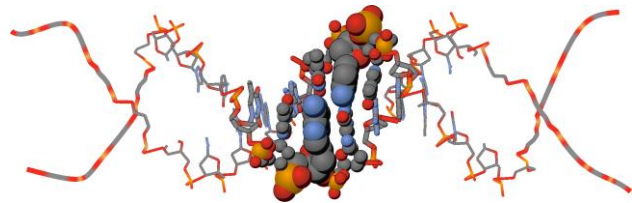**Call for applications for PhD project:**
Spatially Integrated Abstraction of Genetic Molecules

This call for candidates for a PhD position takes place within a scientific initiative of studying, understanding, and formalizing visual abstractions. By considering abstraction as a general transformation from data into meaningful visual stimuli, the project will address aspects of geometric abstraction, illumination abstraction, abstraction in terms of levels of detail, or other relevant aspects of visualization. In particular, this PhD work should focus on visual abstractions that are meaningful in context of studying DNA macromolecular structural composition and its organization into higher-level structures up to chromosomes.

This research project in the field of visualization thus involves a collaboration with researchers in molecular genetics who explore how genetic molecules such as DNA and RNA act and interact with a cell. For example, they are exploring how viruses enter a cell and integrate their viral RNA (or DNA) into the cellular DNA. The challenge in understanding these processes is that only small parts of the long-chained genetic molecules are active at a given time; yet it is important to understand their interactions in the context of their entire structure. Moreover, the active sites change over time so that, for understanding the involved processes as a whole, it is necessary to adjust the depiction accordingly. To fully understand these processes it is necessary to use different types of visualization at different levels of scale to provide both focus and detail at the same time. We thus need to employ abstraction across multiple levels of scale, from the atomic level to the scale of the chromosomes. An interesting aspect of addressing this scientific challenge is that even for the structural abstraction of the molecular data—which intuitively may be assumed to only require the manipulation of a single axis of abstraction—different abstraction axes are required: a visualization at the atomic level will require a different visualization style than at the chromosome level. The specific combination of abstraction axes and abstraction targets will highly depend on the visualization goals and questions asked: in some cases the most detailed representation should use a space-filling or balls-and-sticks or should be inspired by existing techniques. In other cases a representation using the A, C, G, and T abbreviations of the nucleobases, and yet in other cases an abstract chemical structural representations at low levels of scale is needed. Similarly, at high levels of abstraction we will need different forms of depiction to be able to answer different research questions. These forms of depiction could be inspired by scientific illustration or by other existing forms of visualization. Another potential visualization should facilitate the transition from a schematic view that uses a linear layout to the folded and rolled view of chromosomal ordering.

This work is part of a larger research project that is a collaboration between Inria in France and the TU Wien in Austria. This project explores the integrative visual abstraction of multi-aspect molecular data. The future PhD student is thus expected to closely collaborate not only with domain scientists but also with our Austrian project partners, including working on a shared implementation platform.

Required applicants skills

- highly motivated student
- Master's degree (M.Sc., M. Eng, or equivalent) in computer science or closely related fields
- education background in one or more of the following fields: visualization, computer graphics, and human-computer interaction
- interest in applications in structural biology
- previous experience in these fields (in particular, visualization) would be highly beneficial (evident, for example, in form of publications)
- experience in modern computer graphics (GPU) programming
- fluent in written and spoken English (**French language skills are not required** but would be beneficial for living in France and interacting with people outside of the lab)

Application package (to be prepared in English)

- detailed CV (including education, degrees and dates, publications/scientific presentations, skills/experiences in programming languages, project work, academic awards, …)
- motivation letter explaining why you apply specifically for this project and why you are the perfect candidate
- summary of the Master's thesis
- transcript of the grades from the Master's degree
- contact details for two or more academic references
- **prepare all application documents electronically and in English** (transcripts do not need to be translated, these are sufficient in the native language)
- send **a link** (e.g., though DropBox, Box, OneDrive, or similar services) to the application file (**one big PDF file** named **familyname_givenname.pdf**) by e-mail to Tobias Isenberg <tobias.isenberg@inria.fr>

Deadlines:

- **application deadline**: applications are reviewed as they are received; however, for full consideration please submit your application by **February 28, 2017**
- **starting date**: September 1, 2017

Contact: Dr. Tobias Isenberg <tobias.isenberg@inria.fr>
(http://tobias.isenberg.cc/)

Group: AVIZ team, Inria Saclay
(http://www.aviz.fr/)

About us: Inria is the French national institute for computer science and applied mathematics. It is recognized for its world-class contributions to computer science and is and is distributed across eight research centers located throughout France. The Aviz team is part of the research center in Saclay which is located in the greater Paris area, with many connections to universities, other research centers, and companies. Many of the Inria Saclay researchers live in Paris and commute to the lab each day. The Paris region, of course, is a vibrant urban center within Europe that offers many exciting opportunities for cultural activities, sports, and other events.