Curriculum Vitae : Flavio Seno

Dati personali

Nato a Feltre (Belluno), 30 Luglio 1962

Cittadino Italiano

Sposato, con tre figli

Titoli accademici

Laurea in Fisica, Università di Padova , 10 luglio 1987 con il voto di "110/110 e lode"

Dottorato in Fisica, Universitàa di Padova. Esame finale a Roma il 23 settembre 1992.

Posizioni

Dicembre 1987 – Luglio 1988: visiting student presso la Katholieke Universiteit di Leuven, frequentante i corsi di Ph.D. ò

Novembre 1988 – Ottobre 1991: student di Dottorato presso la Università di Padovaò

4 Settembre 1991 – 19 Dicembre 2002: Ricercatore Universitario presso la Facoltà di Scienze MM.FF.NN. della Università di Padova (confermato dal 5 Settembre 1994)

20 Dicembre 2002 – 29 febbraio 2016 : Professore Associato presso la Facoltà di Scienze MM.FF.NN. dell' Università di Padova (idoneità conseguita alla SISSA nel gennaio 2001)

1 febbraio 2016 - : Professore Ordinario (02/B2) presso il Dipartimento di Fisica e Astronomia dell' Università di Padova

Marzo 1992 - Febbraio 1994: ricercatore post-dottorato (in permesso sabbatico) presso il Dipartimento di Fisica Teorica della Oxford University.

Luglio 1988 – Luglio 1989: Servizio Militare

Borse di studio

Borsa di studio della "Fondazione A. Gini" , utilizzati per tre mesi presso la Leuven Katholieke Universiteit (1987-1988);

Borsa di studio della "Fondazione A. Dalla Riccia", utilizzata per 5 mesi presso la Leuven Katholieke Universiteit (1987-1988);

Una European Fellowship nell' ambito del "Science Program" (EU SCIENCE fellowship) utilizzata per 24 mesi presso il Department of Theoretical Physics of Oxford University nel periodo 1992-1994.

Insegnamenti

Ho svolto attività didattica insegnando in vari corsi di studio e a livello di Dottorato. Il giudizio degli studenti sul mio insegnamento è sempre stato molto positivo con votazioni spesso al di sopra dei 9/10.

Come titolare ho insegnato

Struttura della Materia per la Laurea in Scienza dei Materiali
Metodi Matematici per la Laurea inScienza dei Materiali
Fisica Biologica per la Laurea Magistrale in Biologia Molecolare
Fisica Moderna per la Laurea in Fisica
Fisica Biologica per la Laurea Magistrale in Fisica
Fisica Medica per la Laurea in Odontoiatria
Complementi di Matematica e Fisica per la Scuola di Eccellenza " Pietro D' Abano"
Meccanica Statistica per il Dottorato in Fisica

Seminari su invito

Ho tenuto svariati seminari in prestigiose Università italiane e straniere. Su invito ho tenuto seminari in circa 80 Conferenze Internazionali

Organizzazione di Conferenze

Ho co-organizzato con Anne Chaka (NIST , Washington) la Euresco Conference:
"*Biophysics from First Principles: From the Electronic to the Mesoscale"*
San Feliu de Guixols (Spain), 7-12 Settembre 2002.

Sono stato nominato chairman della Sessione di Biofisica della:
"*Psi-K Conference*" Schwabisch Gmund (Germany) 22 -26 Agosto 2000.

Ho organizzato il workshop
"*Fisica Statistica di Bioplomieri*" durante il Convegno Nazionale dell' Istituto Nazionale di Fisica della Materia, Bari giugno 2002.

Ho organizzato (con Silvio Tosatto, Padova) del Workshop:
"*Predicting the Structure and Function of Proteins*", Padova (Italy) 10 -11 Dicembre 2004.

Ho organizzato (con Enzo Orlandini (Padova), Enrico Carlon (Leuven), Jospeh Indekeu (Leuven) til Workshop
"*Interdisciplinary Topics in Statistical Physics",* Venezia (Italia) 16-18 Aprile 2009.

Ho organizzato (con Guido Tiana, Milano) il Workshop
"*Physics of Protein Folding and Aggregation"* Brixen (Italia) 11-12 Febbraio 2010.

Ho organizzato il Workshop: *"Biophysics"* Larnaka (Cipro), 11-15 Luglio 2011, all' interno Sigma-Phi 2011 Conference.

Ho organizzato (con Guido Tiana, Milano) il Workshop
"*Physics of Protein Folding and Aggregation"* Brixen (Italia) 16-18 Febbraio 2012.

Ho organizzato (con R.Metzler, Postdam) la Conferenza:
"Fluctuation on small complex systems" Venezia (Italy) , 21-24 Ottobre 2012.

Ho organizzato (con R.Metzler, Postdam) la Conferenza:
"Fluctuation on small complex systems II" Venezia (Italy) , 10-13 Ottobre 2014.

Ho organizzato come Presidente del Comitato Scientifico il FisMat2015, Conferenzza Nazionale della Fisica della Materia, Palermo 28 Settembre- 2 ottobre 2015.

Ho organizzato (con R.Metzler, Postdam) la Conferenza:
"Fluctuation on small complex systems III" Venezia (Italy) , 3-6 Ottobre 2016
.
Ho organizzato (con R.Metzler, Postdam) la Conferenza:
"Fluctuation on small complex systems IV" Venezia (Italy) , 15-18 Ottobre 2018
.
Ho organizzato (con R.Metzler, Postdam e Gleb Oshanin, CNRS) la Conferenza:
"Anomalous diffusion: bad and wild" Bad Wildbad (Germania) , 23-26 Settembre 2019
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Managment of scientific and educational activities

1994 - 2001: Member of the *Scientific Commission* (Area 02 Physical Sciences) of the Padua University.

1994 - 2004 : Member of the Commission *For the planning of Laurea thesis activity* of the Physics Department of Padua

1994 - 1997 : Representative of Padua Group in the Board (Sezione Ristretta)
of the G-Section (Theory) of the National Institute for Matter Physics (INFM)

In 1997 I opened the *Biophysics Group* of INFM at Padua University and from then, till the closure of INFM, I was the representative of the group in the National Board (Sezione Ristretta)
of the Biophysics Section

1998 - 2001: Member of the *Local Board* (Consiglio di Unitá) of the INFM in Padua.

1999 - 2003: Person in charge of the ERASMUS/SOCRATES exchanges between Padua and Oxford Universities

1999 – 2004: Member of the "*Didactical Commission*" of the Laurea degree in Material Sciences.

1999 - 2003: Member of the "*Special Commission*"(6 persons) in charge of redefining the degree programme in Material Science according the new scheme (3+2).

2004 - 2006 : Chairman of the "*Comitato Ordinatore del Corso di Laurea in Ottica ed Optometria*" of the University of Padua (Committee in charge of creating the new degree course)

2004-2006 : Member of the *Board* (Consiglio di Presidenza) *of the Faculty of Science* of Padova University

2006- 2009 : Member of the *Council* (Giunta) of the Physics Department of Padua University;

2008 - 2011 : Representative of the Rector of Padua University in the National Assembly of CNISM (Consorzio Nazionale Interuniversitario per le Scienza Fisiche della Materia).

2008- 2011 : Director of the Padova Unity of CNISM.

2011 - : Member (by election) of the *Governing Body* (Consiglio di Amministrazione) of CNISM

2013 -2016 : Chairman of the *Scientific Commission* (Area 02 Physical Sciences) of the Padua University.

2013- 2016 Member of the *Scientific Panel* (Commissione Scientifica di Ateneo) of the Padua University

2015 - Member of the *Governing Body* of Collegio D.N. Mazza, one of the 14 Collegi Universitari di Merito (such as Ghisleri and Borromeo in Pavia) officially recognized and supported by the Italian Ministry for Education.

2015-2019 Deputy Director of the Department of Physics and Astronomy of Padua University

2019- Director of the Department of Physics and Astronomy of Padua University

Grants

I won European Fellowship of the "Science Program" (EU SCIENCE fellowship) to be used in Oxford with a supporting grant of 30000 British Pounds .

I have been local coordinator of a grant (ex 40%) (principal investigator: Prof. M. Ferrario - Modena) funded in 1996.

I have been local coordinator of a PAIS Grant - Progetto Avanzato di Interesse Specifico dell' INFM (principal investigator Prof. A. Maritan- SISSA Trieste) funded in 1997.

I have been local coordinator of a PRIN project (principal investigatort Prof. A. Maritan – SISSA Trieste) funded in 2003.

I have been coordinator of a Padova University Grant for Fellowship (Progetto di Ateneo per assegni di ricerca) funded in 2003.

I have been coordinator of a Padova University Grant (Progetto di Ateneo) funded in 2008.

I was participant in PRIN projects granted in 1999, 2001, 2005, 2007, 2009 and 2012.

Other activities

I am referee of the following journals: Physical Review B, Physical Review E, Physica, Physical Review Letters, Journal of Chemical Physics, Journal of Physics, Biophysical Journal, Proteins, FEBS Letters, Journal of Theoretical Biology.

I was Guest Editor of the special issue "New trends in modern statistical physics" of Centr. Eur. J. Phys **10** (June 2012)

I have been an external examiner for several Ph.D. students in Italy. Abroad, I have been on doctoral examining committees at the University of Oxford (July 1996) , University of Toronto (June 2008), University of Lausanne (December 2011) , University of Varanasi (July 2012) and University of Lund (February 2014)

I was invited as visiting Professor (Maitre de Conferences Invitè) to the Universite Henry Poincaré (Laboratoire de Physique du Solide), Nancy (July 1997) where I gave the course "An introduction to the statistical properties of polymers and proteins".

I was invited as visiting Professor (Maitre de Conferences Invite) to the University of Cergy-Pointoise, Paris (July 2003).

I am co-author of a paper: "An optimal protein design procedure", F. Seno, M. Vendruscolo, A. Maritan e J.R.Banavar, Phys. Rev. Lett. 77, 1901-1904 (1996) that was selected as INFM "highlight for the period 1996-1997.

I am co-author of a paper "Design of proteins with hydrophobic and polar amino-acids.", C. Micheletti, F. Seno, A. Maritan e J.R.Banavar, PROTEINS: Struct. Funct. and Gen. 32, 80-87 (1998) which was selected as "Highlight of Biophysics Section of INFM " for 1998.

I am co-author of the paper "Exploring the universe of protein folds beyond the protein data bank". P. Cossio, A. Trovato, F. Pietrucci, A. Maritan, F. Seno and A. Laio, Plos Computational Biology **11** , e1000957 (2010), which was selected as Highlight of CNR for the period 2009-2010.

Patents and licences

I am coauthor (with Silvio Tosatto and Antonio Trovato) of the software PASTA, the licence for which was sold, in 2012, by Padua University to the pharmaceutical society Boehringer Ingelheim. The software aims to predict which portion of a protein sequence is more prone to form a fibrillar aggregate. The software is based on the scientific publications:

A. Trovato, F. Chiti, A. Maritan and F. Seno, Plos Computational Biology 12, 1608-1618 (2006)

A. Trovato, F. Seno and S.C.E. Tosatto, Protein Engineering Design and Selection 20**,** 521-523 (2007)

Research activity

In the early years of my career, I worked on topics related to critical phenomena and phase transitions. Starting in 1996, I oriented my research towards the application of statistical mechanics to biological problems with particular attention to medical and pharmaceutical applications.

The main results I obtained are:

Solution of the theta point problem:

We were able to determine numerically the bulk[a] and surface[b,c] exponents for linear polymers at the theta point, in 2 dimensions. These results stimulated a strong debate since they were in contradiction with the existing theory proposed by Duplantier and Saleur [Phys. Rev. Lett. 59, 3617 (1987)]. Later, we were able to solve the problem exactly[d] by using a mapping on a percolative problem in the presence of a boundary. These results have been completely accepted by the scientific community as the complete solution of the theta point problem and quoted in many reviews, e,g. K. De'Bell and T. Lookman [Surface phase transitions in polymer systems in Reviews of Modern Physics, 65 87, (1993)], and E. Eisenrigler [Polymers near a surface: conformation properties and relation to critical phenomena, Singapore, World Scientific, (1993)] and in the books: C. Vanderzande [*Lattice Models of Polymers*, Cambridge University Press, 1998] and M. Henkel [*Conformal invariance and critical phenomena*, Berlin, Springer (1999)].

[a] F. Seno, A.L. Stella, J. Physique, Vol.49, pp.739-748 (1988)
[b] F. Seno, A.L.Stella, C. Vanderzande, Phys. Rev. Lett., Vol.61, pp.1520 (1988)
[c] F. Seno, A.L. Stella Europhys. Lett., Vol. 7, pp.605-610 (1988)
[d] C.Vanderzande, A.L. Stella, F. Seno, Phys. Rev. Lett Vol. 67, pp.2757-2760 (1991),

Protein design:

We introduced[a] a general method for protein design based on an analysis in sequence space of the Boltzmann weight for a given target structure. We introduced different approaches to implement this method. In particular, by using a free energy expansion based on the amino acid concentrations[b] we were able to successfully design on a cubic lattice (Harvard- San Francisco test) 10 structures of length 48 within the hydrophobic polar (HP) classification of the amino acids. With the same classification of the amino acids, we generalized[c] the method to design real proteins with a success rate of 75% . These results were highlighted in the divulgation journals "Scientific Computing World" (April 1998, p. 8) and "Le Scienze" (July 1998, p. 15).

[a] F.Seno, M. Vendruscolo, A. Maritan, J.R. Banavar, PRL 77, pp.1901-1904 (1996)
[b] C. Micheletti, F. Seno, A. Maritan and J.R. Banavar , PRL 80, pp.2237-2240 (1998)
[c] C. Micheletti, F. Seno, A. Maritan and J.R. Banavar, Proteins: Structure, Function, and Genetics, 32, pp 80-87 (1998)

Topological properties of proteins:

In the work [a] we demonstrated the important role played by the geometrical and topological properties of the native state in determining the folding properties of a protein. Strikingly, by studying the conformational entropy of a backbone it was possible to identify the peptide regions that come in contact at early stages of folding with no detailed information on the sequences that are housed in the target fold. These results regarding the folding nucleus are fully consistent with experimental findings. Even today, this paper is still regularly quoted in the literature (more than 110 citations).

Later on , we introduced a novel and fully automated criteria for an optimal partitioning of a complete data bank of protein fragments . We proved that with only a few dozen of such fragments (length 6 aminoacids), virtually any protein can be reproduced within typical experimental uncertainties.

[a]C. Micheletti, J.R. Banavar, A. Maritan and F. Seno PRL 82, pp. 3372-3375 (1999)
[b] C. Micheletti, F. Seno, A. Maritan, Proteins 40, 662 (2000)

General framework to understand the structural properties of proteins:

In a set of papers[a,b,c] we proposed that native-state folds of proteins can emerge on the basis of considerations of geometry and symmetry. We showed that the inherent anisotropy of a chain molecule, the geometrical and energetic constraints placed by the hydrogen bonds and sterics, and hydrophobicity are sufficient to yield a free-energy landscape with broad minima even for a homopolymer. These minima correspond to marginally compact structures comprising the menu of folds that proteins choose from to house their native states. This result justifies the well-known fact (Denton and Marshall *Nature* 410, 417, 2001) that the number of protein folds is limited and not subject to evolution. The fact that possible folds can be determined only by using a homopolymer was confirmed in a more recent paper [d]. Using a sophisticated numerical approach, we performed an exhaustive exploration of the conformational space of a 60 amino acid polypeptide chain described with an accurate all-atom interaction potential. We found an ensemble of almost 7000 independent structures in which it is possible to find all the folds which are known for similar lengths. However, the ensemble of known folds forms a relatively small corner of this ensemble. Many more proteins are possible. Our analysis suggests that existing proteins were evolutionarily selected under the guidance of a simple principle: reducing the entanglement in the bundle formed by the protein in its folded state. This makes bundles with shorter loops preferable. The set of structures that we make available will potentially open a range of practical applications in biomedical sciences.

[a] T.X. Hoang, A. Trovato, F. Seno, J.R. Banavar and A. Maritan, PNAS USA, Vol. 101, pp. 7960-7964 (2004)

[b]J.R. Banavar, T.X. Hoang, A. Maritan, F. Seno and A. Trovato, PRE **70**, art. N. 041905 (2004)

[c] T.X. Hoang, L. Marsella, A. Trovato, F. Seno, J.R. Banavar and A. Maritan, PNAS USA **103**, 6883-6888 (2006)

[d] P. Cossio, A. Trovato, F. Pietrucci, A. Maritan, F. Seno and A. Laio, Plos Computational Biology **11** , e1000957 (2010)

Interaction potentials for Protein Folding:

An essential ingredient for understanding protein folding and design is the task of deducing the coarse-grained potentials of interaction between the amino acids. In the course of my research work I have published several papers on this topic which were well accepted by the scientific community[a,b,c,d]. Very recently[e, f] we proposed a novel statistical potential constructed by Bayesian analysis measuring a few structural observables on a set of 500 experimental protein structures. Even though employing many fewer parameters than current state-of-the-art methods, our potential is capable of discriminating with unprecedented reliability the native state in large sets of misfolded models of the same protein.

[a] F. Seno, A. Maritan and J.R. Banavar, Proteins: Structure, Function, and Genetics 30, pp.244-248 (1998)

[b] F. Seno, C. Micheletti, A. Maritan and J.R. Banavar PRL 81, pp.2172-2175 (1998)

[c] C. Micheletti, F. Seno, A. Maritan, J.R. Banavar, Proteins 42, 422 (2001)

[d] H.T. Dobbs, E. Orlandini, R. Bonaccini , F. Seno,Proteins 49, 342 (2002)

[e] P. Cossio, D. Granata, A. Laio, F. Seno, A. Trovato Scientific Reports **2,** Art. No. 351 (2012)

[f] E. Sarti, S. Zamuner, P. Cossio, A. Laio, F. Seno and A. Trovato, Comp. Phys. Comm. **184,** 2860 (2013)

Amyloid fibrils:

An increasing number of terrible human pathologies (such as Alzheimer's and Parkinson's diseases) are associated with the conversion of peptides and proteins from their soluble functional forms into well-defined fibrillar aggregates called amyloids. In ref. [a] and [b,c] we developed an algorithm to predict the portions of a sequence, for an initially unstructured polypeptide chain, that stabilizes the cross-beta core of the amyloid fibrils. Our predictions are extremely accurate when compared with experimental findings and they can be used to design mutations that could mitigate the aggregation process and therefore used for therapeutic applications. Our method is available on a web site (http://protein.bio.unipd.it/pasta/) (16000 download). Moreover, the related software we produced (Palmo) was sold, in 2011, by Padua University to the pharmaceutical company Boehringer Ingelheim.

[a] A. Trovato, F. Chiti, A. Maritan and F. Seno, Plos Computational Biology **12**, 1608-1618 (2006)
[b] A. Trovato, F. Seno and S.C.E. Tosatto, Protein Engineering Design and Selection **20**, 521-523 (2007)
[c] I. Walsh, F. Seno, A. trovato and S.C.E. Tosatto, Nucleic acids research **42** , W301-7 (2014)

Modelling of mechanical denaturation of DNA

The recent refinements in experimental tools employing optical tweezers, atomic force microscopes and soft microneedles make it possible to monitor the behaviour under tension and stress of various biopolymers, and then to elucidate the mechanism of some force driven phase transitions occurring at the single molecule level, such as the stretching of single collapsed DNA molecules, and the unzipping of DNA. The large quantity of experimental results was demanding for theoretical modelling. In this field we have proposed and solved, both numerically and analytically[a,b,c,d,e] several models giving a well-recognized contribution to the field. In particular, we have suggested [a,b] the existence of cold denaturation of a double stranded biopolymer (e.g. DNA) under mechanical stress. Such a transition has not yet been seen experimentally, but the accuracy of our calculation was confirmed in an extended range of temperatures. (C. Danilowitz, Y. Kafri, R.S. Conroy et al. [Phys. Rev. Lett. 93, art. 078101 (2004)]).

[a] E. Orlandini, S.M. Bhattacharjee, D. Marenduzzo, A. Maritan, F. Seno, JPA 34, L751 (2001)
[b] D. Marenduzzo, S.M. Bhattacharjee, A. Maritan, E. Orlandini, F. Seno PRL 88, 028102 (2002)
[c]D. Marenduzzo, A. Maritan , A. Rosa and F. Seno , PRL 90 art no -088301 (2003)
[d]A. Rosa, D. Marenduzzo, A. Maritan and F. Seno ,Phys. Rev. E, Vol. 67, art. no. 041802 (2003)
[e]Kapri, S.M. Bhattacharjee and F. Seno , PRL **93,** art. no248102, (2004)

Measure for data collapse.

We proposed [a] a measure to quantify the nature of data collapse, e.g for establishing scaling and extracting the associated exponents in problems showing self-similar or self-affine characteristics, for example, in equilibrium or non-equilibrium phase transitions . Via a minimization of this measure, the exponents and their error bars can be obtained. The methods works remarkably well and it has been used in a variety of problems such as the dynamics of ecological communities and the study of biological networks.

[a] S.M. Bhattacharjee and F. Seno , J. Phys. A, Vol. 33, pp.6375-6380 (2001)

Efimov effect for polymer physics

We proposed [a] and directly verified on an exactly solvable model[b] that the cold atom quantum Efimov effect, namely the possibility of a three body bound state where none of the pairs is bound, can be observed in thermal denaturation of three strand polymeric systems. This observation might have important and unexpected implications in a biological context where many processes involved three polymers (e.g. three helix DNA)

[a] J. Maji, S.M. Bhattacharjje, F. Seno and A Trovato, New Journal of Physics 12, 083057 (2010)
[b] J. Maji, S.M. Bhattacharjje, F. Seno and A Trovato, Phys. Rev. E89, 012121 (2014)

Quorum sensing

Quorum sensing can be described as the regulation of gene expression in response to changes in the bacterial population density. In this emerging field of microbiology we have introduced specific modeling which takes into account the presence of different boundary conditions and our calculations motivated dedicated experiments that we performed in collaboration with experimentalists of our university (Squartini, Brun). Our results have been quoted in the book by Stephen Hagen "The physical basis of Bacterial Quorum Communication"that is the first monography ever written on this subject.

[a] S. Alberghini et al FEMS Microbiology Letters 292, 149-161 (2009) USA
[b] A. Trovato et al. FEMS Microbiol. Lett. 352, 198 (2014)

Padova, 13 novembre 2019

Flavio Seno