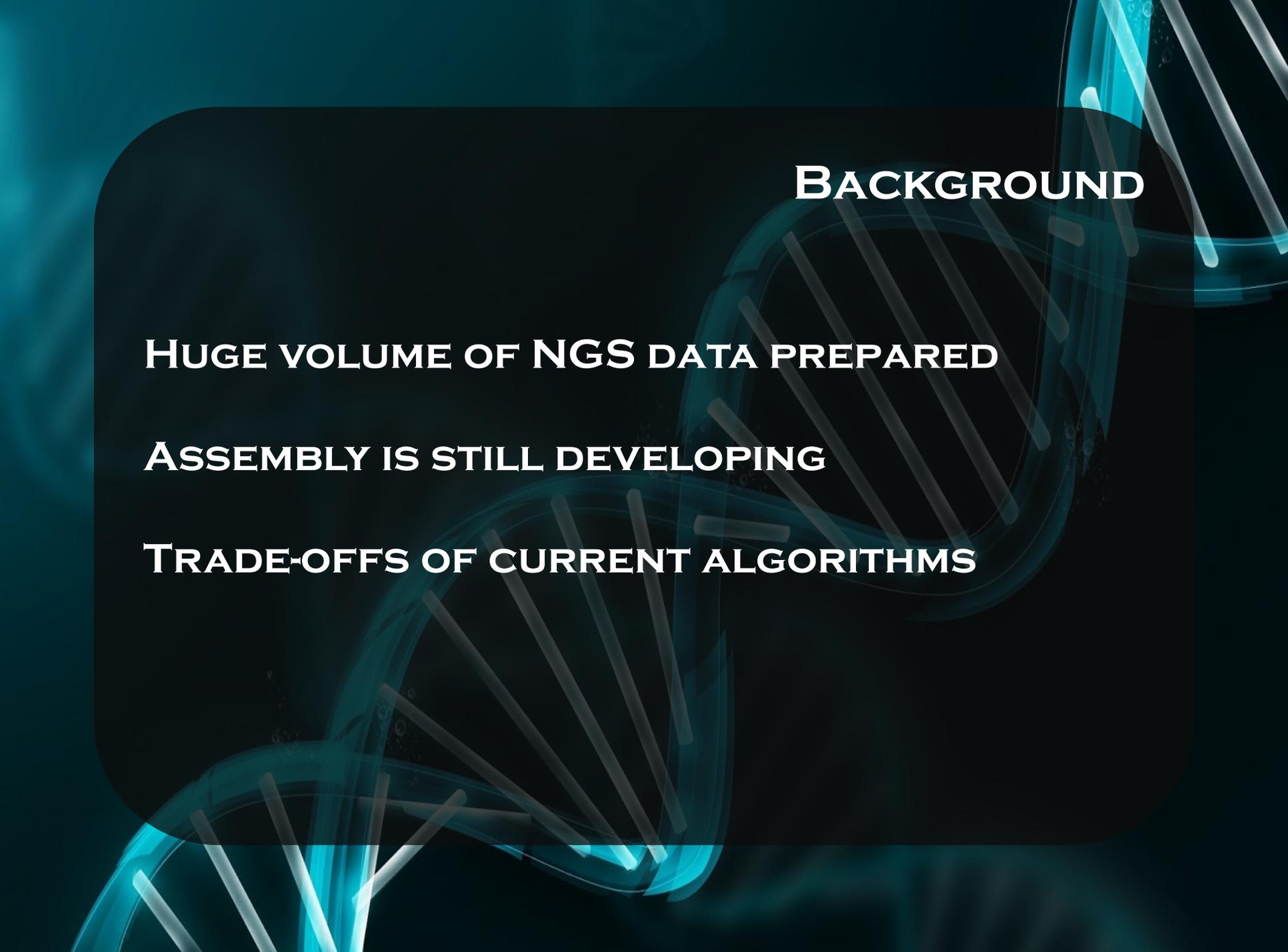


**SEQUENCE ASSEMBLY  
USING THE  
POPLAR SCIENCE  
GATEWAY**

MARY LAUREN HARRIS  
CATHERINE EASON  
BHANU REKEPALLI PHD



## **BACKGROUND**

**HUGE VOLUME OF NGS DATA PREPARED**

**ASSEMBLY IS STILL DEVELOPING**

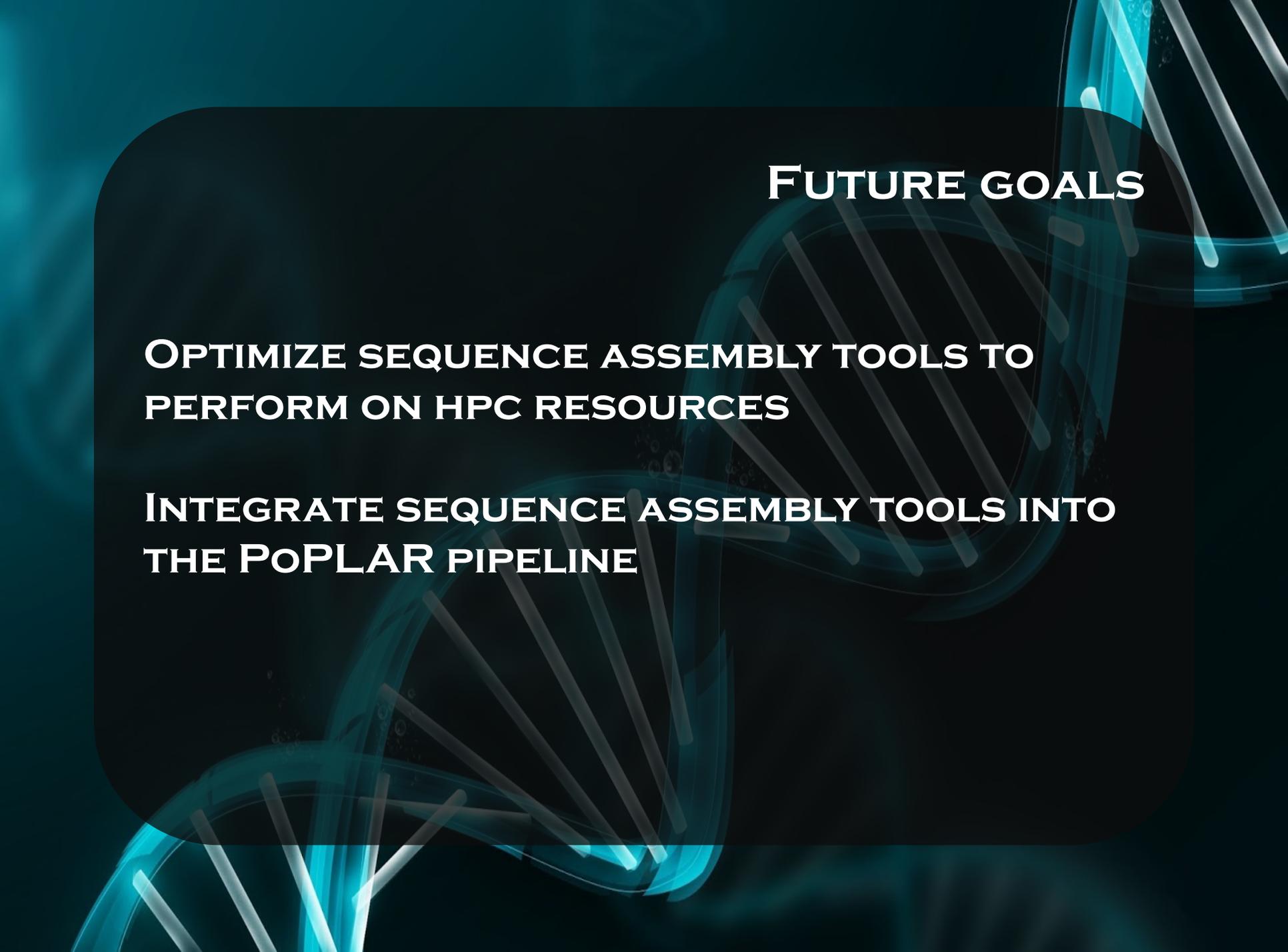
**TRADE-OFFS OF CURRENT ALGORITHMS**

## **CURRENT PROGRESS**

**INSTALLED TWO ASSEMBLY PROGRAMS:  
ALLPATHS-LG AND VELVET**

**RUNNING MPI AND HSP PROGRAMS ON  
DARTER AND NAUTILUS**

**SCALABILITY STUDIES FOR BLAST**



## **FUTURE GOALS**

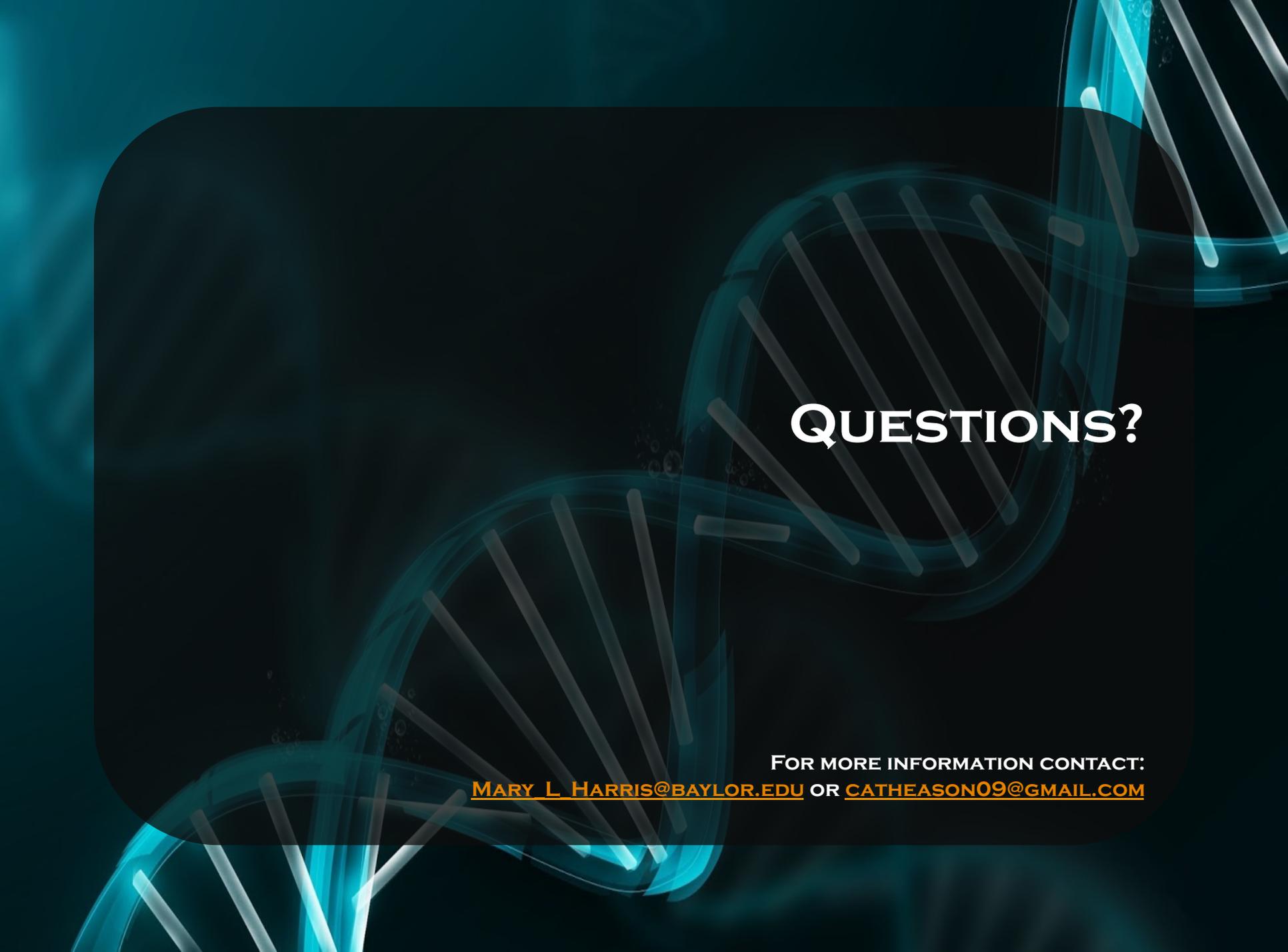
**OPTIMIZE SEQUENCE ASSEMBLY TOOLS TO  
PERFORM ON HPC RESOURCES**

**INTEGRATE SEQUENCE ASSEMBLY TOOLS INTO  
THE POPLAR PIPELINE**

## REFERENCES

**REKAPALLI ET AL.: POPLAR: PORTAL FOR PETASCALE LIFESCIENCE APPLICATIONS AND RESEARCH. BMC BIOINFORMATICS 2013 14(SUPPL 9):S3.**

**NAGARAJAN, N., & POP, M. (2013). SEQUENCE ASSEMBLY DEMYSTIFIED. NATURE REVIEWS GENETICS, 14(3), 157+.**



**QUESTIONS?**

**FOR MORE INFORMATION CONTACT:**

**[MARY\\_L\\_HARRIS@BAYLOR.EDU](mailto:MARY_L_HARRIS@BAYLOR.EDU) OR [CATHEASON09@GMAIL.COM](mailto:CATHEASON09@GMAIL.COM)**