

Call for Abstracts: “Next Generation Sequencing: Challenges for Science and Society”

TATuP special topic in issue 2/2021

Extended deadline for submitting your abstract: 27 October 2020

Today, DNA sequencing has become part of the common knowledge of biological and medical research. Next generation sequencing (NGS), which was established in the mid-2000s, was the most important catalyst for this development. NGS procedures allow for the sequencing of a large number of DNA molecules simultaneously and cost-efficiently. This new procedure and the rapidly decreasing costs generated significant impacts. Knowledge production in molecular based biosciences, in particular evolutionary research but also pharmacogenomics, oncology, reproductive medicine and epigenetics increased significantly.

This TATuP special issue 2/2021 seeks to reflect on these developments. It is about chances and limits of the new method as well as its entanglement with social, cultural, economic and political challenges in the present. Focusing on ‘genetization’ and ‘molecularization’ on both an individual and collective level, actors and their practices, interests and motives as well as structures and knowledge orders need to be considered. As yet, science and technology studies focused particularly on medical, pharmacological and forensic fields of application because sequencing DNA is usually linked with these fields. This proposed special issue, however, aims to go much further. We ask for contributions on fields of application which defy disciplinary classification because they do not belong to clearly delineated disciplines, but often cross-cutting fields, e.g. archaeogenetics, genealogy, research on biodiversity and molecular (palaeo-)epidemiology. Despite the growing significance of NGS in general, its importance is often ignored in fields such as human remains and repatriation studies and genetic history. Particularly, with the establishment of new fields such as archaeogenetics or paleogenetics traditional and long-established historical disciplines are being challenged.

Expected contributions

Since sequencing DNA pervades numerous social fields there is a broad range of possible perspectives. We are looking both for contributions from all fields related to technology assessment/TA (e.g. history of science, history of technology, science studies, science and technology studies), and, particularly, from disciplines and research fields which explore aspects of NGS (e.g. cultural anthropology, sociology, history, archaeology, politics) and address the below mentioned aspects either theoretically and/or empirically or extend with regard to case studies. We also welcome interdisciplinary contributions.

Challenges that could be addressed:

Challenges to sciences: The procedures of DNA sequencing have provoked transformation processes in well-established sciences and fields of research (e.g. prehistoric archaeology). In many cases traditional boundaries have been transgressed. Pars pro toto for this adoption or integration of methods by social and cultural sciences stands the DNA supported historic research drawing on ancient DNA sampling (aDNA). Subsequently, intense debates on disciplinary self-conception and epistemological basics arose, including recent discussions about the relationship between the “two cultures” (e.g. ‘new positivism’) as well as about aspects of boundary work. Moreover, modes of cooperation or a holistic approach, as proposed under the keyword of *consilience*, could also be reflected.

Challenges to society: DNA technology has transformed the hobbyist field of genealogical research, once considered dusty and outdated, into a rapidly growing market. Private genetic analyses (*direct-to-consumer genetic testing*) – including medical services – are in great demand and have become everyday commodities while enterprises such as “MyHeritage DNA” and “Ancestry DNA” act as large-scale collectors of genetic data. What interests does the private sector pursue? How do companies deal with the collected data and how do they handle data security? What forms of regulation and deregulation can be found? Both commercial medical testing and ‘entertainment genetics’ are connected to questions of identity, but in different ways. Ancestry testing and private genetic genealogy draw from and have an effect on current identity discourses. The ensuing ‘biogeographical narratives’ certainly create and convey forms of evidence that remain largely unquestioned. While there still are no empirical analyses on the actual influence on personal identities and political constellations, there is also a lack of reflection on what non-medical applications mean both for the individual and society as a whole.

Challenges to ethics: Next generation sequencing is raising a variety of ethical questions. These days, media attention particularly is focusing on the repatriation of artifacts and human remains from medical, ethnological and anthropological collections in Europe. The mapping of the genome of indigenous peoples is also attracting media coverage. DNA sampling can be a significant power factor here and can gain profound influence on social, cultural and political action. Current provenance research benefits from DNA data when identity and origins are to be determined. Yet, there is also the risk of biologism. One of the difficult questions is who should decide whether an individual or artifact may be studied and what should happen to the obtained data. Obviously, this refers to all research carried out on people who are not in the position to give their consent. NGS analyses are also applied to a broad set of ecological and evolutionary issues. The ethical perspective is of particular importance in species protection and biodiversity research, where DNA analysis is used to implement international conventions and to curb the illegal wild life and animal products trade.

Guest editors of this TATuP special topic

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Submissions

Please send your abstract by email to redaktion@tatup.de by **09 October 2020** at the very latest. The editorial office will correspond with the author submitting the abstract.

Please respect the following directions:

- max. 1 page abstract;
- state all co-authors with their full names, email addresses and institutional affiliations.

Approximate schedule:

09 October 2020: deadline for submitting your abstract

End of October/beginning of November 2020: decision on inviting authors to submit a full manuscript

End of January/beginning of February 2021: deadline for submitting your full manuscript, followed by a double non-blind review process

Beginning/middle of March 2021: feedback from the reviewers, followed by authors' revisions until the beginning/middle of April

Middle/end of April 2021: feedback on revisions

Mid-May 2021: end of revision period

July 2021: publication (print and online)