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# Course summary of Geometry and Topology

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# Course Summary of Geometry and Topology

**by**

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# Abstract

## Course Summary of Geometry and Topology

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The foundation of Luecke's course M: 396 Geometry and Topology is that collaboration amongst mathematicians and biologists caused tremendous gains in DNA research. The field of topology has led to significant strides in understanding of the topological properties of the genetic molecule DNA. Through the integration of biological phenomena and knowledge of topology and Euclidean geometry, biologists can describe and quantize enzyme mechanisms and therefore determine enzyme mechanisms causing the changes. Understanding mathematical applications in contexts outside of mathematics on any level helps to explain why mathematics is a core content area in primary and secondary education. Requiring secondary educators to take such a course could result in mathematics taught with real world application on the secondary level as well as on the graduate level, as shown in Luecke's course.

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# COURSE SUMMARY OF GEOMETRY AND TOPOLGY

## Chapter 1: Application of Geometry and Topology to Secondary Educators

The course, M396: Geometry and Topology taught by John Luecke [**1**] at the University of Texas is very important in the teaching of mathematics in secondary schools because it shows how collaboration amongst mathematicians and scientists can lead to important scientific discovery. Students in secondary education in the United States are often taught that mathematics is the foundation of science, but they are never taught why. This could be due to the separation of the two content areas that occurs since kindergarten.

The NCTM standard on connections in mathematics requires that secondary mathematics educators help students to recognize and apply mathematics in contexts outside of mathematics. Luecke [**1**] hits this standard on a graduate mathematics level, which inspires secondary educators to see the importance of the integration of the mathematics and sciences. The foundation of Luecke's course is that collaboration amongst mathematicians and biologists has caused tremendous gains in DNA research. The field of topology has led to significant strides in understanding of the topological properties of the genetic molecule DNA. Through the integration of biological phenomena and knowledge of topology and Euclidean geometry, biologists can describe and quantize enzyme mechanisms and therefore determine enzyme mechanisms causing the changes. Understanding mathematical applications in contexts outside of

mathematics on any level helps to explain why mathematics is a core content area in primary and secondary education.

## Chapter 2: Summary of Geometry and Topology Course

Luecke [**1**] introduces Knot Theory and its application to the behavior of super-coiled DNA, especially during recombination. Luecke's course starts with a short history of DNA and shows the topological properties of knots. Luecke helps students make connections amongst topology and microbiology through the works of De Witt Sumners [**2**], James White [**3**], and John Luecke [**1**]. The next sections will explain the topological properties of supercoiled DNA and the topological changes that occur during DNA recombination.

### TOPOLOGICAL PROPERTIES OF SUPERCOILED DNA

White [**3**] explains the history of the topological properties of DNA and shows how these views have changed over time. DNA was formally thought to be a twisting of the two sugar-phosphate backbones of the DNA. Figure 1A shows the linear form commonly seen in most visual representations of DNA. The visual representation of DNA evolved to be a closed cylindrical link. Through further experimentation, DNA is found to be most commonly of the form shown in Figure 1C. For the purpose of this paper, the focus will be on the supercoiled closed DNA shown in Figure 1C, and $C$ and $W$ will represent the two sugar-phosphate backbones of the DNA and $A$ will represent the axis curve.

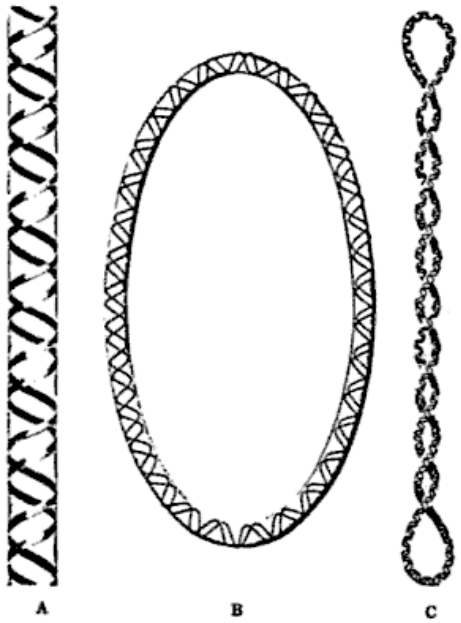



**Figure 1.** A. Double helical model of DNA. B. Relaxed closed circular form of DNA. C. The interwound form of supercoiled closed DNA. [**3**, p. 18]

Luecke [**1**] first explains *linking number* and how it helps in understanding the topological properties of supercoiled DNA. In the study of topology *linking number*, *Lk* is defined as for any curve *C* to be:

$$Lk(C_1,C_2) = \frac{1}{2}\sum_{C\in C_1\cap C_2} SignC. \qquad (1.1)$$

A sign of + or - 1 is given to each crossing of two curves. Figure 2A shows that when the top curve is rotated $90^0$ counterclockwise resulting in the two arrows pointing in the same direction the sign +1 is assigned. Conversely, Figure 2B shows that when the top curve

is rotated 90° counterclockwise resulting in the two arrows pointing in opposite directions a sign of -1 is assigned.

The linking number has two interesting properties. One is the follosing theorem:

THEOREM 1: *Let $D_1$ and $D_2$ represent the parts of a link. $Lk(D_1)=Lk(D_2)$ if and only if $D_1$ can be deformed to $D_2$ (or $D_2$ can be deformed to $D_1$) without breaking a strand.*

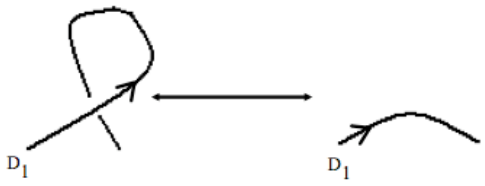
Proof: From M396[**1**]

Let $D_1$ and $D_2$ represent the parts of a link.

There are three deformations (*Reidemeister moves*) that can be done to a link without breaking a strand.

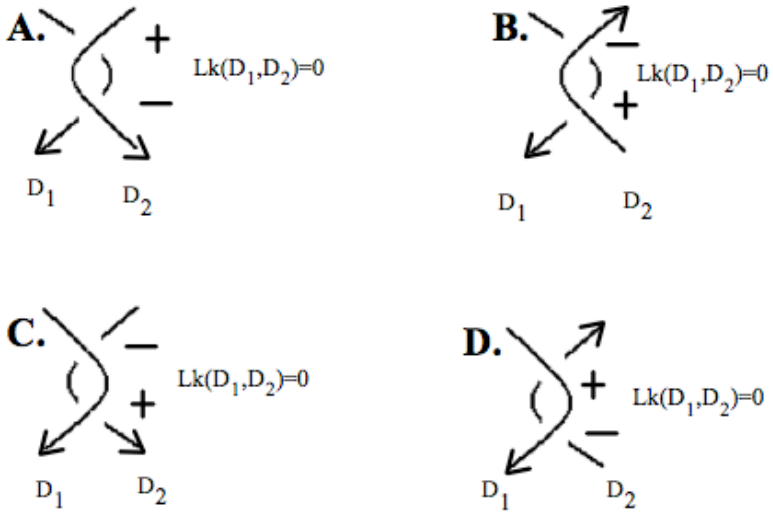
This proof is divided into three cases, one for each Reidemeister move, to show that these deformations do not affect the linking number, $Lk(D_1,D_2)$.

Case 1: Reidemeister move I



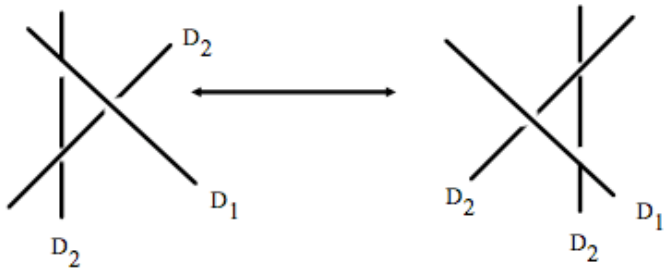

The crossing is not of $D_1$ and $D_2$ as this is irrelevant and does not effect the linking number.

Case 2: Reidemeister move II




In all 4 possible Reidemeister II moves illustrated as A-D, the signs cancel, resulting in $Lk(D_1,D_2)=0$. So this as well does not effect the linking number.

Case 3: Reidemeister move III.




There are many different cases that this move could take on, but without loss of generality, all of them would have the same linking number since the crossings move, but the number of crossings and direction stay the same.

**Q.E.D.**

The second interesting property of linking numbers is that the linking number stays the same regardless of which way you view the link. When working with DNA, the linking number is determined by the crossings of C, one of the sugar-phosphate backbone, and A, the curve axis. The linking number is denoted *Lk(C,A)*. So by determining a strand of DNA's linking number, one can determine if they are the same regardless of the view from which you see the DNA and even when one or both strands have been deformed.

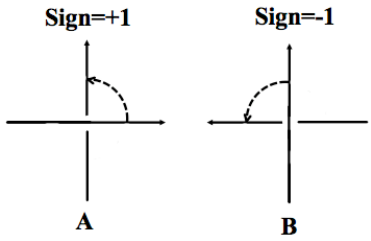



**Figure 2.** A. Positive crossing of two curves. B. Negative crossing of two curves. [**3**, p. 19]

Luecke's course next describes *writhe*, a geometric property that is a measure of distant crossings of the axis curve *A*. Writhe, Wr is a single curve property. (Figure. 3A) Writhe is defined for some curve *H* as:

$$Wr(A') = \sum_{A \in A' \cap A'} SignA \qquad (1.2)$$

Writhe is similar to linking number in that writhe is also the summing of the signs, but it is different from Linking number in that *Wr* does not imply isotopy and similarly isotopy does not imply *Wr*. (Figure. 3)

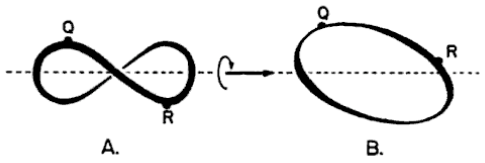



**Figure 3.** A. Illustration of a single curve. B. Illustration of curve A from a different orientation. [**3**, p. 20]

THEOREM 2: *Curve A and Curve B being isotopic does not imply that Wr(A)=Wr(B).*

**Proof:** (by contradiction)

Let Curve A and Curve B be defined as the curves illustrated below.


Curves A and B are isotopic by 1 reidemeister I move.

By definition of writhe, Wr(A)=-1, but Wr(B)=0.

Therefore, by contradiction Isotopic curves will not always have the same writhe.

**Q.E.D.**

## TOPOLOGICAL CHANGES THAT OCCUR DURING DNA RECOMBINATION

Next Luecke explains *Twist*, a geometric property that is a measure of local crossings that requires vector analysis to determine the value of the twist. White [**3**] defines twist as the measure of the change in the vector *Vac*. *Vac* is the unit vector joining the points *a* and *c*, where *a* and *c* are the points on *A* and *C* when you take a perpendicular cross section of the DNA. (Fig. 4) *dVac* is the change in the vector *Vac* as the point *a* moves up the *A* axis.

$$Tw = \frac{1}{2\pi}\int_A dv_{ac} \cdot \mathbf{T} \times \mathbf{v}_{ac} \quad (1.3)$$

Simply, twist is how much *C* twists around *A*.

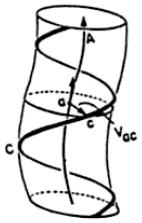



**Figure 4.** Illustration of a cross-section of DNA perpindicular to axis, A.

[**3**, p. 22]

When determining the attributes of supercoiled closed DNA the linking number can be divided into the distant crossings, Wr, and the local crossings, Tw. This is counterintuitive because linking number is isotopic whereas the writhe changes under

deformations. White [**3**] explains that the change in writhe results in an equal in magnitude opposite in sign change in twist. This can be visualized by twisting a rubber band on one side while holding the other side fixed. The rubber band will wind the opposite way onto itself. Therefore the result of DNA twisting is an equal but opposite sign writhing of the DNA. So linking number is the sum of the twisting number and the writhing number, which explains the supercoil of closed DNA.

Luecke explains that enzymes change DNA molecules in interesting topological ways including supercoiling, passing DNA strands through an enzyme-bridged break in DNA, and breaking a pair of DNA strands, then reconnecting to different ends. Luecke shows that direct experimentation of the spatial conformation of DNA, proteins, and protein-DNA complexes in solution has proved to biologists to be very difficult. Biologists consider instead indirect methods to observe the changes to DNA caused by enzyme reactions. The most common method is known as the topological approach to enzymology.

Sumners [**2**] defines the topological approach to enzymology as an experimental strategy used to observe the changes caused by the enzymes onto the Euclidean Geometry (supercoiling) and Topology (knotting and linking) of the DNA. Enzyme experimentation is performed on circular DNA substrate showing the enzymes causing various topological changes in the DNA. Figure 5 shows how an enzyme reaction can change DNA substrates topological and geometrical characteristics. Using this indirect experimentation, one can describe and quantify enzyme mechanisms and therefore determine enzyme mechanisms causing the changes.

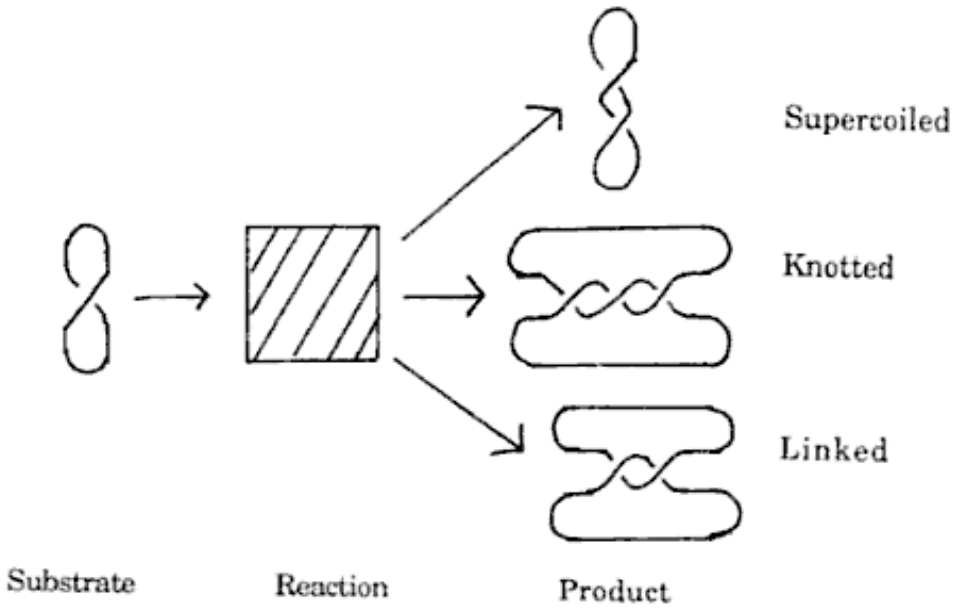



**Figure 5.** The topological approach to enzymology [**2**, p. 55]

*Recombinase* is an enzyme which involves sitespecific recombination of DNA whereas a *recombination site* is a short linear segment whose DNA general sequence is identifiable by the recombinase. Recombinase occurs when two sites get close together and become bound by the enzyme reaction, a process known as *synapsis*. Synapsis results in a protein-DNA complex of the combination of the DNA and the enzyme known as *synaptosome*. The prerecombination of the unbound DNA molecules is known as the *substrate* whereas the postrecombination is referred to as the *product*. Figure 6 pictorially shows what occurs in a recombination event. Through recombination the substrate changes in very interesting topological ways.

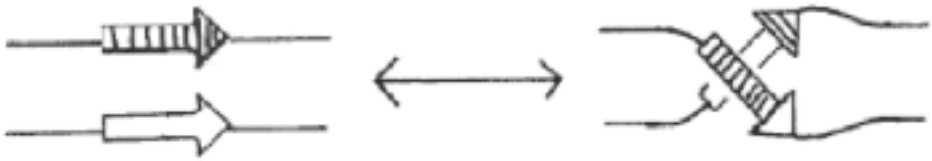


**Figure 6.** A recombination event [**2**, p. 57]

In order to observe the topological changes between the substrate and the product we must experiment on circular DNA to determine the orientation of the recombination site with the DNA. Two observable phenomena explained by Sumners [**3**] are direct repeats which occur when the orientations agree as seen in Figure 7 forming a link, and an inverted repeat that conversely occurs when the orientations do not agree, shown in Figure 8 forming a knot.

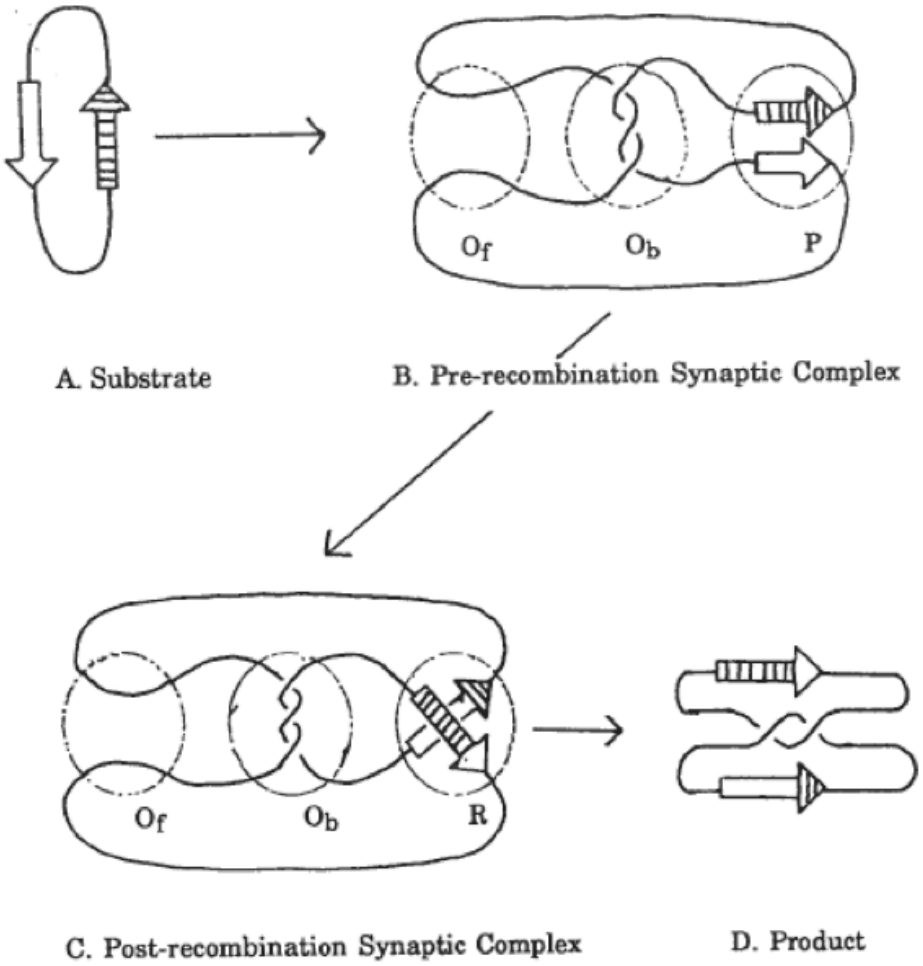



**Figure 7.** Recombination with direct repeats [**2**, p. 58]

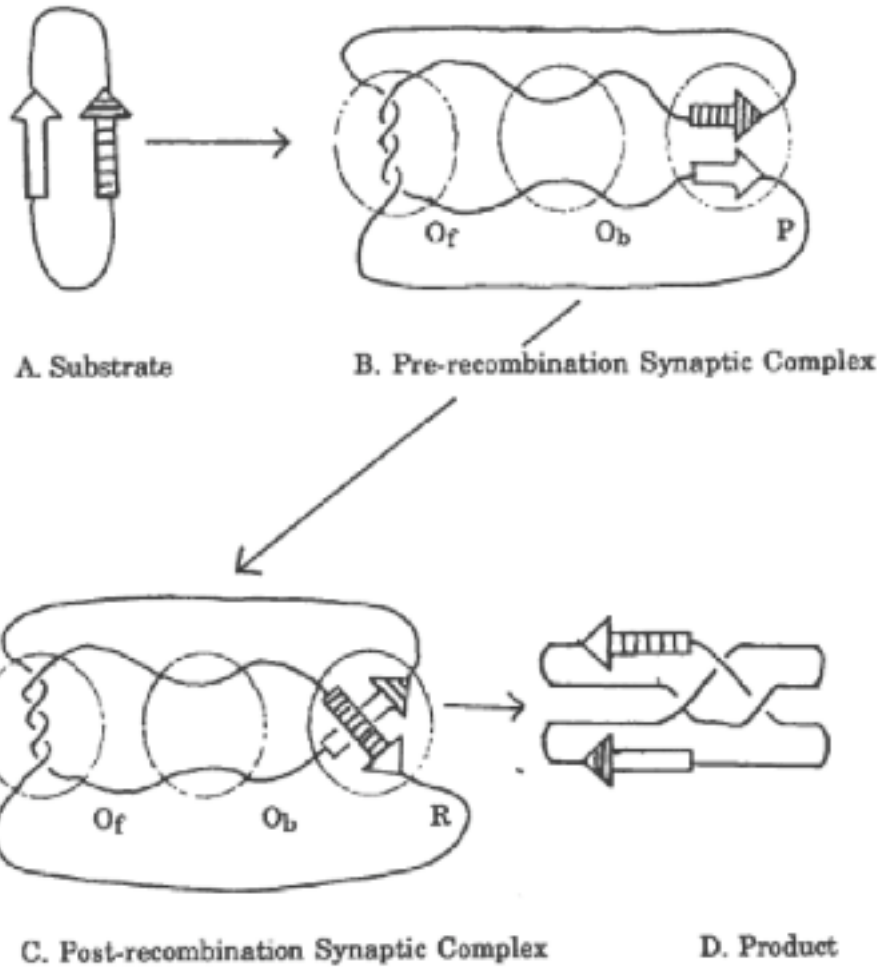



**Figure 8.** Recombination with inverted repeats [**2**, p. 59]

Since the synaptosome is too difficult to observe directly using experimentation with an electron microscope, we must determine topological changes using mathematical knowledge of topology. Using topological properties learned in the beginning of the course Geometry and Topology we can now use the topological properties of DNA to deduce the type of enzyme causing recombination of the DNA substrate.

## Chapter 3: CONCLUSION of How a Graduate Level Mathematics Course can Apply to Secondary Education

Luecke's course Geometry and Topology is different from an introduction to knot theory course because the ongoing theme of the course is the application of mathematics to the study of DNA. Understanding linking number, writhe, twist, and various other topological properties of knots may seem to be useless knowledge until it becomes known that this knowledge gives biologists an indirect way to study changes in DNA due to various enzyme reactions.

Luecke has DNA as the main theme of the course Geometry and Topology, from the beginning of the course, with the explanation of supercoiled DNA through the application of knot theory to studying the topological properties that occur during recombination of DNA.

M 396: Geometry and Topology allows secondary educators to experience being the student in an integrated science and mathematics graduate level class. Since mathematics and science have been taught disjointed for so long, many secondary educators have not had integrated classes. Therefore, they do not know how this could be incorporated into the classroom curriculum. Luecke's course teaches elementary knot theory with an application to supercoiled DNA. By teaching this real-world application of topology and geometry Luecke answers the questions, "Why do we need to know this?"

## References


1. John Luecke, (2009). M396: Geometry and Topology. University of Texas at Austin.
2. De Witt L. Sumners, Knot Theory and DNA, *New Scientific Applications of Geometry and Topology: Vol. 45. Proceedings of Symposia in APPLIED MATHEMATICS* (pp. 39-72). USA: The American Mathematical Society.
3. James H. White, Geometry and Topology of DNA and DNA – protein interactions, *New Scientific Applications of Geometry and Topology: Vol. 45. Proceedings of Symposia in APPLIED MATHEMATICS* (pp. 17-37). USA: The American Mathematical Society.

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Ms. Craig graduated the University of Texas in May 2008 with a B.A. in Mathematics, option: UTeach. She currently is a mathematics instructor at Manor New Technology High School (MNTH) in Manor, TX. MNTH is a project-based high school that incorporates the New Technology Network model by involving the 21st century skills in traditional content areas. Ms. Craig has and continues to facilitate and create project curriculum for the mathematics portion(s) of the following courses: Integrated Algebra 1 and Geometry, Integrated Algebra 1 and Introduction to Physics and Chemistry, Integrated Algebra 2 and Physics, and Integrated Statistics and Research Methods.

In addition to teaching, in November 2009, Ms. Craig helped develop and continues to serve as an instructor for the assessment portion of the Think Forward, Project Based Learning Institute. In addition to leading the training course, she mentors and provides professional development to the teachers implementing project-based learning in their classrooms. Since August 2009, Ms. Craig also provides professional development to secondary and elementary teachers in Manor Independent School District on incorporating various best practices into their classrooms as part of her duties in the leaders in education and development (LEAD) program.

In efforts to share her experiences as a project based instructor and other best practices with teachers outside of Manor, TX, Ms. Craig attends and presents at a variety of secondary teaching and mathematics conferences.

This report was typed by Tara Theresa Craig.