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Mathematics

Numerical semigroups associated with weighted homogeneous complex surface singularities

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The local graded algebra of a weighted homogeneous complex surface singularity defines a numerical semigroup called the semigroup associated to the singularity. In [1] László and Némethi presents an exact formula (up to an algorithmic term) for the Frobenius number of these numerical semigroups.

These singularities can be characterized by a negative definite Seifert 3-manifold, which is called the link of the singularity and is constructed by plumbing via a star-shaped dual resolution graph of the singularity. In [2] Pinkham proves that if the link is a rational homology sphere, then the aforementioned semigroup is topological and can be described using the combinatorics of the resolution graph.

This bridge between local singularities and numerical semigroups is interesting from both perspectives because on one hand the strong machinery of algebraic geometry can be applied to numerical semigroups, on the other hand using numerical semigroup theory we can create some useful transformations on the aforementioned singularities. Therefore it is natural to ask for the study and classification of numerical semigroups representable this way.

This talk will be centered around the properties of these semigroups, more specifically around a special family, called the flat semigroups ([3]). We will prove that they are representable by rather special star-shaped resolution graphs. Moreover, using the properties of these graphs we get a complete description of the generators of flat semigroups and we calculate explicitly their Frobenius numbers regarding their original definition (See [2]) and after that we give a partial characterization of the representable numerical semigroups.

This is a joint work with T. László.

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A note on dense sets in normed spaces

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Given a real or complex normed space $(X, ||\cdot||)$ and a linear (unbounded and not densely defined) operator $A\colon D \subset X \to X$, we show how to define norms $|||\cdot|||$ on X such that $A\colon (D, ||\cdot||) \to (X, |||\cdot|||)$ becomes bounded and D becomes dense with respect to $|||\cdot|||$. The main tool in constructing such norms $|||\cdot|||$ on X is the resolvent $R(\lambda, A)$ of A, where λ belongs to the resolvent set $\rho(A)$ of A. We then apply our results to m-accretive operators, using also some properties of them stated in [1]. Moreover we emphasise that our approach can be included in a more general framework that has some connections with topics presented in [2] and [3].

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A fixed point approach to semi-linear Stokes problems

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The starting point of this study is given by the Navier-Stokes equations which have represented and continue to represent a great point of interest to many scientists from different fields of study due to their theoretical and practical significance [1], [5].

The aim of this paper is to study the following semi-linear Stokes problem describing the Newtonian flow of an incompressible fluid under a reaction type force,

$$\begin{cases} -\mu\Delta u + \nabla p = h(x, u(x)) & \text{in } \Omega \\ \operatorname{div}\, u = 0 & \text{in } \Omega \\ u = 0 & \text{on } \partial\Omega. \end{cases}$$

The problem can be reduced to a fixed-point equation $T(u) = u$, where T is an operator with some specific properties, and we are concerned with finding weak solutions to this problem.

Our approach is based on the operator method that uses abstract results of nonlinear functional analysis (see, e.g. [2], [3], [4]). We first study the problem using Schauder's fixed point theorem and we prove the existence of the solution in case that h has a linear growth in u. Next we try to establish whether the existence of the solution can still be obtained without this growth restriction. Such a result is obtained applying the Leray-Schauder fixed point theorem. We conclude by a summary of the existence conditions and a few directions for future research.

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On some existence results for solutions to bilevel strong vector equilibrium problems

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The purpose of this talk is to present new existence results for solutions to a bilevel strong vector equilibrium problem, by using Fan's lemma and the properly C-upper semicontinuity concept introduced in [1]. Then, as applications, we will provide sufficient conditions for the existence of restricted strong cone saddle-points of a vector-valued bifunction, respectively, for solutions to a Pareto vector optimization problem over constraint sets.

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Strongly regular matrices revisited

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We prove a necessary condition and a sufficient condition for an $n \times n$-matrix A with determinantal rank $\rho(A) = t$ over a commutative ring to be (von Neumann) strongly regular in terms of the trace of its t^{th} compound matrix $Ct(A)$. In particular, a non-zero $n \times n$-matrix A with $\rho(A) = t$ over a local commutative ring R is strongly regular if and only if $\mathrm{Tr}(Ct(A))$ is a unit in R, and in this case we construct a strong inner inverse of A. We derive applications to products of local commutative rings and group algebras. Finally, we count strongly regular matrices over some finite rings of residue classes and group algebras.

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Characterizations of solutions to equilibrium problems via extreme or exposed points

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We consider scalar equilibrium problems governed by a bifunction in a finite-dimensional framework. By using classical arguments in Convex Analysis, we show that under suitable generalized convexity assumptions imposed on the bifunction, the solutions of the equilibrium problem can be characterized by means of extreme or exposed points of the feasible domain. Our results are relevant for different particular instances, such as variational inequalities and optimization problems, especially for best approximation problems. This was a joint work with late professor Nicolae Popovici.

The geometrical optimality test in Interval Branch and Bound method

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This study focuses on solving constrained nonlinear programming problems. The interval branch and bound method (IBB) is the most used method for solving such problems when a rigorous solution is needed. Few IBB implementations use the Karush-Kuhn-Tucker or Fritz-John optimality conditions for eliminating non-optimal boxes. In general, to use them, the solution of an interval-valued system of linear equations is needed. Solving this equation sometimes is difficult because the actual interval box contains more than one result or many unnecessary conditions. In many cases, this has a negative outcome and only increases the computing time.

In this study, the optimality conditions are considered from a geometric point of view. We replace the Fritz-John optimality condition with a geometrical optimality test, aiming to speed up the IBB method and eliminate unnecessary calculations. The main idea is to construct a conic hull from the enclosure of the gradients for the active constraints, and check if the inclusion of the negative gradient intersects with the conic hull. If the intersection is empty, the box cannot contain a local optimum, while if they intersect, the box might be reduced by the optimality conditions. The latter can be done by solving the mentioned interval-valued system of linear equations or by constraint propagation on the same equations.

In this talk, we will focus on a preliminary test that the Fritz-John system of equations is solved only if we are sure that a solution exists in the interval box. We highlight the drawbacks of solving the Fritz-John system of equations for each interval box. We describe a method to construct a conic hull from the enclosure of the gradients in active constraints. The conic hull is used to determine whether each interval box contains an optimal solution. If the test is satisfied, we can solve the Fritz-John system of equations and reduce the interval box. Otherwise, we can discard the interval box because it does not contain an optimal solution. We present the effectiveness of the preliminary test with experimental results.

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Fast synchronization of inhomogenous random automata

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We examine the reset threshold of randomly generated deterministic automata. We claim that an automaton with a random mapping and two random permutation letters has a reset threshold of $\mathcal{O}\left(\sqrt{n \log^3 n}\right)$ with high probability. Our observation is motivated by the breakthrough of Nicaud [1] providing a near-linear bound in a similar case, among multiple other results. Recent numerical analyses [2, 3] have conjectured that the expected reset threshold is closer to $\mathcal{O}(\sqrt{n})$.

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A scaling limit theorem of critical controlled branching processes

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Let Z_0 be a non-negative interger-valued random variable and consider a stochastic process defined recursively by

$$Z_{n+1} = \sum_{j=1}^{\phi_n(Z_n)} X_{n,j}, \qquad n = 0, 1, \ldots,$$

where $\{X_{n,j}\}_{n\geq 0,\, j\geq 1}$ is a sequence of independent and identically distributed non-negative integer-valued random variables and $\{\phi_n(k)\}_{k\geq 0}$, for $n = 0, 1, \ldots$, is a sequence of identically distributed stochastic processes with independent non-negative integer-valued random variables and, also, independent of $\{X_{n,j}\}_{n\geq 0,\, j\geq 1}$. Then $\{Z_n\}_{n\geq 0}$ is a controlled branching process (CBP), a wide family of the branching processes that add the novelty respect to classic Galton–Watson processes that the number of progenitors in each generation is determined by the random mechanism $\{\phi_n(k)\}_{k\geq 0}$.

Assuming that $m = \mathrm{E}[X_{0,1}]$ and $\sigma^2 = \mathrm{Var}[X_{0,1}]$ belong to $(0, \infty)$, the aim of this work is to contribute to the study of weak convergence results in the class of branching processes with Theorem 1, recently published in [1]. The proof makes use of limit theorems for random step processes.

Let $D_{[0,\infty)}[0, \infty)$ be the space of non-negative càdlàg functions on $[0, \infty)$ and $C_c^{\infty}[0, \infty)$ be the space of the infinitely differentiable functions on $[0, \infty)$ which have compact supports. Let $\xrightarrow{\mathcal{D}}$ denote the convergence in the Skorokhod topology. Consider a constant $\alpha > 0$, a standard Brownian motion $\mathcal{W}$ and the stochastic differential equation (SDE)

$$W(0) = 0, \qquad \mathrm{d}W(t) = \alpha\,\mathrm{d}t + \sqrt{\sigma^2 m^{-1} \max\{0, W(t)\}}\,\mathrm{d}\mathcal{W}(t), \qquad t > 0. \tag{1}$$

Taking into account [2], p.235, the SDE (1) has a pathwise unique solution W which is a non-negative diffusion process with generator $Tf(x) = \alpha f'(x) + \frac{1}{2} x \sigma^2 m^{-1} f''(x)$, for $f \in C_c^{\infty}[0, \infty)$.

Theorem 1 *If a CBP $\{Z_n\}_{n\geq 0}$ with $E[Z_0^2] < \infty$ satisfies*

i. $\tau_m(k) = k^{-1}\mathrm{E}[Z_{n+1}|Z_n = k] = 1 + k^{-1}\alpha + o(k^{-1})$ *for* $k > 0$ *as* $k \to \infty$,

ii. $\nu^2(k) = \mathrm{Var}[\phi_n(k)] = o(k)$ *as* $k \to \infty$,

then $W_n(t) = n^{-1} Z_{\lfloor nt \rfloor} \xrightarrow{\mathcal{D}} W(t)$ *for all* $t \geq 0$ *as* $n \to \infty$, *being* W *the pathwise unique solution of the SDE (1) with initial value* $W(0) = 0$.

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Generalized Set-Valued Optimality Conditions

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For a general constrained set-valued optimization problem

$$\min_{G(x)\cap -C\neq\emptyset} F(x) \tag{1}$$

we use a set comparison criterion in order to characterize optimal solutions. It assumes an ordering among the sets $F(x)$, for all $x \in X$, $G(x) \cap -C \neq \emptyset$, which is deduced from an ordering relation on $\mathcal{P}(Y)$. The efficient solutions are defined with the help of generalized interiors of convex cones, a subject previously debated in [2] for unconstrained set-valued optimization problems. The set-criterion approach to set-valued duality was initiated by T. Kuroiwa in the articles [4], [5], [6].

A duality perspective by emphasizing efficient solutions defined with the help of the quasi interior of a convex cone is included. Two set-relations defined with the help of this generalized interior notion are presented and characterized. Then, a general perturbation approach helps delivering the promised generalized set-valued optimality conditions which extend of E. Hernández and L. Rodríguez-Marin [3] for weak efficieny.

An application of the generalized set-valued optimality conditions for a problem stated in $\ell^2(\mathbb{R})$ concludes the presentation.

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The Graham-Kohr extension operator and subclasses of biholomorphic mappings in $\mathbb{C}^n$

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In this paper we discuss about convex combinations of the form $\mathcal{K}_{n,\lambda}^{\alpha,\beta} = (1-\lambda)\Psi_{n,\alpha} + \lambda\Psi_{n,\beta}$ of Graham-Kohr extension operators $\Psi_{n,\alpha}$, where $\lambda \in [0,1]$ and $\alpha, \beta \in [0,1]$. The operators $\Psi_{n,\alpha}$ were defined by I. Graham and G. Kohr in *Complex Variables Theory Appl. 47 (2002), 59-72.* They proved that the extension operator $\Psi_{n,\alpha}$ preserve the starlikeness for all $n \geq 2$ and $\alpha \in [0,1]$. The main idea of this paper is to obtain new extension operators defined by convex combinations of Graham-Kohr operators $\Psi_{n,\alpha}$ that preserve the starlikeness. We prove that a starlike function $f \in S^*$ with $\mathrm{Re}[f'(z_1)] > 0$, for all $z_1 \in U$, is taken to a starlike mapping on the Euclidean unit ball $\mathbb{B}^n$ by the operators $\mathcal{K}_\lambda^0$ and $\mathcal{K}_\lambda^1$, where $\mathcal{K}_\lambda^0$ and $\mathcal{K}_\lambda^1$ are particular forms of the operator $\mathcal{K}_{n,\lambda}^{\alpha,\beta}$. Finally, we give a result which ensures the starlikeness of an arbitrary extension operator Φ_g, respectively the convex combination between the identity I_n and the operator Φ_g.

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Natural convection in a bidisperse porous medium. Effect of internal heat generation

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In the last years, there has been much interest in multiple porosity materials (see, [1]; [2]). A standard porous medium (or monodisperse porous medium-MDPM) is formed by the solid matrix and voids filled with fluid. However, there are cases when a solid body may have a double/triple porosity structure (bidisperse porous medium-BDPM, tridisperse porous medium-TDPM). In these cases, the solid structure of the medium is composed of clusters of large particles that are agglomerations of small particles. Thus, a BDPM is a standard porous medium in which the solid phase is replaced by another porous medium. An example of bidisperse porous medium is a bed of porous or fractured rocks. There is a macro-porosity, ϕ, (voids between rocks) but also a micro-porosity, ϵ, which is linked with fissures and pores in the solid skeleton.

Several applications of BDMP are related to the heat transfer engineering, especially to thermal insulation ([2]) and heat pipes related technologies ([3]). This is due to the fact that the critical Rayleigh number is much higher for a BDPM that for a classical porous medium (MDPM) and that the maximum heat load of bidisperse wick is higher than that for the monoporous wick. Other applications of the bidisperse porous media are related to catalytic chemistry.

In this study we will consider the effect of internal heat generation in a square cavity filled by a bidisperse porous medium. The governing equations are:

Continuity equations:

$$\frac{\partial u_f}{\partial x}+\frac{\partial v_f}{\partial y}=0 \tag{1}$$

$$\frac{\partial u_p}{\partial x}+\frac{\partial v_p}{\partial y}=0 \tag{2}$$

Momentum equations:

$$\frac{\partial p}{\partial x}=-\frac{\mu}{K_f}u_f-\zeta(u_f-u_p) \tag{3}$$

$$\frac{\partial p}{\partial y}=-\frac{\mu}{K_f}v_f-\zeta(v_f-v_p)+\rho g\beta(T-T_0) \tag{4}$$

$$\frac{\partial p}{\partial x}=-\frac{\mu}{K_p}u_p-\zeta(u_p-u_f) \tag{5}$$

$$\frac{\partial p}{\partial y}=-\frac{\mu}{K_p}v_p-\zeta(v_p-v_f)+\rho g\beta(T-T_0) \tag{6}$$

Energy equation:

$$(\rho c)_m\Big(\big(\phi\, u_f+(1-\phi)\varepsilon\, u_p\big)\frac{\partial T}{\partial x}+\big(\phi\, v_f+(1-\phi)\varepsilon\, v_p\big)\frac{\partial T}{\partial y}\Big)=$$

$$=k_m\Big(\frac{\partial^2 T}{\partial x^2}+\frac{\partial^2 T}{\partial y^2}\Big)+q_0''' \tag{7}$$

The previus equations are transformed in dimensionless equations and are solved numerically using central finite difference discretizations along with a SOR iterative technique.
Streamlines, isothermas as well as maximum values for the stream functions and the maximum value of the temperature are obtained.

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Nonlinear Cone Separation Theorems in Real Reflexive Banach Spaces

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The separation of two sets (or more specific of two cones) plays an important role in different fields of mathematics (such as variational analysis, convex analysis, convex geometry, optimization). In the talk, we show some new results for the separation of two (not necessarily convex) cones by a (convex) cone / conic surface in real reflexive Banach spaces. We follow basically the separation approach by Kasimbeyli (2010, SIAM J. Optim. 20) based on augmented dual cones and normlinear separation functions. Classical separation theorems for convex sets will be the key tool for proving our main nonlinear cone separation theorems.

A Stochastic Geometric Optimization Problem for Finite Sample Input Design

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Estimation is one of the core problems of statistics and related fields, such as system identification, signal processing and machine learning. Studying the statistical properties of the estimates is of outmost importance, e.g., they can help building confidence sets quantifying the risk. On the one hand, these properties are determined by the statistical assumptions taken and the estimator used. On the other hand, the excitation driving the experiments also has significant impact on them.

This talk will focus on finite sample system identification, which is an actively studied research area [1, 2, 3, 4, 5], and where the goal is to deliver estimates with certified statistical properties, especially in cases where there are only finite number of observations available for the estimation.

Designing experiments having these recent identification algorithms in mind, e.g., Data Perturbation (DP) methods, results in new input design problems [6]. Using notations from [6], DP confidence regions with level α, $\mathcal{C}_\alpha(X,Y)$, can be constructed from $1/2$ level confidence ellipsoids:

$$\mathcal{C}_\alpha(X,Y) \;=\; \bigcup_{S\in[\mathcal{M}]_q} \Big(\bigcap_{i\in S} \mathcal{C}^i_{1/2}(X,Y) \Big). \tag{1}$$

According to DP theory, any confidence region with (rational) confidence probability $1 - q/m$ can be constructed from $m-1$ instances of $1/2$ confidence regions (in fact, ellipsoids) by taking q of them in every possible way forming their intersections and taking the union of these intersections.

Resolving input design problems with the aim of minimizing some geometric property of the confidence region requires understanding the interaction between the different $\mathcal{C}^i_{1/2}(X,Y)$ sets.

This talk will present the structure of the $\mathcal{C}^i_{1/2}(X,Y)$ confidence sets of DP methods, and it will explore the nature of their relation with respect to the intersections and unions outlined in (1).

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On the strong convergence of the trajectories of Tikhonov regularized second order dynamical systems

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We study some second order dynamical systems with vanishing damping that contain a Tikhonov regularization term, in connection to the minimization problem of a convex, Fréchet differentiable function. We show that for appropriate Tikhonov regularization parameters the value of the objective function in a generated trajectory converges fast to the global minimum of the objective function and a trajectory generated by the dynamical system converges weakly to a minimizer of the objective function. We also obtain the fast convergence of the velocities towards zero and some integral estimates. Nevertheless, our main goal is to extend and improve some recent results from the literature concerning the strong convergence of the generated trajectories to an element of minimal norm from the argmin set of the objective function. Our analysis also reveals that the damping coefficient and the Tikhonov regularization coefficient are strongly correlated.

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On a stochastic Ginzburg-Landau equation with multiplicative noise term

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We consider a method to approximate the solution of the following stochastic complex Ginzburg-Landau evolution equation perturbed by a power-type nonlinearity and a multiplicative noise term

$$dX(t) = \mathrm{i}\Delta X(t)\,dt - \lambda|X(t)|^2 X(t)\,dt + \gamma X(t)dt + \mathrm{i}\sum_{k=1}^{\infty} b_k(t)X(t)\,dW_k(t) \tag{1}$$

with initial condition $X(0) = X_0$. Here, X is a complex-valued stochastic process depending on $t \in [0,T]$ and $x \in [0,1]$; $\lambda, \gamma, T > 0$ are fixed, $(W_k)_{k\in\mathbb{N}}$ is a sequence of independent real-valued Wiener processes and $(b_k)_{k\in\mathbb{N}}$ is a sequence of real-valued functions. Estimates for the approximations of the solution are given.

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Identification of Induction Curves

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A common way to define a norm of a matrix is to take the supremum of the fraction of the vector norms of the matrix-vector product and the nonzero vector, with respect to a given vector norm, i.e. the least upper bound for the norm of the vectors of the transformed unit sphere. Recently induction curves (induction surfaces, induction sets in general) were introduced to provide a visual aid to examine these fractions defining the norm of a matrix, along with the discovery and description of p-eigenvectors [4, 5]. The study of different phenomena in relation to various norms (most importantly with $p = 1$, 2 and ∞) is a traditional and still active topic [1, 2, 3, 6].

In our current investigation we delve into the inverse problem (identification) of induction curves, posed in [4]. Namely: could the elements of the matrix and the used parameter p be reconstructed given the induction curve/surface/manifold, or a sampled subset of such an object. For now we restrict ourselves to induction curves, i.e. the case of 2×2 matrices.

The analytic solution is not possible in most cases already in this planar setting, therefore numerical approximation methods shall be applied. We also examine the problem of the minimal required subset for unique identification. The software package of Matlab/Octave programs available at `https://numanal.inf.elte.hu/~locsi/indsets/` will be extended with new components for the task of identification.

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New Shepard operators in the univariate case

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We obtain new univariate Shepard operators using polynomials that are constructed such that they fit the interpolation data in a weighted least squares approximation way. We study the degree of exactness, the linearity and the remainder for the corresponding interpolation formula. Finally we compare the numerical results with the ones obtained using other combined Shepard operators.

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Differential inclusions on non-compact Riemannian manifolds

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We investigate a large class of elliptic differential inclusions on non-compact complete Riemannian manifolds which involves the Laplace-Beltrami operator and a Hardy-type singular term. Depending on the behavior of the *nonlinear term* and on the *curvature* of the Riemannian manifold, we guarantee non-existence and existence/multiplicity of solutions for the studied differential inclusion. The proofs are based on nonsmooth variational analysis as well as isometric actions and fine eigenvalue properties on Riemannian manifolds.

This is based on joint work [5] with Alexandru Kristály (Department of Economics, Babeş-Bolyai University, Cluj-Napoca & Institute of Applied Mathematics, Óbuda University, Budapest) and Károly Szilák (Institute of Applied Mathematics, Óbuda University, Budapest)

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An exact sequence for the graded Picent group

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In this talk, we consider k to be an associative and commutative ring, with $1 \neq 0$, A to be a crossed product between a finite group G and a k-algebra B, H to be the stabilizer of B as a (B, B)-bimodule and $Z = U(Z(B))$.

We establish the following exact sequence:

$$\begin{tikzcd}1 \arrow[r] & \mathrm{H}^1(G/H, Z) \arrow[r, "\Phi"] & \mathrm{Picent}^{\mathrm{gr}}(A) \arrow[r, "\Psi"] & \mathrm{Picent}(B)^{G/H} \arrow[r, "\Theta"] & \mathrm{H}^2(G/H, Z),\end{tikzcd}$$

which is a version of the Beattie - del Río sequence [1].

This extends the results of [2] and is motivated by [3], where we have proved that there is a link between character triples and a special type of group graded Morita equivalences. These equivalences are obtained via group graded bimodules which satisfy some additional conditions involving how the elements of the bimodule interact with the centralizer subalgebra of the algebras between which we want to obtain the equivalence. Classes of isomorphisms of such bimodules form the graded Picent group, $\mathrm{Picent}^{\mathrm{gr}}(A)$, which is a subgroup of the graded Picard group, $\mathrm{Pic}_k^{\mathrm{gr}}(A)$.

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Absence of periodic orbit for a nonlinear delay differential equation

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The delay differential equation

$$x'(t) = -ax(t) + bf\left(x(t-1)\right) \tag{E}$$

is considered where $a > 0,\ b > 0$ and a continuously differentiable function $f : \mathbb{R} \to \mathbb{R}$ satisfying $f(0) = 0,\ f'(\xi) > 0$ for $\xi \in \mathbb{R}$. It is well-know that if 0 is hyperbolic then it has a neighborhood in which there exists no nontrivial periodic orbit. By using the exponential dichotomy constants, we focus on the estimation of the optimal size of this neighborhood. The aim is to construct the neighborhood as large as possible in order to be able to carry out a verified numerical step for equation (E).

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The convexity flavor of the Hornich-Hlawka functional inequality

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The aim of our talk is to present the following refinement of a result due to Ressel [1]:

Theorem 1 *Suppose that E is an ordered Banach space and $f:\mathbb{R}_+\rightarrow E$ is a continuous function.*

(i) *If f is 3-convex function, then*

$$f\left(x\right)+f\left(y\right)+f\left(z\right)+f\left(x+y+z\right)\geq f\left(x+y\right)+f\left(y+z\right)+f\left(z+x\right)+f(0)$$

for all $x,y,z\in\mathbb{R}_+$.

(ii) *Every function f that verifies the inequality stated at the point (i), also verifies the inequality*

$$f\left(|x|\right)+f\left(|y|\right)+f\left(|z|\right)+f\left(|x+y+z|\right)\geq f\left(|x+y|\right)+f\left(|y+z|\right)+f\left(|z+x|\right)+f(0)$$

for all triplets $x,y,z\in\mathbb{R}$ such that $z\leq 0\leq y\leq x$ and $|z|\geq x+y$.

(iii) *If f is a nondecreasing, concave and 3-convex function, then*

$$f\left(|x|\right)+f\left(|y|\right)+f\left(|z|\right)+f\left(|x+y+z|\right)\geq f\left(|x+y|\right)+f\left(|y+z|\right)+f\left(|z+x|\right)+f(0)$$

for all $x,y,z\in\mathbb{R}$.

The result stated at point (i) admits a generalization for every order of convexity.

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Dinkelbach type approximation algorithms for nonlinear fractional optimization problems

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We establish some approximation versions of the classical Dinkelbach algorithm [1], [2] for nonlinear fractional optimization problems in Banach spaces. We start by examining what occurs if at any step of the algorithm, the generated point desired to be a minimizer can only be determined with a given error. Next we assume that the step error tends to zero as the algorithm advances. The last version of the algorithm we present is making use of Ekeland's variational principle [3] for generating the sequence of minimizer-like points. In the final part, we deliver some results in order to achieve a Palais-Smale type compactness condition that guarantees the convergence of our Dinkelbach-Ekeland algorithm. The presentation is based on a joint paper with R. Precup.

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Closed convex sets with relative boundaries equal to their Pareto-like subsets

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We consider the class of closed convex subsets of $\mathbb{R}^n$ whose relative boundaries are equal to their Pareto-like subsets and characterize them in various ways. Such a set which contains no lines is, according to [2, Proposition 4.8], a Minkowski set, i.e. it can be represented as the convex hull of its subset of extreme points. A set whose relative boundary is equal to its Pareto-like subset is called *strongly Minkowski* and, apart from the mentioned characterizations, we also study the possiblity of the intersection of finitely many strongly Minkowski sets to be strongly Minkowski, or at least a Minkowski set. Some special attention is paid to the intersection of a strongly Minkowski set with a halfflat.

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On the product expansion of normal subsets in simple groups

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By the product expansion of two subsets A and B of a group G, we mean a way of measuring how much $A \cdot B$ grows with respect to the size of A and the size of B. Such questions are related to a conjecture of Thompson, which states that for any non-abelian finite simple group there is a conjugacy class C of G such that $C^2 = G$. Motivation also comes from the theory of expander graphs. If S is a generating set for G and $S^m = G$, then $2m$ is an upper bound on the diameter of the Cayley graph $\Gamma = \Gamma(G, S)$. This in turn translates into bounds on the expansion constant of Γ. After presenting more background and further motivating conjectures, we comment on recent results obtained in [2] and [1] as well as on work in progress with A. Maróti and E. Szabó.

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On the existence of Nash equilibria for nonvariational systems

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Using fixed point arguments together with monotone operators techniques we generalize an existing result regarding the existence of a Nash equilibria for a fixed point type system, where each equation admit a variational structure with respect to each variable. The improvements regard both to the initial conditions and the functional framework, without changing the final conclusion. As an application we consider a coupled system with Dirichlet boundary conditions involving the p-Laplacian, where we show that under mild conditions it has a solution and moreover, it is a Nash equilibrium.

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Ringel-Hall polynomials associated to a quiver of type $\tilde{D}_4$

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Classical Hall algebras associated with discrete valuation rings were introduced by Steinitz and Hall to provide an algebraic approach to the classical combinatorics of partitions. The multiplication is given by Hall polynomials which play an important role in the representation theory of the symmetric groups and the general linear groups. In 1990 Ringel defined Hall algebras for a large class of rings, namely finitary rings, including in particular path algebras of quivers over finite fields. Far reaching analogues of the classical ones, these Ringel-Hall algebras provided a new approach to the study of quantum groups using the representation theory of finite dimensional algebras. They can also be used successfully in the theory of cluster algebras or to investigate the structure of the module category.

In case of Ringel-Hall algebras corresponding to Dynkin quivers and tame quivers we know due to Ringel and Hubery, that the structure constants of the multiplication are again polynomials in the number of elements of the base field. These are the Ringel-Hall polynomials. If we are looking at Hall polynomials associated to indecomposable modules, the classical ones are just 0 or 1, the Ringel-Hall ones in the Dynkin case are also known and have degree up to 5. However we do not have too much information about the Ringel-Hall polynomials in the tame cases.

In this talk we present our process of determining the Ringel-Hall polynomials associated to indecomposable modules over a tame quiver of type $\tilde{D}_4$.

Conditions for starlikeness and convexity of analytic functions

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In this paper we present some simple conditions, which imply the starlikeness or convexity of analytic functions defined in the unit disc. The presented theorems are improvements of some earlier results deduced by differential subordinations. We obtain our results with the method of convolution. Almost all the presented results are sharp.

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Convergence rates for variable step size inexact proximal algorithms

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The proximal point algorithm is a cornerstone of convex analysis, yet its practical value has been debated due to the inconvenience that only a limited number of objective functions admit an explicitly computable prox and, in general, an inexact approximation must be used. An important early contribution is due to Rockafellar [2], who has established convergence given that (computational) errors are summable. Much later, Zaslavski [3], improved existing results by admitting bounded, not summable, errors.

In the present contribution, we investigate inexact proximal point algorithms with increasing step size by combining above ideas with the pioneering work of Güler [1]. The main conclusion of our analysis is that for bounded errors, one can achieve arbitrary convergence rates by taking an unbounded sequence of step sizes which increases fast enough. This is quite counter-intuitive, as one would naively expect that larger step sizes amplify computational errors, but this isn't the case.

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Computer Science

Network optimization problem applicable for breast cancer screening cost minimization

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We investigate the problem of breast cancer screening optimization, using various techniques applicable in domains where the data format is not defined in advance. The aim is to minimize the cost related to the screening of patients, while maximizing the beneficial effect of the process regarding some key breast cancer indices. Our model can be easily adjusted to other similar network optimization tasks where a goal function has to be minimized across a geographical surface. We present the problem's key similarities to the Travelling Salesman Problem, and underline the fact why we choose a deterministic algorithm compared to a Simulated Annealing-based solution. Furthermore, we present the usefulness of the Elastic stack regarding this application, and offer a concrete solution to the problem defined by our generated dataset, respecting the European data distributions in this domain.

Towards feature extraction for lesion type detection in mammograms

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The efficient analysis of digital mammograms has an important role in the early detection of breast cancer and can lead to a higher percentage of recovery. The process of mammogram analysis can be divided into two steps. In the first step, we define if the tissue contains abnormalities or not. In the second step, determine the nature of the lesion. This second step of a computer-aided diagnosis system is important in order to select the best treatment to the patient to achieve the highest change of recovery. In general, image processing consists of preprocessing, feature extraction, feature selection and classification. Two main type of feature extraction are shape features and texture features. In the current paper, we present several experiments in order to compare the performance of different feature extraction methods from the two types mentioned previously. As data we use images from Digital Database for Screening Mammography (DDSM), which has precise ground truth for the cancerous tissue. For classification Decision Trees and Random Forest methods are used to evaluate the performance using the different extracted features.

A compartmental model for COVID-19 to assess effects of non-pharmaceutical interventions with emphasis on contact-based quarantine

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Relative to the number of casualties, COVID-19 ranks among the ten most devastating plagues in history. The pandemic hit the South Asian nation of Bangladesh during the early March, 2020, and has greatly impacted the socio-economic status of the country. In this article, we propose a compartmental model for COVID-19 dynamics, introducing a separate class for quarantined susceptibles, synonymous to isolation of individuals who have been exposed and are suspected of being infected. The current model assumes a perfect quarantine based on contacts with infectious individuals. Numerical simulation is conducted to investigate the efficiency of disease control by segregating suspected individuals and other non-pharmaceutical interventions. In addition, we assort quantitatively the importance of parameters that influence the dynamics of the system. Fitting the system to the early phase of COVID-19 outbreaks in Bangladesh, by taking into account the cumulative number of cases with the data of the first 17-week period, the basic reproduction number is estimated as 1.69.

Risk probability in blockchain technology

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Despite the technological advancements that have occurred in blockchain technology, it still faces a significant challenge when it comes to entering the business operations of large corporations. One of the main reasons why this is so is that it still hasn't demonstrated its resilience. Distributed ledger technology is commonly used in cryptocurrencies such as Bitcoin. Although it has not been proved that all Bitcoin transactions are fraudulent, many of them have been accessed by third parties, which resulted in user losses. This thesis aims to demonstrate the trustworthiness of blockchain algorithms when it comes to performing secure transactions in Bitcoin. When it comes to analyzing the risks associated with Bitcoin transactions, a security perspective is important. This paper aims to provide a comprehensive analysis of the prbability of the various security threats that affect the operations of blockchain technology. It also explores the challenges that will face the financial sector when it comes to using blockchain technology for international payments [1, 2, 3, 4, 5, 6].

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An Extension of Dynamic Time Warping for Images: Dynamic Image Warping

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Dynamic time warping (DTW) is probably the most successful distance metric for time series classification. It has been used as an essential component of various time series classifiers, including neural networks, see e.g. [1] [2] [3] and the references therein. The core idea behind DTW can be summarized as follows: based on dynamic programming, DTW aims to find an optimal alignment between time series so that it allows for shiftings and elongations when it compares two time series. This is essential because in case of data captured under real-world conditions, we can not expect the same pattern to be repeated *exactly* (see e.g., the ECG of a patient, movements during handwriting or dynamics of keystrokes). A similar issue arises when we compare images or parts of images.

In this talk, we present a generalisation of dynamic time warping for the comparison of images. A digital image of $n \times m$ pixels may be seen as an intensity matrix with n rows and m columns. We consider such a matrix a sequence of n row vectors (or as a sequence of m column vectors, respectively). In principle, two sequences can be compared with DTW, however, we have to take into account that, in our case, items of the two sequences are not real numbers, but vectors. Therefore, we propose to use DTW as inner distance within the main DTW, i.e., for the comparison of the aforementioned row (or column) vectors. Thus, we can summarize our approach as *"DTW with DTW as inner distance"* or *"double DTW"*. For simplicity, we call it dynamic image warping or DIW for short.

We made a reference implementation (Python and Cython source codes) of our approach publicly available in our github repository:

https://github.com/kr7/diw

We performed initial experiments in the context of recognition of handwritten digits. The results show that, compared with other distance metrics, such as Euclidean or Manhattan distances, DIW is especially beneficial in cases when few training instances are available.

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Feasibility of using machine learning algorithms for yield prediction based on seeding date for sunflower and corn crops

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Study Aim. In this research, our objective is to identify the relationship between the date of seeding and the production of corn and sunflower. We aim to assess the feasibility of using prediction models on a set of identified crop yields each year and plant phenology data in several states of the US.

Related work. Machine learning can be used successfully to identify factors that increase crop production [3]. However, there are limited available data and inadequate research on the impact of the seeding date on crop yield. Many crops have a wide window of ideal plating date (60-90 days), but crop success can be influenced by changes in climate or soil composition. Recent research shows that early seeding is beneficial for several crops, resulting in increased production [2], but it also presents major risks.

Methods. The data used in this study have been extracted from the US National Agricultural Statistics Service [1]. Data preprocessing involved the aggregation of yield data (in lb/ac) for each state and year with the seeding date (calculated as a weighted average based on percentages of the crop planted each week, as they were available). As a result, we obtained $n = 88808$ instances for corn (from period 1979-2022) and $n = 1108$ for sunflower (from period 1950-2021), each containing 5 features: year, state ANSI, crop type (irrigated, non-irrigated, total), yield and planting date. In the case of sunflower, there were only 312 entries containing information on planting date, therefore, the non-available data was completed using the forward fill method. The algorithms XGBRegressor, HistGradientBoostingRegressor, DecisionTreeRegressor, and RandomForestRegressor have been trained and validated using a data split of 20% for testing, and k-fold cross-validation with $k = 10$.

Results. The best results to predict the yield were obtained by the XGBRegressor (with $R^2 = 0.969$ and the percentage Mean Absolute Percentage Error $MAPE = 9.42\%$ for corn and $R^2 = 0.905$ and $MAPE = 9.76\%$ for sunflower) and the HistGradientBoostingRegressor ($R^2 = 0.969$, $MAPE = 8.945\%$ for corn and $R^2 = 0.884$ and $MAPE = 10.71\%$ for sunflower).

Conclusion and future work. The algorithms used in the prediction show a good correlation between the selected characteristics (year, state, planting date, type of crop) and yield. The seeding date might also have a higher influence based on specific climate conditions and precipitations, so further work involves correlating it with meteorological data for the specific regions involved.

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Object-Oriented Complexity Metrics Overview

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The complex software systems developed nowadays require a way to assess their quality or proneness to errors. Reducing the code complexity is never ending problem, especially in today's fast pace of software system development. Therefore, the needs of the industry are to find a way to determine the qualities of a software system, the degree of difficulty in developing new functionalities or proneness to errors. One way of measuring and predicting the quality attributes of a software system is to analyse the software metrics values for it and the relationships between them. More precisely, we should analyse the metrics that measure and determine the degree of complexity of the code. The complexity of the code is an essential aspect because it can affect the progress in different phases of the development lifecycle, such as developing, testing and maintaining the system. The objective of this paper is to analyse some of the most common object-oriented metrics used for measuring the complexity of the code and their particularities. We will also present possible effects these metrics can have on software quality attributes, such as testability, maintainability, or understandability.

Malicious Web Link Detection - Comparison between ML Algorithms

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The beginning of the XXI century has been strongly influenced by the evolution of web technology that forced most businesses and industries to move most of their content online. Technology is continuously evolving at a high speed, and for humans it is becoming more and more difficult to adapt to the many changes brought about by the new online age. Web applications help individuals socialize, read news, do their remote work, online education, everyday shopping, payment of invoices, taxes, watch media and entertainment services and do other online activities. Therefore, most consumers need to surf the Internet daily for their bare necessities. Because of this, individuals with low digital education and no defense methods can become easy targets for many malicious organizations which share threats into the online world mostly to gain financial advantages.

One of the most challenging categories of threats circulating into the online world is social engineering, with malicious web links, fake news, clickbait and other not-so-well-intended tactics. Malicious links are disseminated into the online world to lure users into clicking them. This opens a malicious web page that may run its malware code into the browser to deceive the user (e.g. with a fake bank login page) or download a malware program without the user's consent. Malware URLs are extremely dangerous because they represent the main propagating vector for web malware, and they may violate user's personal data, even leading to huge data breaches. Malicious web links detection is a challenging task because the detection mechanism should not influence the consumers' online experience. As stated in [1], the proposed solutions must be sensitive enough to any small piece of code injected into the web page that might be malicious, and fast enough to perform the detection mechanism before the user accesses the link and downloads its content.

The main purpose of this paper is to compare several machine learning algorithms such as Random Forest, Decision Tree, K-Nearest Neighbor and analyze the best configurations. Moreover, these ML approaches will be compared with relevant results previously obtained in the literature and will draw significant conclusions on how to approach the problem of malicious web links detection. The experiments are based on the dataset provided by [2] and used in similar researches such as [3]. In addition, we will make important observations about the most relevant features of a web link that are used in malicious/ benign classification. This analysis can help everyday users with low digital experience to identify malicious links far easier and security researchers to give them an small presentation of this domain from an experimental point of view.

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Dynamics of Herpes and Chlamydia Co-Infection in a Population

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A mathematical model was formulated to investigate *Chlamydia trachomatis* (*C. trachomatis*) and herpes simplex virus (HSV) co-infection in a population; taking into account that HSV can induce a viable but non-cultivable state of *C. trachomatis* in a host. A complete description of the global dynamics is given for the sub-systems where only one of the diseases is present. For the co-infection model, we show that the extinction or persistence of HSV is determined solely by the basic reproduction number of HSV, regardless of *C. trachomatis* prevalence. On the contrary, *C. trachomatis* can not always invade a HSV-endemic population even when it could invade a susceptible one, and this is determined by a newly introduced threshold parameter. By a limiting system approach, the existence of a co-infection steady state is shown when all reproduction numbers are greater than one. Applying the theory of asymptotically autonomous systems, we prove global stability results for the disease free and the boundary equilibria.

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MEC - Applications deployment and testing using Simu5G

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Mobile (or Multi-Access) Edge Computing (MEC) can provide higher computing speed and lower end-to-end delay (latency) in comparison with traditional networks and cloud/fog computing. In cloud computing, the servers of the cloud are usually part of data centers that are located at long distance from most end users' devices. This distance is one major reason behind the weakness of cloud services, in terms of latency. In addition to the delay problem, the cloud needs to have more "base stations" between the users and the cloud servers to transfer the data and manage the requests; these base stations load extra energy, increase installation and maintenance costs, and cause a delay accumulation. MEC is put forward to solve these problems. The users' requests will be managed in the local network edge, instead of being delivered to the remote "core" cloud server, to maintain low latency [1]. In comparison to fog computing, MEC is a more powerful and wider technology that involves the 5G radio access network. MEC is the key technology of the smart vehicle era, under the advent of 5G. The crucial issue with smart vehicles and smart cities is the sensitivity to delay, and MEC breaks this delay (and the extra energy and cost problems in the traditional cloud services) so that the core technology of the cloud can be upgraded with 5G/6G MEC. Governments have started the steps to build smart traffic and smart city with various infrastructures based on 5G networks, which pave the way for vehicles, infrastructures and applications to step forward into the intelligent era (6G) [2]. MEC is considered as an enabling technology that will provide new chances for innovative services and brand-new ecosystems, and as of now MEC can be involved to leverage Internet of Things (IoT) services in 5G networks. Moreover, MEC supports a rapidly increasing number of application areas such as agriculture, smart parks, smart factories, smart traffic, etc. The advantage of using MEC in IoT is that; as more IoT devices enter the commercial market, the mobile network will be under more load as devices are added to cloud servers. Having mobile user equipment (UE) connect to centralized cloud services, independently from their current location, may restrict IoT use cases that require low latency and high capacity/bandwidth. This highlights the significance of edge computing paradigms such as MEC, a novel, and evolving networking paradigm that the European Telecommunications Standards Institute is currently standardizing (ETSI). In summary, the goal of MEC is to bring the cloud's capabilities to the edge of cellular networks [3].

MEC is implemented and tested in OMNeT++ with the Simu5G simulator. Simu5G [4] can quickly setup a 5G network, and can be used as a real-time network emulator, or to interface with a real time application. In this paper, we show how to design and deploy an application into a simulated MEC infrastructure in 5G network using Simu5G.

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Graphical User Interface Element Detection using Faster Region-based Convolutional Neural Network Models

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Automation of tasks is becoming common in everyday activities. This process involves using software or tools in performing simple tasks. By having the computer take over redundant tasks, manual involvement is reduced, thus increasing human productivity. Detecting Graphical User Interface (GUI) elements is the first step in automating complex processes [1]. Obtaining the positions of GUI elements and accurately classifying them is essential in the automation process, as these processes require interaction with these elements to perform tasks. The object detection process represents the localization of the presence of objects using a bounding box and the recognition of object classes located in these boxes. Convolutional neural networks are a real interest in image processing and object detection [2]. In our research, the focus was the application of Faster Region-based Convolutional Neural Network models for the detection of several classes of GUI elements [3]. A Faster Region-based Convolutional Neural Network is characterized by the combination of two networks, the Region Proposal Network, and the Convolutional Neural Network. The first network aims to generate region proposals, while the second one uses these proposals for object detection [4]. In the experiments, we used a public dataset containing screenshots of various websites. This method provided good results, obtaining very good metrics in the evaluation, and thus, the hypothesis of their application on this type of task has been fulfilled.

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Generating semantic webpages from knowledge graphs

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Making human-readable information meaningful for machines is the main goal of the Semantic Web. However, web developers are still creating and publishing websites that are rather visual appealing to humans then RDF-friendly. Therefore, extracting meaningful machine reasoning information from most of the human readable publicly exposed data can still be difficult.

In this context we propose an alternative concept to the typical webpage development process. An approach that begins from the semantics of the information instead of plain data. In order to prove this concept, we have implemented a web content management system that allows authenticated users such as the members of an organization to easily create machine meaningful webpages while maintaining the common visuals and usability.

Since the content of the page is stored as knowledge-graph in a NoSQL graph database, the owner of the page can visualize and navigate the structure of the webpage as a graph. This allows for identification of orphan pages while they appear as disconnected graphs leading to a better understanding of the web-development process even for non-programmers.

Managing the information and the structure of the webpage could be made easy for everyone since there will be multiple possibilities to create content. In our proof-of-concept implementation, the user can create pages and add data using SPARQL queries in GraphDB Workbench, using APIs inside a programming language, uploading RDF-formatted information such as Turtle files, using our implementation's embedded editor or just sending emails to the webpage's backend engine.

Supporting debugging in Erlang with symbolic execution

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Fault localization is a process of identifying the locations of faults in a program. Although bugs in the software are usually discovered due to some faulty behavior (e.g. a runtime error occurs), finding the origin of the fault is a non-trivial task. Error detection mechanisms are vital for building highly reliable systems. Given the size and complexity of large-scale software systems today, manual fault localization becomes more and more futile, so effective automatic methods are needed. Dynamic and static tools could provide help in this task.

Static source code analysis techniques may help the programmers in various tasks: code comprehension, testing, debugging, etc. They often need to reproduce executions that result in faulty behaviour. Program analysis techniques with symbolic execution can help to solve this task. In a concrete execution a program is evaluated on a specific input, and a single control-flow path is explored. Symbolic execution [1] uses unknown symbolic variables in evaluation, allowing to simultaneously explore multiple paths that a program could take under different inputs. We can use symbolic execution to help us in fault localization.

In this paper we propose a method to select an appropriate execution path from the static control-flow graph that may lead to a given runtime error in Erlang software. We build our tool on the RefactorErl[2] static analyser framework.

Because of the path-explosion problem, it is infeasible for symbolic execution tools to explore all execution paths of any nontrivial programs. Therefore, search heuristics are required elements of symbolic execution. Using a good search heuristic can maximize code coverage and improve the effectiveness of the analysis in practice. We have implemented our prototype algorithm using backtracking and demonstrated how it finds an execution path to a given expression containing an error [4]. We are using the SMT solver of Z3 [3] to solve the constraints we gather during our analysis. In this paper, we explore different heuristics to improve the path finding in order to make our method feasible for error detection in larger software bases.

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Report on a Field Experiment of the Memory Retention of Programmers Regarding Source Code

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In the life of a programmer, source code comprehension activities take up a significant amount of time during working hours [1, 5]. Program comprehension has been a continuously important research topic in computer science since the spread of personal computers, and several program comprehension strategies, models have been identified as possible directions of active code comprehension [8, 7, 3]. However, there has been little to no research as to how much programmers remember the code they have once written. Towards the end of the 19th century, Ebbinghaus defined a so-called "forgetting curve" [2], which was aimed to model the memory retention of humans over time. Ebbinghaus conducted experiments with people who had to remember random series of words, and had to repeat them back several times after a number of minutes. The validity of the forgetting curve has since been confirmed by more recent studies [4, 6].

One of the diverting factors when we try to remember source code that we wrote or read in somebody else's work is that source code constitutes coherent content, so we do not just try to remember random words, but class, function, variable identifiers on the more refined level, or actual algorithms on a more abstract level. This means that the forgetting curve cannot be automatically adjusted to the retention of source code.

We conducted two experiments with a group of Computer Science MSc students. In the first experiment, we examined the code comprehension strategies applied by the participants, and draw conclusions on the general direction of these strategies in the case of junior programmers. The students were given a task to implement a minor feature in a relatively small C++ project, *tinyXML2*. The students had one hour to complete the task. In the second experiment - which is the relevant one to this paper -, we asked the students almost 3 months later to complete the same task again. Before starting the clock, we asked the students to fill a questionnaire which aimed to measure program code-related memory retention. In the questions, we were curious about how much the students remembered the code, down to the smallest relevant details, e.g. the name of functions and variables they had to find to complete the task.

After the second experiment, we could compare the solution times of those students who participated in both parts. As one result, we could see that these students could solve the task in shorter time than they did in the first experiment. We also looked at the results of the questionnaire: the vast majority of students could not precisely remember more than two or three identifiers from the original code. In this talk, we will show how this result can be compared to the forgetting curve.

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XRaying the Execution of C++ Code for an Improved Visualization

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The formation of C++ source code is the mold of sequential execution, so it is very painful to realize which code parts are able to run parallelly [2]. The constructs of concurrency cannot explain properly how the code snippets can be overlapped, therefore a single static analysis tool cannot give precise feedback about the parallel execution [4]. Moreover, parallelization can be the root cause of many runtime problems (interferences, deadlocks, etc.), therefore software maintenance of multithreaded code requires many experiences. Code comprehension tools may mitigate these difficulties.

XRay is a function call tracing system that can be used with C/C++/Objective-C code. The system uses instrumentation based on the Clang compiler and contains tools for analysing the retrieved traces [3].

In this paper, we present an approach which takes advantage of XRay and traces are used to estimate the details of parallel execution. We highlight and visualize the results in the Monaco Editor which is Microsoft's open-source browser based code editor [1]. We show how this approach improves the code comprehension when threads are in-use.

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Detecting programming flaws in student submissions with static analysis of the source code

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The demand for IT professionals is constantly increasing globally, as software development and maintenance is required in various fields, ranging from the banking sector through healthcare and automotive industry to agriculture. As a direct consequence, more and more people are enrolling each year in computer science degree programs and other IT and programming related courses at universities. This increment of students significantly increases the workload of university teachers and makes the manual grading of each student submission unsustainable. As a result, the usage of automatic grading systems for programming assignments have gained focus in the past years. Whether they are developed commercially, open-source or in many cases as an internal project at a university, these systems are becoming indispensable for instructors.

Non-trivial run-time errors in programming submissions are often missed by instructors and automatic testers, because these kinds of errors are not always easy to find and reproduce. Furthermore, there are solutions with functionally correct and bug-free code that does not follow the conventions and guidelines of the given programming language. These kinds of errors can be avoided and the application of the given guidelines can be forced using static code analyzers. In our paper we evaluate student submission from previous semesters written in C++ and C# programming languages, by executing various static code analysers on them [1].

The C++ projects were collected from the *Object-oriented programming* and *GUI programming with QT* courses at our university. All together 555 programming submissions were analyzed. We have run three tools on these submissions: *Clang-Tidy*, *Clang Static Analyzer* and *Cppcheck* [2, 3]. Typical programming errors which have been overlooked by the grading instructors previously, but found by static analysis included:

- narrowing conversion (e.g. `unsigned int -> int`);
- result of integer division used in a floating point context;
- comparison of signed and unsigned integers;
- memory leaks in dynamic memory management;
- multiple calls of delete for the same reference;
- delete calls on abstract classes without virtual destructor;
- out of bound indexing;
- object slicing;
- calling virtual methods in constructors.

In the case of C# projects, 183 programming submissions were collected from the *Event-driven programming* course, where students have to develop Windows Forms and WPF applications. For these submissions, we have used both first-party (*Microsoft NetAnalyzers*) and third-party (*Roslynator Analyzers* and *SonarAnalyzer CSharp*) analyzers built on top of APIs provided by the *Microsoft Roslyn* compiler platform [4, 5]. Typical programming errors which have been overlooked by the grading instructors previously, but found by static analysis included:

- fields with public visibility;
- incorrectly implemented properties (e.g. setter body is empty);
- disposable objects are not disposed;
- disposable objects are used after disposed (or returned from a using statement/declaration);
- both Close and Dispose called on the same object;
- asynchronous calls are not awaited;
- infinite recursions (e.g. setter of a property calls itself);
- incorrect overrides of `Equals(Object)` and `GethashCode()`.

Bases on these findings, in our paper we argue to include static analysis of programming submissions in automated grading and evaluating systems at universities, as these could increase the quality of programming assignments and raise the attention of students on various otherwise missed bugs and other programming errors.

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Competitive influence maximization in trust-based social neworks with deep Q-learning

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Social network analysis is a rapidly evolving research area having several real-life application areas, e.g. digital marketing, epidemiology, spread of misinformation. Influence maximization aims to select a subset of nodes in such manner that the information propagated over the network is maximized. Competitive influence maximization (CIM) describes the phenomena of multiple different actors competing for resources within the same infrastructure. The CIM problem may be solved with a greedy approach proposed by [1], which selects the seed nodes utilizing the influence strength between nodes. Recently, deep reinforcement learning methods were applied for estimating the influence strength. A controller is trained to select a node list of given length as the initial seed set for the information spread. Embedded node representations are beneficial as an input for such systems to ensure that the learned models are efficient on network with structures differing from the training samples. We show empirically that deep Q-learning methods are suitable to analyze the competitive influence maximization on trust- and distrust based social networks. We apply several memory representations for social networks to maximize the performance of training a deep Q-network.

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Clustering of countries based on the associated social contact patterns in epidemiological modelling

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Social contact patterns is crucial in influencing the transmission rates of infectious diseases. Quantifying these patterns during an evolving pandemic is key for planning, evaluation, and assessment of age specific interventions in different settings. They have also been used to inform public health decisions through identification of setting-specific social contacts. However, their comparisons from country to country is yet to be established.

Here, we fill this gap by introducing an approach that groups countries into clusters based on the social contact matrices derived from [1] with a disease transmission model [2], that describes the contact rates between age groups in household, school, work, and other settings. We demonstrated the effectiveness of this methodology by deducing countries from the algorithm that can be compared during a pandemic situation like COVID-19.

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Ensemble methods and their interpretability in demand forecasting

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Decision trees are one of the main options for solving classification and regression problems. They are not the most suited for predicting continuous values[1], however they are one of the easiest interpretable models[2]. This aspect is an important factor for business-oriented applications, because the rules learned by the model can give insights to the business. Decision tree ensembles are meant to overcome several limitations of singular decision trees, but they are called opaque or black box models as their internal working is not straightforward.

Our main research focus is to use ensemble models for demand prediction and use different interpretability techniques to gain knowledge on the model insights. While some of these interpretability techniques are model specific like SHAP tree explainer, others are model agnostic like permutation feature importance or Mimic explainer. These techniques aim for providing feature importance values for the entire model(global explanation) or individual data point(local explanation) predictions. In our experiments we used these techniques to evaluate different boosting ensemble methods like Adaboost, XGBoost and bagged decision trees like Random Forest for solving a regression problem of demand forecasting.

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On composing asynchronous operations

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Asynchronous operations are very useful for actions that wait for an external event or work for a long time, to avoid blocking the thread that launches them. Unfortunately, whether they report their termination via callbacks or via completing a future, composing several asynchronous calls is difficult and error prone. The continuations mechanism (provided, for example, in C# Task Parallel Library via `ContinueWith()`) offers limited support for scheduling a sequence of operations. In this paper we try to improve this mechanism with better support for sequencing operations, and with support for conditionals and loops, together with separating from the executor mechanism and covering the specifics of a C++ implementation.

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Malware analysis and static call graph generation with Radare2

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A powerful feature used in automated malware analysis is the static call graph of the executable file. Elimination of sandbox environment, fast scan, function call patterns beyond instruction level information – all of these motivate the prevalence of the feature. Processing and storing the static call graph of malicious samples in a scaled manner facilitates the application of complex network analysis in malware research. IDA Pro is one of the leading disassembler tools in the industry [7, 8] which offers the generation of the call graph via *GenCallGdl* and *GenFuncGdl* APIs – a tool which we used in our previous works [6]. In this paper we offer an alternative analysis using another disassembler tool, Radare2[1], an open-source Unix-based software, which is also frequently used in this domain [5, 2, 3, 1, 4]. Radare2 has Python support (among other languages as well), via the *r2pipe* package, thus enabling full scalability on Linux-based servers using containerized solutions.

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A tale of controllability: evolving network motifs in random Complex Networks

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Network motifs are patterns of interconnection that are found in real-world networks. Their existence is mainly attributed to the apparent chaotical behavior of the atoms in the systems that the networks are modeling, behavior that emerges in patterns that will be encoded in the network. Motifs were not formalized as structures due to their rarity but only explained through their contextual appearance in the networks. A series of experiments [1][2][3][4] managed to prove that their existence is correlated with various micro-scale but also macro-scale properties of the network topology. In this paper, we propose a new null model that generates random networks with a specific concentration of motifs based on two micro-scale properties, Assortativity degree, respectively Local Clustering Coefficient. Such a model could significantly improve the study of network motifs by generating any number of synthetic networks that can serve as experimental material for the community of researchers.

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Internet Wizard for Enhancing Question Answering Chatbot Knowledgebase

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Currently, chatbots are used in many different fields to automate tasks. This is because machines can outperform humans due to their availability and consistency. Education is one of the areas where chatbots are used. However, all types of chatbots, including domain-specific and open-domain questions-answering chatbots, have limitations due to their knowledge base. Rather than being static, knowledge grows dynamically. New information is coming in every day, even every minute. Static modeling languages do not account for these updates in their knowledge base. This is because statistical models are trained based on the knowledge that has been gathered from the time the dataset was collected and frozen. The massive dynamic knowledge available on the World Wide Web can play a crucial role in improving the chatbot knowledge base. In this research, we explore the use of the internet wizard by taking advantage of search engine features Data Science, and Natural Language Models to develop a mechanism capable of dynamically accessing the vast knowledge of the Internet, with alternative components for generating responses. A model which generates real-time, up-to-date answers from web documents for user queries in a chatbot that answers open-domain questions. To test the developed chatbot, a pilot study will be conducted the data of which will be analyzed and evaluated to investigate the adaptability of chatbots in education.

Global dynamics of a within-host model for Usutu virus

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In this work, we propose a within-host mathematical model for the Usutu virus with Crowley–Martin functional response. The basic reproduction number R_0 is found by the next-generation matrix method. The model exhibits one or two equilibria, depending on the basic reproduction number. The local stability of the two equilibria is discussed using the Routh–Hurwitz criterion. Global stability is also established by constructing appropriate Lyapunov functions and using LaSalle's invariance principle. Numerical simulations are presented to illustrate the results and a sensitivity analysis of the $\mathfrak{R}_0$ was also completed, and a model fit to actual data is established.

Key words: Usutu virus, Virus dynamics, Stability analysis, Lyapunov function, Crowley–Martin functional response.

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Dynamics of an SIRWS model with immune boosting and secondary infections

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SIRS models capture transmission dynamics of infectious diseases for which immunity is temporary. The SIRWS model is formulated by adding a W compartment for individuals with waning immunity. Earlier studies of this model in [3, 4] assumed identical waning rates from R to W and from W to S. A detailed analysis of this model, where we relax this restriction and allow an asymmetric partitioning of the total immune period is found in [5]. We find rich dynamics: Hopf bifurcations, double endemic bubbles, regions of bistability. In this work, we investigate the dynamics of an SIRWJS model, which is a further extension of the SIRWS model by adding a J compartment for individuals experiencing secondary infections. Stability analysis of both the disease free and endemic equilibria are investigated. Relying on Theorem 4.1 of [2] based on center manifold theory [1], we prove that the disease free equilibrium undergoes a transcritical bifurcation of forward or backward kind when the basic reproduction number is one i.e. $\mathcal{R}_0 = 1$. For the endemic equilibrium, numerical continuation methods are applied to track bifurcations along the equilibrium branch. We find that the double endemic bubbles in the previous analysis collapse into a single bubble. Our results highlight that the length of the period in which waning immunity can be boosted is a crucial parameter significantly influencing long-term epidemiological dynamics.

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Evolutionary algorithms for solving Traveling Salesman Problems

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This paper proposes an incursion in the field of evolutionary computation methods for solving optimization problems, more precisely the study of the evolutionary algorithms in solving the traveling salesman problem. The traveling salesman problem (TSP) is a well-known and intensively studied NP-hard problem. Numerous research studies have focused over the years on solving TSP using evolutionary algorithms, transforming the algorithm from a general to a specific one tailored to this problem. New types of crossover and mutation operators have been proposed to improve the performance of evolutionary algorithms [2].

This paper aims to analyse the comparative performance of different crossover and mutation operators in the evolutionary search process. To generate new individuals, the crossover operator is used to create offspring which inherit either the relative order or the absolute position of cities from the parental chromosomes [3]. The role of the mutation operator is to maintain diversity in the population, establishing uniform populations able to evolve and escaping from the local minima's trap [4]. In this paper, the analyzed crossover operators are the order crossover [1], the partially-mapped crossover [3] and the cycle crossover [3], and the mutation operators considered are the swap mutation [4] and the reverse order mutation [4].In order to analyze the performance of these operators, a series of experiments are performed on various problem instances from the TSP library. The fitness of each individual is based on the total distance of the route solution encoded and stays at the core of the selection strategy used by the evolutionary algorithm. The role of this selection is to enrich the population with better individuals [4].

Computational experiments performed for the TSP library show that the best results were obtained for the use of the cycle crossover operator together with the reverse order mutation operator and the worst results for the use of the cycle crossover operator together with the swap mutation operator. Therefore, the best mutation operator for these datasets was the reverse order mutation. Regarding the reverse mutation operator, the best results were obtained for the cycle crossover operator and the worst results for the partially-mapped crossover operator. For the swap mutation operator, the best results were obtained for the order crossover operator and the worst results for the cycle crossover operator.

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Image segmentation techniques

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Image processing and image segmentation represent a subfield of computer vision that is closely related to extracting information from images or videos. Each domain has its own specific characteristics which requires the adaption of the well-known algorithms. Detecting the breast cancer, or finding tumors are examples of fields of study where specialized methods are needed.

At the beginning, the research briefly presents the state-of-the-art of state-of-the-art algorithms used in image segmentation. First, unsupervised methods such as K-means, histogram thresholding, graph-based segmentation and region-based methods are presented. Based on the obtained results, the algorithms could be compared in terms of their performance. In the following, some metrics that are widely used for validating image segmentation results are presented.

Next, the study presents a review of recent studies in the medical field based on the presented methods. A comparison of these methods based on the segmentation method, seed selection and input images is also presented.

An overview of prototype-based self-explaining models

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Interpretability or explainability of deep neural network (DNN) models is of central importance when applied in safety-critical situations, like medical decisions or driver assistance systems. In these domains it would be crucial to open up the black-box of DNN models in order to be able to analyze the root causes in case of failure and to fulfill regulatory requirements towards safety-critical systems.

In our work we present a general self-explainable model following the work of Alvarez-Melis and Jaakkola [1]. Then we study some existing self-explainable models [4, 3, 2] and analyze them in the light of the presented general self-explainable model. We attempt to reproduce the results published for the models considered and test these on other datasets as well. We also aim to compare the self-explainable models with their non-interpretable DNN backbones to analyze the performance gap between them.

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Evaluation of the Traquest model

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There are many protocols and software architectural styles [1] for distributed systems and communication between computing nodes or processes. SOAP [2], REST [3], GraphQL [4] and RPC [5] are probably the most common ones just to name a few. The current architectural styles differ in many aspects, but they all have one thing in common, they all wait for a request and they give a final response to it.

The ACID (Atomicity Consistency Isolation Durability) [6] properties are very well known and crucial in many distributed systems. Being able to convey atomic operations reliably in a distributed system is essential in many use cases. Yet, nesting processes in an ACID way using the current architectural styles is practically impossible due to the final nature of their responses. For instance, if a process has two sub-processes, and the first one succeeds but the second one fails, the first process should rollback as well, but it is impossible since it already gave a final response. Currently the most common solution to this problem is the use of multi-tier architectures [7] with stateless servers, where the whole complexity and responsibility of ensuring ACID properties is delegated to the persistence layer. Therefore, there are many ACID database engines, but on the other layers we can hardly find any ACID technologies. There are no ACID message brokers, cloud functions, stream processors or other technologies belonging to layers other than the persistence layer.

Our approach is called the Traquest Model [8]. In the Traquest Model we refer to the processes as Traquests. A Traquest is capable of giving a temporary response to a request instead of a final one. Traquests can be nested into larger Traquest trees. A Traquest tree represents an atomic operation. A whole Traquest tree can be committed at once or before the commit any branch of the tree can be rolled back. Therefore the Traquest model can nest processes in an ACID way. The Traquest Model can ensure the ACID properties not only in a database in the persistence layer, but on all higher layers as well. This new approach allows us to create completely new kinds of distributed architectures or create architectures similar to the currently existing ones, but make them magnitudes faster.

We created a prototype similar to the serverless architectures [9] with a Traquest based key-value database and a Traquest based cloud function service. In canse of optimal data topology using the Traquests allows us to reach the database without using network communication or even without leaving the runtime environment. Under optimal circumstances reaching the global state can be executed in memory time.

Our preliminary tests showed, that if eventual consistency is enough in some cases our Traquest model based database can be 200 times faster than Redis [10] which is one of the fastest in memory databases. If keeping full ACID properties is a requirement our database can be still four times faster than Redis providing only eventual consistency.

Of course comparing distributed systems or evaluating the correctness and reliability of a new distributed technology is a much more complex question. The goal of the current research is to give a more holistic evaluation and comparison of the Traquest Model.

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Analysis of recent complex network centrality measures

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Network science has pervaded many domains of scientific, economic, social and technological interest in recent years. It consists of a valuable toolkit for mathematical analysis of graph-based structures and of the interactions thereof. Transforming data stemming from sources of a diverse nature into a graph (complex network in *Network science* jargon), essentially lends itself to complex network analysis. The interdisciplinary nature of *Network science* facilitated the rapid development of the field, with novel techniques initially restricted to one field of science finding an easier path to generalization through the fusion enabled by a strong scientific community in the domain of Network science.

Centrality measures are an important part of network analysis, which consist of a variety of functions utilized in providing a ranking of the network nodes, more precisely a quantifiable measure of their impact to the network topology, along with their importance to the communicability and maintenance of the relations within the network. Different fields of research may require their own measure of *importance* of individuals in a community, hence the abundance of studied centrality measures. We start our discussion with a number of classical centrality measures (degree, closeness, betweenness, subgraph centralities - [8], [9]), and afterwards consider a number of more recent measures that either improve upon the aforementioned centralities ([1], [4], [7]), define novel methods of determining the important nodes of a network ([2], [3], [5]), or even derive their *interestingness* measure from a blend of literature-established measures with insights of domain-specific problems (as is the case with [6]).

We consider that selecting the proper tools for achieving the desired network analysis is a difficult process, encompassing both knowledge of recent advancements to the field, as well as a capability for adapting the current state-of-the-art to the specific problems addressed. While we acknowledge that an exhaustive analysis of centrality measures is virtually impossible, given the fruitful development of the field, especially in recent years, we attempt nevertheless a simple comparative study of a number of recent centrality measures, and try to show that providing adaptations and hybridizations of methods found in the literature can be achieved straightforwardly.

To this end, we constructed a testing base that can be easily parameterized to include any networks and centrality measures in the analysis. We intend to provide an in-depth analysis of the selected measures, applied on a data set of real-world, as well as synthetic networks (random, scale-free networks of various sizes and densities). The analysis will include a discussion on the run times of the algorithms, as well as their efficiency in detecting the central nodes of networks with respect to choosing the onset of an epidemic simulation, such that a rapid spreading on the network is ensured. Furthermore, we will be assessing their impact in determining the nodes central to maintaining communicability within the network (i.e. discovering the nodes that, once eliminated sequentially from the network, diminish the communicability within). In addition, we discuss the properties of the subgroup of nodes ranked highest in each network by every centrality measure, as well as the sensibility of these measures to slight variations of the analysed graphs.

This work is intended primarily for directing interested parties towards selecting the most appropriate method for their specific network data analysis requirements, while at the same time providing an overview of recently developed centrality measures.

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Evaluating the Join Operation on Data Streams

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In the traditional data processing paradigm, *one-time queries* [3] are executed on finite tuple sets stored in their entirety. In fields like astronomy, health care or finances, to name a few, *continuous queries* [1] are running perpetually against potentially infinite streams of data.

The join operation is one of the fundamental operations in SQL, allowing the combination of data from several relations, with multiple algorithms having been proposed [6].

In the continuous processing context, a data stream can be joined with other streams or with conventional stored relations. Joins come with unique challenges in this setting, as there's the time component to consider and the ephemeral nature of the data. Tuples arriving on a data stream are processed by the system and subsequently discarded. A *tuple-based* sliding window with parameter N on a stream holds, at each time instant, the last N tuples that arrived on the stream, whereas a *time-based* sliding window with parameter T on a stream contains, at each time instant t, the tuples on the stream with timestamps between $t - T$ and t [2].

Joins have received a lot of attention in the streaming world, with multiple papers [5, 4, 7] proposing different algorithms, ways of describing and executing joins, and operators.

In this paper, we adapt several of the classical join algorithms to the data stream context, tackling challenges posed by continuous data processing. We focus on a sliding window-centered approach to data stream processing.

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Predicting Indoor Radon Levels in Romania using Machine Learning Algorithms

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Predicting the indoor concentration of Radon aligns with the global initiative of reducing humans' exposure to health hazards. Increased levels of indoor Radon are the second major factor causing lung cancer [1]. Detecting the presence of this radioactive, odorless, and tasteless gas in households is high-priced and requires experts' aid. Creating an accurate prediction based on easy-to-gather geo-climatic data could inform residents of possible endangerment and guide them for specialized assistance in a faster and cheaper manner [2]. We tackle this regression problem by training and comparing three machine learning models to find a realistic prediction (Neural Networks, Support Vector Machine, and Random Forests). The aim is to train a model which can reliably outline the households with dangerous indoor Radon values. The input features were provided by researchers from Babeş-Bolyai University, Environmental Science and Engineering Faculty, who recorded and measured Radon levels periodically in multiple locations from Romania. The initial dataset contains the Radon concentration alongside indoor temperature and humidity at various timestamps. Another dataset was provided, containing CO2 measurements at the same locations. We further introduce the value of the outside temperature, wind direction, and altitude from the sensors' GPS coordinates. Preparing the data for the training consisted of merging the CO2 and Radon datasets into a comparable time-based metric, as well as normalizing the values. After this merge, we obtain 48 149 937 rows and 8 columns. We use Grid Search to tune the parameters of our RF and SVM models. The NN's depth and layers are adjusted based on visually observing the experiments. Out of these three algorithms, the Neural Network yields promising results with the fastest training times. The comparison between the results was based on both computing the mean percentage error and accurately classifying the values that posed a real danger (the values exceeding 250 Bq/m3).

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Algorithmic approaches with the use of modeling for improvement and optimization of business process

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One of the most important factors that businesses consider when it comes to improving their productivity is the continuous improvement of their formal and informal processes. This paper introduces a new method that can help businesses improve their processes and enhance the transparency of their business operations. Through the DMAIC method, we suggest algorithmic approaches to improve organizational processes and enhance their efficiency. These algorithmic approaches convert the XML meta-model of a UML activity diagram into a more accurate and useful version. We first used the Papyrus tool to represent an activity diagram. We then used Acceleo to extract and improve the non-improved XML. We then produced an improved version of the activity diagram using the updated XML. To demonstrate the viability of our approach, we showcase the operation of our method in the financial domain. Our research plan is to apply the proposed technique for the process improvement and digitization of business processes in the financial realm. We want to pay attention the blockchain technology too and investigate the integration of blockchain patterns, and workflow patterns for digital transformation in the case of financial enterprises.

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