Second CI²MA Workshop
"Mathematical Models in Epidemiology"
Supported by MINEDUC project UCO 1202 (REDOC.CTA) and Conicyt projects CMM-Basal, Fondecyt 11140708 and 1130154

July 6 and 7, 2016
Auditorio Alamiro Robledo
Facultad de Ciencias Físicas y Matemáticas, Universidad de Concepción

Organizers: Raimund Bürger (UdeC) and Luis Miguel Villada (UBB)

Programme

Wednesday, July 6, 2016

15.45 **Mauricio Castro** (CI²MA & Departamento de Estadística, Facultad de Ciencias Físicas y Matemáticas, UdeC):
Censored mixed-effects models for irregularly observed repeated measures with applications to HIV viral loads

16.30 **COFFEE BREAK**

17.00 **Fernando Córdova-Lepe** (Facultad de Ciencias Básicas, Universidad Católica del Maule, Talca):
Vacunación por pulsos. Frecuencia dependiente de la incidencia.

17.45 **Gerardo Chowell-Puente** (School of Public Health, Georgia State University, Atlanta, GA, USA):
Characterizing epidemic growth dynamics to improve epidemic forecasting

20.30 **Seminar Dinner**

Thursday, July 7, 2016

09.30 **Luis Miguel Villada** (CI²MA, UdeC, & Departamento de Matemática, Facultad de Ciencias, Universidad del Bío-Bío, Concepción):
Modelling the spatial-temporal progression of the 2009 A/H1N1 influenza pandemic in Chile

10.15 **Mauricio Sepúlveda** (CI²MA, & Departamento de Ingeniería Matemática, Facultad de Ciencias Físicas y Matemáticas, UdeC):
Finite volume method for a model of indirectly transmitted diseases with nonlocal cross-diffusion

11.00 **Coffee break**

11.15 **Elvis Gavilán** (CI²MA, UdeC, & Departamento de Ingeniería Matemática, Facultad de Ciencias Físicas y Matemáticas, UdeC):
A computational approach to a spatio-temporal and gender-structured model for hantavirus infection in rodents

12.00 **Concluding discussion and closing of the workshop**

Seminar participants who would like to join dinner should register with CI²MA secretary:

Ms Angelina Fritz, CI²MA
E-mail: afritz@ci2ma.udec.cl, Phone: (041) 266 1324

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CENSORED MIXED-EFFECTS MODELS FOR IRREGULARLY OBSERVED REPEATED MEASURES WITH APPLICATIONS TO HIV VIRAL LOADS

MAURICIO CASTRO

Abstract. In some acquired immunodeficiency syndrome (AIDS) clinical trials, the human immunodeficiency virus-1 ribonucleic acid measurements are collected irregularly over time and are often subject to some upper and lower detection limits, depending on the quantification assays. Linear and nonlinear mixed-effects models, with modifications to accommodate censored observations, are routinely used to analyze this type of data. This paper presents a framework for fitting LMEC/NLMEC with response variables recorded at irregular intervals. To address the serial correlation among the within-subject errors, a damped exponential correlation structure is considered in the random error and an EM-type algorithm is developed for computing the maximum likelihood estimates, obtaining as a byproduct the standard errors of the fixed effects and the likelihood value. The proposed methods are illustrated with simulations and the analysis of two real AIDS case studies.

This contribution is based on joint work [1] with L. Matos and V. Lachos from Universidade Estadual de Campinas, São Paulo, Brasil.

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CI²MA, Universidad de Concepción, and Departamento de Estadística, Facultad de Ciencias Físicas y Matemáticas, Universidad del Concepción, Concepción
E-mail address: luiscastroc@udec.cl

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VACUNACIÓN POR PULSOS: FRECUENCIA DEPENDIENTE DE LA INCIDENCIA

FERNANDO CÓRDOVA-LEPE

Abstract. Presentamos una estrategia de vacunación impulsiva para una enfermedad tipo SIS en la que el tiempo entre vacunas es función de la incidencia [1]. Esta función nos permite encontrar una condición umbral entre los parámetros para asegurar la convergencia de las trayectorias a la solución libre de infección. Se ilustran los resultados con algunas simulaciones numéricas. El formalismo matemático está dentro de cierto tipo de Ecuaciones Diferenciales Impulsivas [2, 3].

References

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Facultad de Ciencias Básicas, Universidad Católica del Maule, Talca, Chile
E-mail address: fcordova@ucm.cl

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CHARACTERIZING EPIDEMIC GROWTH DYNAMICS TO IMPROVE EPIDEMIC FORECASTING

GERARDO CHOWELL

Abstract. A better characterization of the early growth dynamics of an epidemic is needed to dissect the important drivers of disease transmission, refine existing transmission models, and improve disease forecasts. In this talk, I will discuss recent efforts aimed at improving the ability of mathematical models to forecast the spread of epidemics in the context of recent infectious disease emergencies including the 2014-15 Ebola epidemic in West Africa and the ongoing Zika epidemic spreading in the Americas.

References

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School of Public Health, Georgia State University, Atlanta, GA
E-mail address: gchowell@gsu.edu

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MODELLING THE SPATIAL-TEMPORAL PROGRESSION OF THE 2009 A/H1N1 INFLUENZA PANDEMIC IN CHILE

LUIS MIGUEL VILLADA

Abstract. A spatial-temporal transmission model of 2009 A/H1N1 pandemic influenza across Chile, a country that spans a large latitudinal range, is developed to characterize the spatial variation in peak timing of that pandemic as a function of local transmission rates, spatial connectivity assumptions for Chilean regions, and the putative location of introduction of the novel virus into the country [3, 5]. Specifically, a metapopulation SEIR (susceptible-exposed-infected-removed) compartmental model [1, 4] that tracks the transmission dynamics of influenza in 15 Chilean regions is calibrated. The model incorporates population mobility among neighboring regions and indirect mobility to and from other regions via the metropolitan central region ("hub region"). The stability of the disease-free equilibrium of this model is analyzed and compared with the corresponding stability in each region, concluding that stability may occur even with some regions having basic reproduction numbers above 1. The transmission model is used along with epidemiological data to explore potential factors that could have driven the spatial-temporal progression of the pandemic. Simulations and sensitivity analyses indicate that this relatively simple model is sufficient to characterize the south-north gradient in peak timing observed during the pandemic, and suggest that south Chile observed the initial spread of the pandemic virus, which is in line with a retrospective epidemiological study. The "hub region" in our model significantly enhanced population mixing in a short time scale.

This contribution is based on joint work [2] with R. Bürger (U. de Concepción, Chile), G. Chowell (Georgia State University, Atlanta, Georgia, USA), and Pep Mulet (Universitat de València, Spain).

References

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[5] E. Pedroni, M. Garcia, V. Espinola, A. Guerrero, C. Gonzalez, A. Olea, M. Calvo, B. Martorell, M. Winkler and M. Carrasco, Outbreak of 2009 pandemic influenza A/H1N1, Los Lagos, Chile, April–June 2009, *Eurosurveillance* **15** (2010), paper 19456 (9pp).

CI^{2}MA, Universidad de Concepción, and Departamento Departamento de Matemática, Facultad de Ciencias, Universidad del Bío-Bío, Concepción
E-mail address: lvillada@ubiobio.cl

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FINITE VOLUME METHOD FOR A MODEL OF INDIRECTLY TRANSMITTED DISEASES WITH NONLOCAL CROSS-DIFFUSION

MAURICIO SEPÚLVEDA

Abstract. In this paper, we are concerned with a model of the indirect transmission of an epidemic disease between two spatially distributed host populations having non-coincident spatial domains with nonlocal and cross-diffusion, the epidemic disease transmission occurring through a contaminated environment. The mobility of each class is assumed to be influenced by the gradient of the other classes. We address the questions of existence of weak solutions and existence and uniqueness of classical solution by using, respectively, a regularization method and an interpolation results between Banach spaces. Moreover, we propose a finite volume scheme and proved the well-posedness, nonnegativity and convergence of the discrete solution. The convergence proof is based on deriving a series of a priori estimates and by using a general L^p compactness criterion. Finally, the numerical scheme is illustrated by some examples.

This contribution is based on joint works [6, 7].

References

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CI^{2}MA & DIM, Universidad de Concepción
E-mail address: mauricio@ing-mat.udec.cl

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A COMPUTATIONAL APPROACH TO A SPATIO-TEMPORAL AND GENDER-STRUCTURED MODEL FOR HANTAVIRUS INFECTION IN RODENTS

ELVIS GAVILÁN

Abstract. Hantavirus represents a health problem in Chile. In particular the transmission dynamics of this virus among rodents, has not been studied sufficiently. In this presentation, we will present a preliminary model of the spatio temporal transmission in a gender structured rodent population.

The purpose of this work is to take a deterministic model and apply some ideas of a predator prey model [3] and we utilize a spatio-temporal version of the gender-structured model for hantavirus infection of [2]. The non-linear system consists of a non-local conservation law for male-gender coupled with a parabolic equation for female-gender. The non-local conservation law describes the movement of the males that can be directed toward region with high female density, and in the direction opposite to region with high male density.

This contribution is based on joint work with R. Bürger (U. de Concepción, Chile), G. Chowell (Georgia State University, Atlanta, Georgia, USA), Pep Mulet (Universitat de València, Spain) and Luis-Miguel Villada (U. del Bío-Bío,Chile).

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CI²MA and Departamento de Ingeniería Matemática, Universidad de Concepción
E-mail address: egavilan@ing-mat.udec.cl