Bladder cancer is the primary form of cancer in the urinary system, accounting for about 3.2% of all cancer cases worldwide. It ranks as the seventh most common cancer among men. The cause of bladder cancer involves a combination of environmental and genetic factors, with cigarette smoking identified as the most significant risk factor. Established causes of bladder cancer include occupational exposure to aromatic amines, previous pelvic area radiotherapy, use of pioglitazone for diabetes, and chronic bacterial and parasitic infections of the urinary bladder. The primary treatment for bladder cancer is a surgical procedure that involves removing the bladder. One of the most challenging aspects for surgeons is the final stage of this procedure: reconstructing the urinary tract to enable urine elimination from the body. The preferred solution involves using a segment of the gastrointestinal tract—such as the stomach, small intestine, or large intestine—to create continent diversions. Over half of the patients who undergo bladder removal surgery face complications, with 30% needing rehospitalization and 2.3-8% dying within three months post-surgery. Utilizing the intestine to restore the urinary system's functional continuity raises the risk of urinary tract infections, electrolyte imbalances, and urinary system stones, potentially leading to deteriorating kidney function. Urinary tract infections (UTIs) are among the most frequent complications following bladder removal surgery. The balance or imbalance of the microbial community can influence the treatment's outcome. The procedure entails a radical 'microbiome shift' from the gastrointestinal tract to a vastly different body niche with distinct functions within the urinary tract.

The main goal of this project is to elucidate the gut-bladder axis and comprehend how the intestinal phageome transitions into the urinary tract phageome, as well as its impact on the bacterial part of microbiome and the clinical outcomes of treatment. This will be accomplished by identifying changes in microbial communities following transplantation and adapting gut tissue for the role of urine diversion in patients who have undergone bladder removal surgery due to bladder cancer.

This goal will be achieved through:

- the collection of microbiome material from resected urinary bladders and intestinal tissues used for reconstructions, as well as from patients' catheterized urine samples before surgery, and at one, six, and twelve months afterward,
- the bioinformatic analysis of bacterial microbiome and phageome structures, with their profiles identified through Next Generation Sequencing (NGS),
- comprehensive, multi-directional statistical analysis that incorporates patients' medical data to associate phageome structures with clinical outcomes.

We plan to employ NGS technology for virome profiling and utilize a state-of-the-art pipeline for profile analysis. This project will conduct high-throughput analyses of various virus groups and examine the virome transformation as the human intestine adapts to a new biological function within the urinary tract. Learning from the changes caused by the surgery, we will be able to understand impact of this medical intervention on the microbiome. Furthermore, correlation of phageome changes to the success, or lack thereof, of surgical procedures, we will be able to propose how to improve existing procedures for bladder removal surgery and the creation of a novel form of urinary diversion. Consequently, the findings will contribute to enhancing surgical procedures for patients with bladder cancer undergoing bladder removal surgery. The current state of knowledge regarding bladder removal surgery and the creation of new urinary diversions does not offer clear insights into the occurrence and risk factors for urinary tract infections, the differences in bacterial microbiomes among various urinary diversions, and the optimal type of perioperative antibiotic prophylaxis.