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Se debe indicar de forma fiel cómo va a ser desarrollada la docencia. Esta guía debe ser elaborada teniendo en cuenta a todos los profesores de la asignatura. Conocidos los espacios y profesorado disponible. Los detalles de la asignatura serán informados por el Campus Virtual.

Se recuerda la importancia que tienen los comités de título en su labor de verificar la coherencia de las guías docentes de acuerdo con lo recogido en la memoria de verificación del título y/o en sus planes de mejora. Por ello, **tanto la guía, como cualquier modificación** que sufra en aspectos "regulados" (competencias, metodologías, criterios de evaluación y planificación, etc..) deberá estar **informada favorablemente por el comité** de título **ANTES** de ser colgada en la aplicación web de la UVa. Se ha añadido una fila en la primera tabla para indicar la fecha en la que el comité revisó la guía.

Asignatura	**BIOINFORMATIC APPLIED TO FORESTRY**		
Materia			
Módulo	Optional, Block I		
Titulación	*Forest Management based on Data Science*		
Plan	428	**Código**	**54284**
Periodo de impartición	1st semester (2nd Period)	**Tipo/Carácter**	OP
Nivel/Ciclo	MASTER	**Curso**	2º
Créditos ECTS	3		
Lengua en que se imparte	English		
Profesor/es responsable/s	Julio Javier Diez Casero (https://investigacion.uva.es/CawDOS/jsf/actividades/proyectos.jsf) Aroa Suarez Vega Jonatan Niño Sánchez		
Datos de contacto (E-mail, teléfono…)	Julio J. Diez Casero jdcasero@pvs.uva.es 979108420 http://sostenible.palencia.uva.es/users/jdcasero		
Horario de tutorías	http://www.uva.es/export/sites/uva/2.docencia/2.02.mastersoficiales/ 2.02.01.ofertaeducativa/2.02.01.01.alfabetica/Mediterranean-Forestry-and-Natural- Resources-Managemeent-Medfor-Erasmus-Mundus/ https://pod.uva.es/pod/redireccionTutorias.doc		
Departamento	Producción Vegetal y Recursos Forestales/Ciencias Agroforestales		
Fecha de revisión por el Comité de Título	20 de julio de 2023		

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1. Situación / Sentido de la Asignatura

1.1 Contextualización

Biodiversity stands for all living things on earth. It refers to the range of variations among a set of entities and is commonly used to describe variety and variability of living organisms in terms of genetic diversity, species diversity and ecological diversity. In simple terms, Biodiversity is the vaste variety of natural plant and animal life existing in any region. The biodiversity is usually studied now by taxonomist who takes great pains in collecting, identifying, documenting and describing the elements of diversity. Pathogens may also limit the sites on which species can be grown successfully outside their natural range as has been experienced with red band needle blight (*Mycosphaerella pini*) and western gall rust (*Endocronartium harknessii*) infecting *Pinus radiata.*

RNA-seq enables to assess and quantify the expression levels of differentially expressed genes under contrasting environmental con ditions (Ekblom and Galindo 2011) and/or to detect previous ly unidentified genes and splice variants. A growing number of studies focused on the assembly and quantification of differential expression of mRNA have been conducted to date for different organs or tissues of tree species using RNA-seq. Data bases, whether regional, national, or worldwide, which must be known, used and mined, as a key support for diagnostic and scientifically sound decision making in forest health management.

1.2 Relación con otras materias

The curse on Bioinformatic is basically related to other in the optional module that focus on data bases general management, as *Bases de datos relacionales y SQL* y *Fundamentos de programación con Python*, and particularly to *Cambio global y bosque*, where several issues related to the introduction of alien invasive species are dealt to. Within the optional module, the action of bioinformatic is linked to other curses dealing with the processes that occur in forest communities, as *Conservación de Flora y Fauna* y *Dinámica de sistemas forestales*. Besides, they are also related the group of tools highly valuable in monitoring and damage evaluation caused by such organisms.

1.3 Prerrequisitos

None

2. Competencias

2.1 Generales

G1 Knowledge of the basic elements of professional work in practical form, analysing and synthesizing relevant data and organizing and planning teams and processes
G2 Ability of communicate in spoken and written forms, either in specialized forums or with non expert people.
G3 Knowledge, abilities and skills on computer and on technologies of information and communications (TIC)
G4 Ability of team and individual working, within a local, regional, national and international framework.
G5 Ability of taking initiatives and developing entrepreneur skills

2.2 Específicas

E8 Ability to quantify and understand the effects of several impacts in forest systems.

E11 Ability to look for, select, generate and manage suitable data bases to obtain relevant information of forest management problems.

3. Objetivos

To know the strategies, tactics and scientific and research advanced methods for the identification of organisms, genes and their function, everything applied to the management of forest pests and diseases. To find, manage, analyze and discuss the relevant information contained in national and International gene data bases.

Main concepts related to identification genes by sequencing and the control mechanisms of conifers and broadleaves related with growth, defence and growth and their importance for the competence and natural selection.

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4. Tabla de dedicación del estudiante a la asignatura

ACTIVIDADES PRESENCIALES	HORAS	ACTIVIDADES NO PRESENCIALES	HORAS
Theoretical classes	15	Autonomous learning and documentation	23
Practical classes (classroom)	5	Elaboration and preparation of individual reports	12
Practical classes (Computer Room)	10	Collaborative and group learning	10
Collaborative and group activities		Forum , virtual debate, self evaluation ,	
Seminars			
Evaluations			
Total presencial	30	**Total no presencial**	45

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5. Bloques temáticos

Bloque 1:

Forest Pests and Diseases

Carga de trabajo en créditos ECTS: 3

a. Contextualización y justificación

Described in 1.1

b. Objetivos de aprendizaje

Described in 3

c. Contenidos

1. Diagnosis of Forest Pest and Diseases: NCBI: GeneBank. Introduction to BLAST and their use to diagnostic of organisms. Bioinformatics analysis of sequencing data using MG-RAST, and Galaxy bioinformatics tools.
2. Solve given biological problems by using appropriate bioinformatic methods and databases.
3. Methods in sequence bioinformatics such as sequence alignment, phylogenetic analysis and pattern recognition.
4. Account for and use methods in structural bioinformatics such as classification of protein structures, structure prediction, simulations and structure based drug design.
5. Use and design simple scripts in R.
6. Analyze and compile results of bioinformatic analyses.
7. Next Generation Sequencing: platforms and their specific applications.
8. High-throughput sequencing, and their use for the identification of genes.
9. RNAseq and their applications to the understanding of gene expression on trees.

d. Métodos docentes

. Presentation in the classroom of concepts, contents, and practical cases

. Group discussion in the classroom

. Practical work on data bases and web sites in classroom

. Computer practices

. Seminars on current forest bioinformatic applications to forestry

. Field trip visits to microcomputer facilities

. Preparation on a written report

e. Plan de trabajo

Presential:

Attendance and discussion of concepts, contents and cases in the classroom: 15 hours.

Attendance and participation on seminars: 5 hours

Attendance, participation and discussion on issues during external visits and field trips: 10 hours

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Non Presential:

Personnel study of material and bibliographic references provided: 25 hours

Research on websites and data bases, preparation of individual report: 20 hours

f. Evaluación

Evaluation will be based on the one hand the active participation (questioning, discussion, debate) in presential activities in the classroom, seminars and field trips (40%). On the other hand, qualification will be completed by individual exercise/report prepared by the students on assigned study cases (35 %). In the exercise report, quality and suitability of contents, skills of the student and formal aspects of the report (editing, graphical information) will be valued. Furthermore, the student will be scored by a specific knowledge test (25%) about the main topics of the subject.

g. Bibliografía básica

- *Sim, A. Y. L.; Minary, P.; Levitt, M. (2012). "Modeling nucleic acids". Current Opinion in Structural Biology. 22 (3): 273–278. doi:10.1016/j.sbi.2012.03.012. PMC 4028509. PMID 22538125.*
- *Dawson, W. K.; Maciejczyk, M.; Jankowska, E. J.; Bujnicki, J. M. (2016). "Coarse-grained modeling of RNA 3D structure" (PDF). Methods. 103: 138–156. doi:10.1016/j.ymeth.2016.04.026. PMID 27125734.*
- *Kmiecik, S.; Gront, D.; Kolinski, M.; Wieteska, L.; Dawid, A. E.; Kolinski, A. (2016). "Coarse-Grained Protein Models and Their Applications". Chemical Reviews. 116 (14): 7898–936. doi:10.1021/acs.chemrev.6b00163. PMID 27333362.*
- *Wong, K. C. (2016). Computational Biology and Bioinformatics: Gene Regulation. CRC Press/Taylor & Francis Group. ISBN 9781498724975.*

- *Hall, L.O. (2010). Finding the right genes for disease and prognosis prediction. System Science and Engineering (ICSSE),2010 International Conference. pp. 1–2. doi:10.1109/ICSSE.2010.5551766. ISBN 978-1-4244-6472-2.*

- *McDonagh, J.L; Barker, D; Alderson, R.G. (2016). "Bringing computational science to the public". SpringerPlus. 5 (259): 259. doi:10.1186/s40064-016-1856-7. PMC 4775721. PMID 27006868.*

- *Robson, J.F.; Barker, D (2015). "Comparison of the protein-coding gene content of Chlamydia trachomatis and Protochlamydia amoebophila using a Raspberry Pi computer". BMC Research Notes. 8 (561): 561. doi:10.1186/s13104-015-1476-2. PMC 4604092. PMID 26462790.*
- *Wregglesworth, K.M; Barker, D (2015). "A comparison of the protein-coding genomes of two green sulphur bacteria, Chlorobium tepidum TLS and Pelodictyon phaeoclathratiforme BU-1". BMC Research Notes. 8 (565): 565. doi:10.1186/s13104-015-1535-8. PMC 4606965. PMID 26467441.*

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h. Bibliografía complementaria

http://metagenomics.anl.gov/

https://blast.ncbi.nlm.nih.gov/Blast.cgi

https://usegalaxy.org/

www.cabi.org Commonwealth Agricultural Bureaux International CABI

www.iufro.org International Union of Forest Research Organizations

https://www.bioinformatics.org/

https://toolkit.tuebingen.mpg.de/#/

http://www.ascidea.com/

www.ncbi.nlm.nih.gov/genbank/

i. Recursos necesarios

. Virtual Campus

. Classroom with audiovisuals (digital board, projector)

. Computer rooms

. Bioinformatic laboratories

. Forest sites containing experiences and cases

. Computer facilities in the Autonomous Community

.Tutorial support during the curse within the assigned timetable

6. Temporalización (por bloques temáticos)

BLOQUE TEMÁTICO	CARGA ECTS	PERIODO PREVISTO DE DESARROLLO
Bioinformatic Applied to Forestry	6	November-December 2016

7. Sistema de calificaciones – Tabla resumen

INSTRUMENTO/PROCEDIMIENTO	PESO EN LA NOTA FINAL	OBSERVACIONES
Participation in lectures, practical activities, seminars and field trips	40%	
Individual Report	35%	Written and oral presentation
Specific knowledge test	25	

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8. Consideraciones finales

Those students that did no pass and require a 2nd chance, will be asked to fulfill the same requisites as in the first evaluation.

More information is offered on the webpage of the Sustainable Management Research Institute: http://sostenible.palencia.uva.es/gfs/formacion/maestrias/7/default.aspx