

Synecdochic and metonymic chains in the organizing narratives of PRC forensic genetic research targeting Uyghurs in Xinjiang

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In this paper, I demonstrate how synecdochical and metonymic chains function in the semiotic narrative schema of forensic genetics articles. Greimas's narrative schema and work on categories provides a framework that can be synthesized with cognitive linguistic advances on synecdoche and metonymy chains to understand how meaning is created in organizational interactions through the circulation of objects of value. Based on an empirical analysis of controversial forensic genetic articles involving Uyghur subjects on ancestry inference marker and phenotype (visible appearance) inference marker research projects, it shows how scientists from the Chinese Ministry of Public Security and other scientists organize through a shared manhunting narrative schema. In this schema, Society and/or Humanity send scientists quests to protect society by improving forensic genetic technologies to variously track down and capture or kill criminals, separatists, insurgents and terrorists. Utilizing recent advances in theorization of synecdoche, the article shows how synecdoche functions in the categorization of Uyghurs as "Eurasian" and "mixed East Asian and European" populations. It also shows how synecdoche and metonymy function through syllogisms to mediate relations and the exchange of objects of value such as Uyghurs' genetic materials and data between the phases and sub-narratives of the scientific articles' narrative schema.

Keywords: metonymy; synecdoche; synecdochical and metonymic chains; narrative schema; forensic genetics; Uyghurs; cognitive linguistics

1. Introduction

Through an analysis of Chinese Ministry of Public Security forensic genetic journal articles, I here consider if a central aspect of A.J. Greimas's narrative theory, the exchange of objects in a narrative schema, conceptually fits with cognitive linguistic analysis of metonymy as inferential relations based on different forms of contiguity. Greimas provided a crucial insight in identifying how contiguity relies on exchanges of objects that connect a sequence of events that make up a narrative. He considered that a narrative involves "a syntagmatic sequence of *enonces* [i.e., utterances or statements] bringing about the transfer of an object of value" (Budniakiewicz, 1992, p. 92; Greimas, 1971, p. 804). Greimas' conception accords in ways with some recent work on metonymy in the field of cognitive linguistics. For example, Al Sharafi (2004) uses the concept of *textual metonymy* to demonstrate the role of metonymic chains of subjects and pronouns in linking together successive sentences. Through an analysis of international news coverage, Brdar-Szabo and Brdar (2011) show how textual metonymic chains function through contiguity with source terms like "Russia", "Moscow" and "the Kremlin" all referring to the same target, the Russian government, or similarly "the US", "the White House" and "Washington" referring to the US government (Brdar-Szabo & Brdar, 2011, pp. 231-3).

Not only do metonymic chains provide a repetition function that is important in cohesion along the syntagmatic (time) axis and forward movement of the narrative schema but also each metonymic usage reveals further information about the signified (Denroche, 2015, p. 20). Denroche's explanation of what he terms *discourse metonymy* is useful in that it identifies the relationship between sentences at the paragraph level (Denroche, 2015). However, despite using the term "discourse", it does not provide a stronger overall understanding of how metonymy functions at the level of an entire scientific article.¹ Similarly, Littlemore (2015) discusses the role of metonymy at the textual level, but again remains rather vague in terms of methodology. The

¹ Denroche's use of the term "discourse metonymy" is problematic if we consider discourse as a sort of meta-concept that covers a particular field or discipline. I would rather suggest that his particular examples are at the sub-narrative level.

importance of metonymy in narrative is summarized by the cognitive linguist Gerard Steen as follows:

Metonymy is important for narrative as a mode of narration; then it plays a *structural* role in narrative. Thus, the chronological and causal sequencing of distinct events in a plot has been analysed as so many metonymic moves by the narrator, taking the addressee from one situation to another, with the situations constituting contiguous parts evoking a larger whole that is left unexpressed [...]. A similarly metonymic function has been attributed to the narrator's switching from characters to settings to events themselves [...]. [emphasis in original] (Steen, 2005b, p. 307)

Yet for all the significance of these chains in narratives, there is no model in cognitive linguistics to account for how these chains function overall in articles or books. In this article, through an analysis of controversial Chinese Ministry of Public Security forensic genetic research articles, I suggest that the exchange of objects of value in Greimas's narrative schema fits well with cognitive linguistic analysis of how synecdoche and metonymy provide forms of contiguity that are vital to textual cohesion and coherence of forensic genetic research articles. A synthesis of Greimas's semiotics and narratology with cognitive linguistics' metonymic theories has two major advantages.

First, cognitive linguistic theorizations of synecdoche and metonymic chains can help account for Greimas narrative exchanges of objects of value, which is of significance to semiotics. Recent re-theorizations in the field of cognitive linguistics on how metonymy and synecdoche form chains can be developed further by synthesizing them with Greimas's narrative schema. This integration creates a concise model of analysis for empirical application. The transfer of objects of value involves an economy of communication in which argumentation, particularly syllogisms, is crucial for the coherence of each utterance and the one that precedes it and the one that follows relies on the metonymic contiguity of events in a narrative that Steen (2005b, p. 307) refers to. These chains are often intertwined and implicated in each other (Brdar-Szabo & Brdar, 2011, p. 229-33). Within traditional cognitive linguistics (e.g., Lakoff & Johnson, 1980), it is customarily assumed that metonymy implies a conceptual mapping from a source concept (e.g., CAPITAL) to a target concept (e.g., GOVERNMENT). However, Wachowski (2019, p. 29) rejects such an account, instead arguing that metonymy works through inference: "In a metonymic relationship both the source and the target are conceptually present. The target then is not substituted by the source but is conceptualized by means of its relation to the source" (Wachowski, 2019, p. 29).

Second, Greimas' universal (canonical) narrative schema's emphasis on exchanges of objects of value among actants can explain the way in which metonymic chains provide cohesion and coherence in texts, which is of significance to cognitive linguistics. It contributes a response to critiques (e.g., Fisher, 2003, pp. 495-6) that cognitive linguistics often resorts to extensive lists of metonymic transfers and yet fails to deal with the larger context and the attendant role of tropes as rhetorical devices that are crucial to understanding thought processes.

In this article, I show how synecdochic and metonymic transfers that are crucial to the exchanges of objects function through syllogisms within the organizing narrative schema. However, rather than follow the idea of synecdoche as a form of metonymy, as espoused by, for example, Jakobson (1956), I will draw on more recent theorizations that distinguish between synecdoche as based on categorization and metonymy as rooted in partonomy (Bierwiazzonek, 2020, p. 228; Wachowski, 2019, pp. 67-73).

Greimas's narrative schema has been criticized as being too structuralist or rigid due to its origins in Vladimir Propp's studies of Russian folklore; indeed, folklore is often highly formalized in terms of its plot structures and elements (Wales, 2011, pp. 53-4). However, scientific research articles are also highly formalized, which makes them ideal for analysis using

Greimas's narrative schema.² Yet applying this analytical model to Chinese Ministry of Public Security scientists' forensic genetic research papers on Uyghurs from the Xinjiang Uyghur Autonomous Region in northwest China is anything but routine in its findings. For these are not just routine articles; rather some have been retracted by prominent international journals due to major controversies over informed consent and other ethical concerns due to Chinese government mass repression in Xinjiang (Moreau, 2019, p. 38; Normile, 2024; Wee, 2021). In fact, these Chinese Ministry of Public Security articles are accounts of repression that semiotics and cognitive linguistics can provide insights into. For as legal theorist Raphael Lemkin advocated in his development of the concept of genocide, it and other crimes against humanity are all too common and therefore require detailed and systematic analysis (Lemkin, 1944, pp. 80-1).

Using this synthetic approach of semiotics and cognitive linguistics allows understanding how scientists select and enrol Uyghur research subjects and take biometric and ancestry data and blood samples. These blood samples are processed in labs into data and analysed to create findings. However, this metonymic chain maintains its Uyghur identity from donors to blood samples and findings. It is not a matter of "substitution", but rather the internal cohesion of the scientific article relies on this chain in which blood samples are taken and processed through various means. Indeed, some of the experimental processes are outlined very briefly or schematically and rely on readers' ability to use Idealized Cognitive Models to understand the missing information (Wachowski, 2019, pp. 25-26).

The remainder of this article is organized into four main sections. In Section 2, I provide a brief introduction to the crisis over crimes against humanity in Xinjiang and how it developed out of the so-called War on Terror. In Section 3, I provide a brief literature review of synecdoche in forensic genetic analysis to set up an extended analysis of Chinese Ministry of Public Security articles and how synecdoche and metonymy function through syllogisms to articulate the phases within the narrative schema in these articles. Section 4 summarizes these findings in terms of deductive synecdoche transfers and inductive synecdoche-metonymic transfers linking together the various stages of forensic genetic article narrative schemas. Finally, I conclude with the main findings in Section 5.

2. Context: Crimes against Humanity in Xinjiang

After the George W. Bush Administration's declaration of the so-called "war on terror" in 2001, the People's Republic of China (PRC) quickly coopted this war-on-terror discourse, claiming that China was a victim of international terrorism in the Xinjiang Uyghur Autonomous Region from Uyghur extremists operating in northwest China (Roberts, 2020, pp. 66-88).³ In July 2009, Han Chinese-Uyghur interethnic riots broke out in which some 200 people were killed in the Xinjiang provincial capital of Urumqi (Roberts, 2020, pp. 146-8). In addition, there were a series of terrorist attacks the Chinese government blamed on Uyghur separatists, which some Xinjiang scholars like Smith Finley (2019) and Roberts (2020, pp. 161-197) argue were reactions to escalating Chinese repression. Since 2017, there has been increasingly genocidal Chinese state political and cultural repression against the Uyghurs and other largely Muslim peoples in Xinjiang. This repression has included mass imprisonment in reeducation camps, destruction of mosques, cemeteries and other holy sites, use of residential schools for children and a host of other measures that seek to forcibly assimilate these peoples (Byler, Franceschini, & Loubere, 2022; Clarke, 2021; Roberts, 2020, pp. 199-235).

² Further, the founders Actor Network Theory, Bruno Latour (1987) and Michael Callon (1986), make extensive use of Greimas's semiotic theories (Cooren, 2000, pp. 183-7).

³ By contrast, before the 9/11 attacks, such separatist movements and any local clashes with PRC police over land and resources and police abuse had been framed by the Chinese government as the actions of "counterrevolutionaries" (Roberts, 2020, pp. 66-88; Rodríguez-Merino, 2019).

In the early 2010s, the Chinese state security apparatus began extensive biometric research and development targeting Uyghurs and other Indigenous peoples as well as Han Chinese (Clarke, 2021; Munsterhjelm, 2023; Wee, 2019).⁴ As part of these efforts, the Chinese Ministry of Public Security's Institute of Forensic Science and other Chinese state security agencies began long-term programs on individual, ancestry and phenotype marker research (Munsterhjelm, 2023, pp. 141-3; pp. 199-210; Wee, 2019). These programs eventually involved thousands of Uyghurs and other Indigenous peoples as research subjects (Wee, 2019). In the time since, there have been hundreds of forensic genetic articles published by Chinese security agency affiliated scientists (sometimes in cooperation with Western scientists) that have used Uyghurs and other Xinjiang Indigenous peoples as research subjects (Moreau, 2019, p. 38; Normile, 2024).

However, since 2018-19, the resulting articles have become highly contentious with many articles retracted and many more under review with significant coverage of these controversies in major media outlets (e.g., Moreau, 2019; Wee, 2021). These conflicts also played out in international diplomacy, with the US government imposing sanctions in 2020 against the Chinese Ministry of Public Security's Institute of Forensic Science over repression in Xinjiang, then lifting them in 2023 in order to gain Chinese government cooperation on reducing the export of fentanyl related chemicals (Alper & Martina, 2023).

3. Synecdoche and Metonymy in Forensic Genetic Articles

Before I provide detailed analysis of the Chinese Ministry of Public Security articles, it is useful to review some of the research that mentions synecdoche done in security studies and science and technology studies. The references I have found only mention “synecdoche”, not “metonymy”, but given that the concepts are understood differently in the literature, some of these studies also deal with metonymy, as understood in the present article. A number of analysts have conceptualized how the human body is represented in forensic genetic technologies using a *part for whole relationship*. Pugliese (2010) includes DNA profiles as part of a “biometric template” along with fingerprints, photos and other measurements of the body. He describes these in terms of being “body-bits” that act to represent the individual as a legal subject, both in criminal proceedings and counterinsurgency (2010, p. 23, 73, 97). Pugliese, Sherwin and Wagner (2014, pp. 651-2) consider the significance of “synecdoches of the legal category of the subject. In particular, the biometric template must be conceptualised as juridico-political entity as it synecdochically functions to constitute and reproduce the legal category of the person-as-subject.” Lynch et al. (2008, pp. 273-4) analysed so-called “John Doe” warrants filed by prosecutors based on DNA profiles of unknown suspects, the first being filed in California in 2000. They comment that such “synecdoche for an unknown person is a further instance of the contemporary trend to treat ‘DNA’ as the essence of a person.” In their analysis of murdered and missing victims of Mexico's drug war, Smith and Garcia-Deister (2017, p. 691) mention how, “DNA samples in biobanks can become a synecdoche for the body itself and for the missing more broadly.” In his study of forensic genetics in the use of DNA dragnets (mass sampling) in the Dutch justice system, Toom (2012, pp. 163-4) uses the concept of sample/ID packages in which, a “DNA profile represents a known body and, as such, stands proxy for an identified individual” through synecdoche. Approaching genetics in terms of tropes, Judith Roof discusses how synecdoche functions in forensic science in the representation of individuals through a limited number of DNA markers called short tandem repeats, such as the 13 STR markers used in the US Federal Bureau of Investigation developed CODIS (Combined DNA Identification System) criminal databases (Roof, 2007, pp. 189-90). Therefore, we can see how analysts have identified the function of synecdoche – understood in a broad, Jakobsonian fashion – in representing individual criminal suspects.

⁴ Professional disclosure: I cooperated with Wee on the 2019 *New York Times* article, which is based on my research (Munsterhjelm, 2023, pp. 278-281).

The polysemy of DNA also means that changing markers allows access to different forms of identity, including racial categories. In their analysis of working definitions of race and ethnicity used in genetic research (including forensic genetics), Panofsky and Bliss (2017, p. 68) found that in research articles, “the methods section reveals synecdoche, whereby smaller populations defined by distinct logics are taken to be representative of larger ones. Claims about ‘Africans’ are thus based on a ‘West African’ sample that is actually made up of 120 people from ‘Ibadan, Nigeria.’ ‘European’ claims are based on a ‘North European’ sample composed of 120 ‘European American chromosomes’ from individuals of ‘North European’ ancestry, from ‘Utah, USA.’” Forensic geneticists have made use of established racial categories since its initial invention in 1984 (Kahn, 2015). During the late 1980s and 1990s, early forms of individual testing, like those using restriction fragment length polymorphisms, were phrased in terms of random match probabilities of two individuals having the same set of markers within a given racial population, e.g., “Caucasian” or “Native American” (e.g., Track, Ricciuti & Kidd, 1989, p. 340, 344).⁵

After the September 11, 2001, terrorist attacks, in the name of public safety and national security, scientists expanded the scope and overtness of racial categorization into ancestry informative marker and phenotype informative marker research, development and commercialization with large-scale efforts by the US, European Union and Chinese security apparatuses (M’charek, 2008; Munsterhjelm, 2023; Panofsky and Bliss, 2017; Sachs, 2004). In these security discourses, including forensic genetic papers, Chinese and Western scientists have asked the question: *what if there are no matching individual genetic profiles in any databases to identify suspects?* (e.g., Zhao Wenting et al., 2017, p. 260). In their projects, scientists have sought to develop technologies to infer (estimate) unknown suspects’ possible ancestry and visible appearance and use these as forms of intelligence to help police and security agencies guide investigations (Kruger, 2013, p. 238). However, critical analyses of forensic genetics, such as those by Panofsky and Bliss (2017, p. 68) and Pugliese (2010, pp.17-18, 122-3) and other researchers, has not taken up how synecdoche functions in any sort of technical detail.

Conventional definitions consider synecdoche and metonymy to be forms of figurative language use, in which *synecdoche* is defined as part for whole and whole for part (e.g., <https://www.merriam-webster.com/dictionary/synecdoche>), while *metonymy* is defined as a substitution of one word by a related word (e.g., <https://www.merriam-webster.com/dictionary/metonymy>). However, these definitions have been challenged since the 1950s in semiotics, cognitive linguistics, and other fields. Central to these challenges is the idea that synecdoche and metonymy are actually modes of thought and central processes in cognition. The influential linguist Roman Jakobson proposed this thesis based on his comparative analysis of various language use disorders, which has since been developed extensively in cognitive linguistics (Jakobson, 1956; Lakoff, 1989; Steen, 2005a).

In the following section, I outline my adaptation of these tropes within the manhunting narrative schema of forensic genetic research articles. Combining this with Greimas’ semiotics, as outlined in Section 1, the transfer of objects of value in the narrative schema occurs through synecdoche and metonymy, which link together the events of the narrative schema. Through these exchanges, the scientists as receiver-subjects demonstrate the modal attributes of *wanting-to-do* in the narrative schema’s manipulation and commitment phases, *knowing-how-to-do* and *being-able-to-do* in the competence phase and *to-do* in the performance phase (Cooren & Fairhurst, 2004, p. 798). This sequence of modal attributes in a typical article includes scientists selecting and enrolling Uyghurs (and/or other Xinjiang Indigenous peoples), taking blood samples and biometric measurements from them and then processing the samples into genetic data, which is then analysed using advanced statistical techniques, and the findings discussed. These articles

⁵ Restriction Fragment Link Polymorphisms are repeating sequences of DNA that are unique to individuals, a trait that made them useful in early DNA testing technologies. Some readers may have seen news photos or TV reports featuring DNA bands in gels lit up by ultraviolet light used in this early technology, images that were common in 1990s coverage of DNA testing.

involve the coproduction of the various actants, particularly, the genetic researchers as scientists, through the synecdoche of members of their class or category while Uyghur research subjects represent particular populations and geographic regions and are also targets of investigation when these technologies are deployed in policing and national security applications (Greimas, 1971, p. 804; Reardon & TallBear, 2012, p. S235; TallBear, 2013, p. 17). This way of utilizing the universal narrative schema provides an understanding of how synecdochic and metonymic chains allow shifts in meaning that are crucial to the syntagmatic articulation of the narrative schema.

3.1. The Universal Narrative Schema Adapted to Manhunting

Forensic genetics has been shaped by an organizing narrative schema of *hunting* people, particularly those deemed threats to society (Bundgaard, 2007, pp. 252-3). This cognitive schema of state security agencies, police and military hunting terrorists and criminals is central to contemporary counterterrorism and security discourses. This was typified by US President George W. Bush's 2003 statement, "We're at war - in a different kind of war. It's a war that requires us to be on an international manhunt. We're on the hunt. It's a war that causes us to need to get the enemy on the run. We got them on the run. And it's just a matter of time before we bring them to justice" (Bush, 2003). Its modern variants involve governments protecting society from the anti-subjects of criminals, separatists, insurgents, terrorists, and others who prey on society (Chamayou, 2012, pp. 26-7, 36; Young, 2003).

These manhunt narratives can be analysed using Greimas's deep level of narrative grammar which posits two opposing quests by the subject and the anti-subject respectively. These involve what Greimas terms *isotopic spaces* "i.e. the loci where the performances unfold" and they are "equivalent, at the deep level, to contradictory terms" (Greimas, 1987, p. 78), as shown in Figure 1.

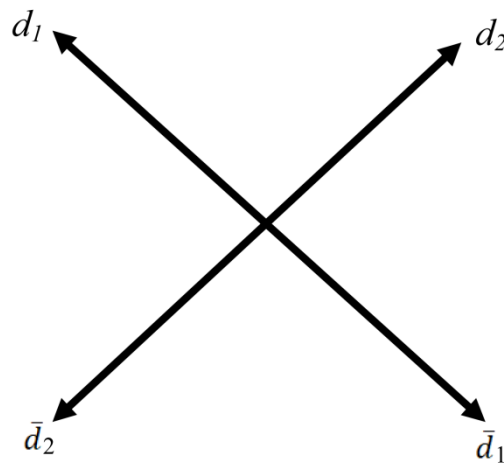


Figure 1. Semiotic square based on Greimas (1987, p. 78)

Greimas (1987, p. 78) discusses how in Vladimir Propp's Russian folktale analysis: "Society (d_1) experiences a lack, the traitor ($\bar{d}_1$) kidnaps the king's daughter (O) and takes her elsewhere in order to hide her (d_2). Greimas summarizes these functions as in (1).

$$(1) \quad F(d_1 \rightarrow O \rightarrow \bar{d}_1) \rightarrow F(\bar{d}_1 \rightarrow O \rightarrow d_2)$$

In response to the traitor's actions: "The hero ($\bar{d}_2$) finds the daughter of the king (O) somewhere (d_2) and returns her to her parents (d_1)" (Greimas, 1987, p. 78). These circulation of object-values functions involve the schema in (2).

$$(2) \quad F(d_2 \rightarrow O \rightarrow \bar{d}_2) \rightarrow F(\bar{d}_2 \rightarrow O \rightarrow d_1)$$

In particular, “The Russian folktale thus shows a circular transmission of values by successively using two performing subjects and by valorising one of the conformed spaces (that of the hero) at the expense of the other (that of the traitor)” (Greimas, 1987, p. 78). The hero’s recovery of the object (*O*), in this case the kidnapped princess, demonstrates the modal values of being-able-to-do and knowing-how-to-do, which are required to complete the quest (Greimas, 1987, p. 79). Like Russian folktales, the narrative structure of forensic genetic articles is also highly formalized and can be analysed using the same approach. In particular, we may adapt Greimas’s example to forensic genetics as follows: Society (*d_I*) experiences a lack of security in which criminals and/or terrorists (*d_I*) prey on and inflict harm on innocent members of society (*O*) and take their property and/or lives and then hide through anonymity (*d₂*). In response to the criminal and/or terrorist actions the scientists (*d₂*) help restore public safety and/or find justice (*O*) by finding the perpetrators’ identity somewhere (*d₂*) and aid police in capturing the perpetrators and making them face justice for their crimes against society and/or preventing perpetrators committing further crimes (*d_I*) (adapted from Greimas, 1987, p. 78).

Thus, scientists seek to defend society by advancing these technologies to improve police and security forces abilities to track down and capture or kill those deemed to threaten the state and its citizens (Foucault, 2003, pp. 89-90; Snoeck Henkemans, 2005, p. 435; Young, 2003). These state manhunts are justified as both punishing these anti-subjects’ unauthorized hunts for humans and trying to prevent these anti-subjects from any further unauthorized hunting of humans. These goals fit with the sociologist Max Weber’s concepts of the modern state’s claims of a monopoly over the exercise of legitimate violence (Weber, 1978, p. 56).

Having outlined the above relationship of opposing quests carried out by the subjects and the anti-subjects, next I will consider the narrative schema and its phases. In the field of organizational communication, Cooren and Fairhurst (2004) reconceptualise Greimas’s universal narrative schema as five phases, each with their respective modalities in parentheses:

- Manipulation phase: X has to or is requested/invited by Y to perform an action A (having-to-do)
- Commitment phase: X decides or agrees to perform A (wanting-to-do)
- Competence phase: X needs to know how to perform A (knowing-how-to-do), and X needs to be able to perform A (being-able-to-do)
- Performance phase: X performs A (to-do)
- Sanction phase: X is assessed by Y regarding [X] performing A. (Cooren & Fairhurst, 2004, p. 798)

Each of these phases has its own respective set of actants (human and non-human actors). The *sender*, who corresponds to Y in the above summary, sends the quest to the *receiver* who (or which) is X in the manipulation and commitment phase above. In the competence phase, the receiver is the *subject* seeking the *object* (*O*) of their quest, aided by *helpers* and resisted by *opponents* (Cooren, 2000, pp. 72-4). In the analysis that follows below, I will use this schema to analyse articles by Chinese Ministry of Public Security scientists involving Uyghurs and other Indigenous peoples.

3.2. Manipulation Phase

The manipulation phase involves a state of imbalance or situation that needs assistance. In forensic genetic organizing narratives, Society, or rather the government acting on behalf of Society, Humanity or some other entity needs help in hunting criminals, terrorists and/or insurgents (Neocleous, 2021, p. 40). The latter are, in semiotic terms, *anti-subjects* who disrupt social/political order (Smeets, 2021, p. 157). The anti-subjects' quest corresponds to (1) above. In the organizing narratives of ancestry inference and phenotype inference markers research and development, scientists frame this quest as being able to gather intelligence to direct investigations when there is no matching genetic profile in a criminal DNA database (e.g., Zhao W. T. et al., 2017, p. 260). The scientists' quest corresponds to (2).

3.3. Commitment Phase

In the commitment phase, the scientists accept this quest from Society creating a fiduciary contract (Cooren, 2000, pp. 67-8). The involved scientists coproduce their own synecdochically defined categorical role as authors by using samples and/or data from Uyghur donors as synecdochic representatives of the Uyghurs (and of other Indigenous and non-Indigenous peoples) as their objects of value. This co-production is possible through metonymic chains that retain traces of the agency of the involved scientists (e.g., they process Uyghur DNA extract into Uyghur genetic data) and so *articulate* (both in the sense of to utter and to link together) the various phases and the disparate time-spaces (e.g., experimental steps done in different places) that make up the narrative schema.

As understood in modern research, synecdoche relies upon the use of taxonomies in which higher-level more general categories already include lower-level categories (Bierwiazzonek, 2020, p. 228; Wachowski, 2019, pp. 67-73). There is a taxonomy of actant roles within the narrative schema with Greimas discussing how the asymmetrical relation between the sender and receiver is a way of transforming "transcendent values into immanent values" (Greimas, 1987, pp. 102-3). In particular, the sender is representative of a type of hyperonym (category or class) who by giving the quest for the object of value to the receiver transforms the receiver into a hyponym (member of the category or class) (Greimas, 1987, p. 103). The hyperonym and hyponym relation involves the synecdochical metonymy of a category or class and a member of that category or class (Bierwiazzonek, 2020, p. 228; Greimas & Courtés, 1983, p. 145). In cognitive linguistic terms, Bierwiazzonek argues:

Genus–species transfer, i.e. synecdoche, is based on the conceptual relation of hyponymy, i.e. the kind-of relation, while ordinary metonymy is based on various sorts of meronymy (or partonymy), i.e. the part-of relation, and thus has different logical properties, e.g. a hyponym entails its hyperonym, which is not the case in ordinary metonymic source-target relations, usually characterized by what Panther and Thornburg (2003) call "contingency." (Bierwiazzonek, 2020, p. 228)

Bierwiazzonek's approach is particularly useful in understanding the role of synecdoche in the categorical syllogisms that articulate the manipulation phase with the commitment phase. Synecdoche is crucial in the commitment phase because the scientists' reception and acceptance of the quest for the object of value (which creates a wanting-to-do modality) transforms the involved researchers into receivers (hyponym) and so into members of that category (Greimas, 1971, pp. 103-4). Therefore, in forensic genetic discourses, acceptance of the quest for security and public safety transforms involved scientists into forensic genetic researchers serving Humanity and Society. If security and public safety are transcendent universal values articulated by the sender representing Society and/or Humanity, then the forensic genetic researchers as receivers are engaged in the immanent enactment and realization of these values. The scientists' enactment involves a form of fiduciary contract that derives from accepting the quest (Cooren,

2000, p. 74), something that is expressed through transcendent values in the manipulation phase and therefore defines the hyperonym. According to the cognitive semiotician Per Aage Brandt (2020, p. 47), metonymy is a vital element in professionals' identity as they leave behind indices, indicators and traces of their agency, and these – I would add – are evident in their research articles, which are scientists' accounts of their knowledge production, as discussed further below.

Use of synecdochical transfer can underpin the syllogism that is the basis of the claim to be engaged in a quest for forensic genetics knowledge. For example, in a Chinese journal *Hereditas* (Beijing) article on facial morphology (shape), Li Y et al. (2018) enrolled and sampled 715 Uyghurs from Tumxuk in southwest Xinjiang. This article was coauthored by Chinese scientists from the Chinese Academy of Sciences-Max Planck Society Partner Institute of Computational Biology in Shanghai, the Beijing Institute of Genomics and Chinese Ministry of Public Security's Institute of Forensic Sciences in Beijing. The authors use a strong deductive synecdoche-based syllogism shown in (3).

- (3) *Major premise.* The authors define the importance of the quest for understanding the genetics of facial shape traits among human populations (hyperonym).

Minor premise. They now engage in what is termed a specialization synecdoche and specify the lack of studies on non-European populations means the findings may not be generalizable outside Europe.

Conclusion. The authors submit to the quest through their research projects in a hyperonym (category) to hyponym (member of category) synecdochic relation that articulates the manipulation and commitment phases of the forensic genetic narrative schema.

This set of synecdoche-based transfers is enacted through a series of syllogisms that define and coproduce not only the researchers as scientists but also the Uyghur research subjects whose blood samples and information function as objects of value. The scientists use the Uyghurs as objects of value by moving from the general hyperonymic category of human populations to regional continental groupings like European and East Asian and Eurasian. These continental designations blend these two larger racial continental categories that define Uyghur as European-East Asian or Eurasian in a CATEGORY FOR MEMBER OF CATEGORY synecdoche.

3.4. Competence Phase

The competence phase occupies most of an article and includes sub-narratives (like scenes in a movie) for the steps through which the scientists accomplish their specific quest to aid the general good of Society and/or Humanity. Each of these sub-narratives can in turn be analysed using the same five-phase model (Cooren & Fairhurst, 2004). The competence phase's series of sub-narratives are articulated (linked together) through inductive syllogisms that move incrementally from the frame of the scientists' specific project to return to the frame (time-space) of universal scientific knowledge. In particular, these syllogisms involve generalizing synecdoches, which move inductively from member of category to category, as involved scientists situate their specific research paper within the larger field of scientific research by arguing they have advanced knowledge of forensic genetics through their research project. This inductive sequence of syllogisms involves the shift MEMBER OF CATEGORY FOR CATEGORY. This shift blends both synecdoche (categorization-based) and metonymy (contiguity-based) in that the donors are synecdochic representatives of the Uyghurs in a series of metonymic source-to-target contiguous transfers like Uyghur genetic data FOR Uyghur DNA extract FOR Uyghur donors' blood samples. The scientists conduct statistical tests and analyse the results to create findings, which are systematic and viable explanations that fit the available evidence and theoretical paradigms. These claims involve a metonymic chain of transfers that link together the various sub-narratives into a coherent whole.

Each process step in this synecdoche guided metonymic chain of transfers elaborates further information (Denroche, 2015, pp. 120-122) about Uyghurs and other peoples. Likewise, in each step new forms of attributes and attendant forms of scientific researchers' agency are enacted as the input from the previous step is processed into an output. For example, blood samples are processed into DNA extract, which is then processed using lab equipment and chemicals and analysed using genetic sequencers and/or other scientific instruments. So, each step elaborates new attributes and forms of agency in a metonymic chain of Product FOR Source. It is here that Wachowski's (2019) conceptualization of metonymy, mentioned in Section 1, and the notation of Y THROUGH X rather than as not Y FOR X. Still, for the purposes of this article I will retain the established cognitive-linguistic notational use of X FOR Y. In this metonymic chain each object of exchange like blood samples is contiguous to the ones that preceded it and followed it by virtue of its place in the process chain. For example, scientists conduct statistical analysis of data produced by genetic sequencing equipment by processing DNA extract made from blood samples of Uyghurs and other Indigenous peoples. This processing involves a type of plasticity in which the Uyghur blood samples and derivative products like data carry the traces of scientists' and their equipment's agency, thereby demonstrating their modal abilities (e.g., knowing-how-to-do and able-to-do in the competence phase). Cumulatively, these demonstrations of modal abilities allow the various phases with their respective modalities to be connected into a cohesive and coherent whole (Cooren & Taylor, 1997, pp. 247-8). So, for example, the metonymic chain in which scientists take Uyghur test subjects' blood and then process those blood samples into DNA extract transforms them physically, but they still retain the identification of Uyghur as a type of synecdochical categorization. The inductive syllogisms allow the exchange of objects between temporally and spatially distinct sub-narratives of the sampling of Uyghurs in Tumxuk or Urumqi in Xinjiang in the northwest of the People's Republic of China to scientists processing these blood samples in laboratories thousands of kilometers away in Beijing or Shanghai or other major cities and subsequent transformation into data and research papers available internationally in the field of forensic genetics.

In cognitive-linguistic terms, this series of transformations involves a metonymic chain of source to target transfers as shown in (4).

(4)	Source (S)	→	Target (T)
•	Population (S1)	→	Donors (T1)
•	Donors (S2)	→	Blood Samples and Biometric Data (T2)
•	Blood Samples (S3)	→	DNA Extract (T3)
•	DNA Extract (S4)	→	Genetic Data and Biometric and/or Ancestry Data (T4)
•	Genetic Data and Biometric and/or Ancestry Data (S5)	→	Findings (T5)

Since all stages of this chain involve synecdochic categorization, these transfers can be diagrammed as in Figure 2.

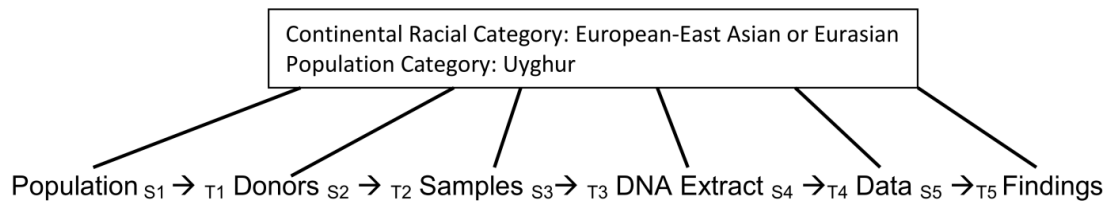


Figure 2. Sequence of subject to target transfers in competence phase of genetic article (based on Brdar-Szabo & Brdar, 2011, p. 233).

These material, textual and cognitive traces allow the organization to extend across time-space. The organizing properties of objects through the synecdochic chains and metonymic chains that creates contiguity between the materiality of blood samples and data allows the forensic genetic research assemblage as an “organization to transcend the bounds of local interaction, which is inherently ephemeral, transitory” (Cooren & Taylor, 1997, p. 247). The synecdoche-metonymic chain in (4) and Figure 2 involves the following five transfers, in the reverse order of each step.

3.4.1. DONORS (T1) FOR POPULATION (S1)

In forensic genetic research, involved scientists claim that they obtained free and informed consent from participating Uyghur research subjects. For example, Li et al. (2018, p. 1026) state: “The study has been reviewed by the Ethics Committee of the Ministry of Public Security’s Physical Evidence Identification Center, and all subjects have signed informed consent” (translated from Chinese). A typical informed consent claims involves a PRODUCT FOR PROCESS metonymy in which the subjects’ signing informed consent form stands FOR the subjects’ approval to participate having undergone after the informed consent process and thereby be willingly enrolled in the project. This is an example of what Radden and Kövecses (1999, p. 39-40) call a Production Idealized Cognitive Model, which can be analysed as a narrative schema, a sub-narrative nested within the overall article organizing schema.

The following is a typical statement about the enrolment of research subjects: “The samples were collected from Tumxuk City, Xinjiang Uyghur Autonomous Region, with a total of 715 Uyghur individuals, including 688 males and 27 females. The ages ranged from 16 to 59 years old with an average age of 35.5 years old” (Li Y. et al., 2018, p. 1026; translated from Chinese). Li et al. (2018, p. 1026) describe the donors as Uyghurs as “a typical mixed East Asian and European group” using the synecdoche CATEGORY FOR MEMBERS OF CATEGORY. This categorizes potential donors by asking them questions about their ancestry, which shows the synecdoche of Uyghur FOR Eurasian (MEMBER OF CATEGORY FOR CATEGORY) in the ancestry criteria that all their parents and grandparents were of Uyghur origin. Furthermore, it is stated that those enrolled did not have any medical conditions that might affect their appearance like thyroid disease or gigantism (Li et al., 2018, p. 1026). These criteria involve the synecdoche TYPICAL MEMBER OF CATEGORY FOR CATEGORY in that scientists seek to select prototypical members of this category who are representative of normal genetic variation in the population (Bierwiazek, 2020, p. 227; Lakoff, 1989, pp. 12-14; Radden & Kövecses, 1999, p. 35; Wachowski, 2019, pp. 63-4). As well, there is a polemical aspect to this prototypical categorization of the normal versus the pathological as discussed by Canguilhem (1978 [1966]).

3.4.2. BLOOD SAMPLES, ANCESTRY AND BIOMETRIC DATA (T2) FOR DONORS (S2)

In phenotyping research on the face, scientists take 3-D facial images from which they calculate various distances between facial landmarks like the inside and outside of the eyes, bridge and base of the nose, corners of the mouth, along with weight and height and other biometric measures of the Uyghur donors. This emphasis on the face involves a general FACE FOR PERSON metonymy and also MEASUREMENTS FOR PERSON MEASURED (Barcelona, 2005, p. 315).

Researchers draw blood from the selected donors, and these blood samples are immediately refrigerated or frozen, which involves a metonymy of SALIENT BODY PART FOR PERSON (e.g., Li et al., 2018, p. 1026) (Barcelona, 2011, pp. 14-15). The scientists now have the blood samples and biometric data needed for the genome wide association testing, which seek to find associations between genetic markers and facial features. However, blood samples first require further processing.

3.4.3. DNA EXTRACT (T3) FOR SAMPLES (S3)

The scientists process the blood samples using a centrifuge to spin the samples at high speed to extract DNA. This processing also seems to use a SALIENT BODY PART FOR PERSON metonymy (Barcelona, 2011, pp. 14-15).

3.4.4. GENETIC DATA (T4) FOR DNA EXTRACT (S4)

Scientists next use genetic sequencers and other testing equipment to process the DNA extract into genetic data. This can involve a couple of distinct types of transfers depending upon the type of genetic sequencing for individual, ancestry, and/or phenotype (physical traits).

- a. ANCESTRY SINGLE NUCLEOTIDE POLYMORPHISM (SNP) DATA FOR DNA EXTRACT. Ancestry DNA testing involves relatively few markers called *single nucleotide polymorphisms* (SNPs) that are differences in a particular base pair in the DNA sequence.⁶ There are millions of SNPs within human genomes. For example, Li Caixia and her colleagues at the Ministry of Public Security's Institute of Forensic Science developed a 27-SNP marker ancestry inference panel by using blood samples and data from hundreds of Uyghurs and other Xinjiang peoples, as well as Tibetans (Jiang Li et al., 2017; 2018; Wee, 2019).
- b. PHENOTYPE SNP DATA FOR DNA EXTRACT. In phenotype inference SNP markers research, the scientists used US-made Illumina chip-based genetic systems to test DNA extract for large numbers of SNP markers, 650,000 or more (e.g., Li et al., 2018, p. 1026). In the next stage of testing, forensic scientists combined biometric 3D facial mapping measurements with the SNP genetic data. In this stage, the scientists used the statistical techniques of linear regression and principal components analysis to test for associations between SNP markers and particular facial features. This stage tries to link different variants of genes with particular physical traits, like chin shape or ear shape (Peng et al., 2016, pp. 102-6), and involves the metonymy of CONTROLLER FOR CONTROLLED (Radden & Kövecses, 1999, p. 40), in which genetics control physical appearance traits. Facial and other visible trait phenotype research relies upon ideas that genetics are inherited and control physical appearance. This also seems to interact with the metonymy SALIENT PROPERTY FOR CATEGORY (Radden & Kövecses, 1999, p. 36).

⁶ For example, in a G for C substitution, a guanine (G) nucleotide replaces a cytosine (G) nucleotide in a base pair. There are over three billion base pairs in the human genome.

3.4.5 FINDINGS (T5) FOR GENETIC DATA, BIOMETRIC AND/OR ANCESTRY DATA (S5)

In the discussion sub-narrative, the involved scientists argue that they have helped advance knowledge about their intended topic of ancestry or phenotype genetics as part of the conclusion of this inductive argument. They do this by placing their findings in relation to other already published research, particularly how their findings are significant. There are two transfers involved here:

- a. SPECIFIC GENETIC FINDINGS FOR GENETIC DATA. The scientists combine and process data from the different populations using software programs like STRUCTURE to produce statistical findings, graphs, and heatmaps and other visualizations that allow comparisons between populations.
- b. UNIVERSAL GENETIC FINDINGS FOR SPECIFIC GENETIC FINDINGS. They further analyse and discuss the significance of their findings in relation to the field. For example, Li et al. (2018, p. 1031) state that variants of the gene they identified affect chin shape, which is relevant to developing forensic genetic phenotyping so police will have “more initiative and more intelligence” to use in investigations.

3.5. Performance Phase

The preceding competence phase with its sub-narratives involves a sequence of inductive syllogisms about the sampling, processing and findings about Uyghurs and other Indigenous and non-Indigenous peoples. In the performance phase, the scientists assert they have demonstrated the necessary competences (and attendant modalities) and thus they make a claim of completing their quest for knowledge and restate what contribution they have made in relation to the field of forensic genetics. Yet the quest is not complete because it could be rejected in the following phase.

3.6. Sanction Phase

Sanction is the reward or punishment depending on the success or failure of the research. Editors and peer reviewers act as representatives of the sender of Society and/or the discipline. Positive sanction is implicit in the journal publication that the researchers have succeeded in their quest. However, their paper may be challenged or even discredited later, a form of negative sanction (Latour, 1987, pp. 91-2), which has occurred with Western publishers like *Springer* retracting articles by Chinese security agency researchers, including the Ministry of Public Security’s Institute of Forensic Science (Wee, 2021).

4. Summarizing the Deductive and Inductive Transfers

In this section, I concisely summarize the model of how synecdoche-mediated syllogisms in the narrative schema progress *deductively* from the manipulation phase to commitment phase, while other synecdoche-mediated syllogisms, combined with metonymy, function in the *induction* that run from the competence phase to the sanction phase. The narrative map shown in Figure 3 provides a way of visually conceptualizing how a typical scientific article, such as those here analysed, hierarchically articulates, both in the sense of uttering and linking, a series of disparate actants in their respective time-spaces into a circuit of genetic research production and accumulation. In this circuit, forensic genetic researchers, in their centers of accumulation like labs in Beijing, act upon and thereby govern Indigenous peoples at a distance (Latour, 1987, p. 223). With the narrative mapping, it is possible to visualize how these exchanges across different forms of time-space hierarchically articulate and govern this sequence of disparate time-spaces (what Greimas called “isotopic spaces”) into a coherent whole in articles on ancestry inference SNP markers (AISNPs) and Phenotype Inference SNP markers (PISNPs).

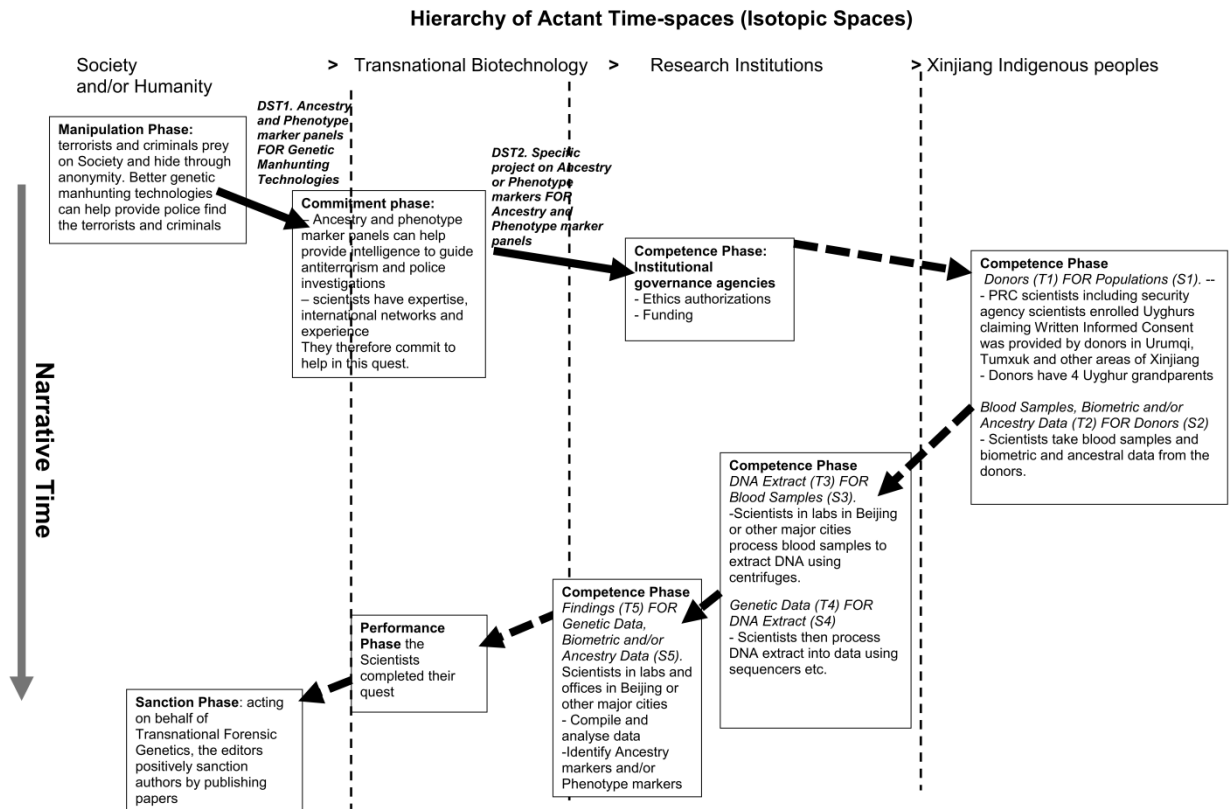


Figure 3. Map of synecdochical and synecdochical-metonymic transfers through syllogisms in forensic genetic articles. The solid black arrows indicate deductive syllogisms while the broken black arrows indicate inductive syllogisms.

The general point is that forensic genetic research articles begin by moving deductively through a series of syllogisms from the universal field of knowledge to the specific forensic genetic research project of the authors, which are mediated by the series of deductive synecdochical transfers (DST) shown in Figure 3:

- DST1. Manipulation Phase to Commitment Phase. This deductive transfer involves global knowledge of ancestry and/or phenotype genetic markers FOR forensic genetic knowledge.
- DST2. Commitment Phase to Competence Phase. Here, the deductive transfer involves specific project on Uyghurs and/or other peoples' Ancestry Inference SNP markers or Phenotype Inference SNP markers FOR Global Knowledge of Genetic Markers. Thereby, scientists have responded to Society's and/or Humanity's call for protection from criminals, terrorists and/or insurgents. This response by scientists involves a role defining act of submission, which involves a contract and so creates a hierarchical relation:

The existence of a relation of unilateral presupposition between the presupposed sender-term and the presupposing receiver-term makes communication between them asymmetrical. Thus the paradigmatic status of the sender in relation to the receiver is defined by hyperonymic relation whereas the status of the receiver in relation to the sender is characterized by hyponymic relation. (Greimas, 1987, p. 103)

Such an asymmetrical hyperonym and hyponym relation is enacted in the deductive synecdochical transfers through syllogisms that link the Manipulation Phase, in which Society as the sender asks for protection from criminals and terrorists, to the Commitment Phase, in which

forensic genetic scientists accept the quest and become receiver-subjects. This asymmetrical linkage involves a sequence of deductive synecdochical transfers from the general category of the sender to the specific receiver-subject, which is consistent with Greimas and Courtés (1983, pp. 68-9):

The deductive method can be viewed as a succession of cognitive operations leading to a “rigorous conclusion.” It is traditionally identified with syllogism. As such, deductive method is characterized by its “downward” movement, passing from the general to the particular, from the class to its components, etc., and, more specifically, by its character as a construction, which avoids constantly calling upon “experiential data.” (68-9)

Thus, in this case experimental data is not significant in the synecdochical mediated linkages between the manipulation phase and the commitment phase that define the forensic genetic authors’ quest. However, this experiential data as experimental data becomes pivotal in the inductive stages of the narrative schema from the Competence Phase to the Sanction Phase that were analysed in Section 3.4:

1. DONORS (T1) FOR POPULATION (S1)
2. BLOOD SAMPLES, BIOMETRIC AND/OR ANCESTRY DATA (T2) FOR DONORS (S2)
3. DNA EXTRACT (T3) FOR BLOOD SAMPLES (S3)
4. GENETIC DATA (T4) FOR DNA EXTRACT (S4)
5. FINDINGS (T5) FOR GENETIC DATA, BIOMETRIC AND/OR ANCESTRY DATA (S5)

Induction in scientific reasoning is a vital process in the development of new knowledge: “a series of cognitive operations, carried out at the moment of description (of the construction of a model), which consists in passing from a component to a class, from a particular proposition to a more general proposition, etc.” (Greimas & Courtés, 1983, p. 155). This movement is evident in Figure 3 beginning in the Competence Phase, in which the sequence of inductive syllogism metonymic transfers syntagmatically moves forward from the details of the authors’ specific forensic genetic research project to the universal scope of current scientific knowledge.

Because of the materiality of the donors, their blood and derived DNA extract, there is a metonymic contiguity based on indexical concepts of heredity and genetics that is crucial to the cohesion of the article. These synecdoche and metonymic chains link the phases of the narrative schema together through reference to synecdoche defined categorizations, which are typical of racial taxonomies shown in (5).

- (5) *Superordinate (Hyperonym)*: Eurasian or Admixed European-East Asian
Subcategory (Hyponym): Uyghurs in Xinjiang
Sub-subcategory: Uyghur research subjects enrolled in Tumxuk City or Urumqi in Xinjiang

This hierarchy of synecdoche-defined categorizations in forensic genetic research papers operates consistently with Wachowski’s contention that synecdochical shifts back and forth between superordinate categories (e.g., Eurasian) to subcategories (e.g., Uyghur) and these involve shifts (in linguistic terms: “Genus to Species”) from more inclusive to less inclusive categories (Wachowski, 2019, pp. 63-7). These all involve synecdoche transfers, not metonymy, which is also consistent with Greimas and Courtés (1983, p. 145) on the hyperonym and hyponym relation.

Conventional accounts of scientific method tend to posit that it involves deduction alternating with induction, which I largely follow in the analysis proposed above. Space does not allow for an extended discussion, but I would like to briefly point out that the observed sequence of argumentation forms in forensic genetic articles follows Charles Peirce’s sequence of scientific

method of abduction-deduction-induction (Burch, 2024). Abduction occurs in the manipulation phase when scientists create hypotheses based on available evidence such as literature reviews and their own experience. However, in contrast to the natural sciences, the important puzzle or surprising phenomena that the Chinese Ministry of Public Security scientists and their colleagues investigate is not primarily driven by their own intellectual curiosity but rather the demands of the Chinese state security apparatus. Therefore, in the Commitment Phase (Section 3.3) the scientists point out the lack of knowledge about the Uyghurs as a Eurasian population and/or discuss the lack of studies of facial shape related phenotype markers outside of European populations. The remainder of my analysis fits with the Peirce's deduction moving from the general to the specific case and the subsequent inductive experimentation that test hypotheses make up the competence phase and performance phase.

5. Conclusion

I have here argued that forensic genetic research articles' cohesion relies on reiteration through deductive synecdochic chains for classifying and categorizing the various steps, such as Uyghur donors' blood samples. In turn, synecdochic and metonymic chains are central to the inductive sequence of transformations and translations that occur through the selection and enrolment of donors, sampling and testing and processing of the samples and subsequent statistical analysis and findings. In these chains, the series of transformations, from population to subjects to blood samples to processed DNA extract to data and finding, involves Indigenous populations as objects of value circulating through a series of transformations that allows them to retain traces of scientific agency in the different time-spaces (e.g., donors in their homeland and scientists processing genetic materials in different labs around the world). This, in turn, allows the various phases with their respective modalities to be connected into a cohesive and coherent whole (Cooren & Taylor, 1997, pp. 247-8). The plasticity of the objects of value (e.g., the processing of blood samples from Uyghur donors into DNA extract and then data) in the research experiments relies upon the series of transfers that reveal further information about the Indigenous people. The syllogisms are vital to the narrative schema's polemical aspects by allowing the exchange of objects between sub-narratives and their respective time-spaces (frames), thereby ensuring the overall cohesion of the article.

Thus, synecdoche and metonymy are cognitively crucial to the manhunting organizing narratives of forensic genetics. In particular, the articulation and organization of these disparate agencies and scientists in the production circuits of forensic genetic research papers is based on the processing of Uyghurs and other Indigenous peoples as human objects of value, genetic resources in the production of scientific knowledge. The involved scientists refer to "the Uyghurs", representing these populations through possessing their blood samples, biometric and ancestry data. This possession as the basis of representation demonstrates the metonymic chain of SAMPLES FOR INDIVIDUALS and the synecdochic chain of DONORS FOR POPULATION. These synecdochic and metonymic chains articulate and thereby syntagmatically connect the distinct phases of research articles' narrative schemas.

In conclusion, analytically and theoretically, incorporating developments in metonymy and synecdoche into the narrative schema has relevance to both cognitive linguistics and semiotics. For cognitive linguistics, this synthesis provides ways of analysing how the shifts and transfers that make up metonymy and synecdoche chains fit within longer texts. For semiotics, attention to synecdochical and metonymic chains provides ways of understanding how receiver-subjects interact with objects of value to fulfil the various shifts in modality within the narrative schema. When combined these approaches can provide important insights into how scientists and their security agencies organize research that uses and targets Indigenous peoples and other racialized groups.

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