800–1820, Opaque watercolor and gold on paper, 38.5 × 28 cm, Victoria and Albert Museum, London, Given by Mrs. Gerald Clark.



Figure 9: The Equivalence of Self and Universe (detail), folio 6 from the *Siddhasiddhāntapaddhati* (Bulaki), India, Rajasthan, Jodhpur, 1824 (Samvat 1881), 122 x 46 cm, RJS 2378, Mehrangarh Museum Trust.

Chapter 4

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