

Computational Pharmaceutics-New Approach of Medicine Delivery

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ABSTRACT

Due to the longer time, greater cost and decreased productivity of novel molecular entities (NMEs).Pharmaceutics and drug delivery have assumed growing importance in the pharmaceutical business in recent decades.However contemporary formulation development still depends on time consuming, expensive and unpredictable classical trial and error studies.In the last ten years, a new field known as “computational pharmaceutics” has emerged in response to the exponential growth of computing power and algorithms. This field integrates big data, artificial intelligence, and multi-scale modeling techniques into pharmaceutics, and has the potential of fundamentally alter the way the drugs are delivery to the patients. Pharmaceutical scientists can use multi-scale lenses provided by computational pharmaceutics to disclose in the clinic includes revealing physical, chemical, mathematical, and data driven. Details ranging across pre-formulation studies, formulation screening, in-vivo prediction in the human body and precision medicine in the clinic.the current studies offers a thorough and in depth overview of all aspects of computational pharmaceutics including artificial intelligence and machine learning techniques , molecular modeling ,mathematical modeling , process simulation, and PBPK modeling. In addition to summarizing these technologies, theories and advancement, we also reviewed the legal requirements, existing difficulties, and potential future developments in the field, such as talent training and a cultural shift in the pharmaceutical sector.

Keyword: AI and machine learning,molecular modelling,process simulation,pbpbk modelling and simulation in drug development,future of computational pharmaceutics.

COMPUTATIONAL PHARMACEUTICS

A recent field of study called computational pharmaceutics with artificial intelligence and multi-scale modeling methods and it has the potential to fundamentally alter how formulations are developed. Today computational pharmaceutics is able to provide multi-scale lenses to pharmaceutical scientists , revealing physical ,chemical, mathematical, and data driven details ranging across chemical stability ,polymorphism , formula screening and precision medicine computational approaches play an essential role in all areas of pharmaceutics , involving but not limited to quantum mechanisms (QM) ,molecular dynamics simulation ,mathematical modeling , physiologically based pharmacokinetic (PBPK) modeling, process simulation , artificial intelligence (AI) , and machine learning algorithms .

By using Schrodinger equation quantum mechanics accurate description of electrons spatial positions, and other atomic and molecular scale things. It can forecast the physiochemical and structural characteristics of molecules under Newton rules of physics; molecular dynamics simulation simulates the motion of atoms and molecules. The molecular mechanism of formulation based on molecular mechanics and the empirical force field can be investigated using molecular modeling, which can also explore the structural, dynamic and energetic feature of the medication and excipient .The numerical simulation of a physical process , such a production line is called process molding ,PBPK simulation can forecast how formulation will behave in terms of pharmacokinetic / pharmacodynamic (PK/PD) in humans.Large volumes of accumulated experiments data can be cycled to develop a quantitative formulation prediction model using machine learning and AI algorithms to produced data-driven predictions. The development process can be

gently accelerated by a well designed AI system, which can also optimize formulations, reduce costs, maintain product consistency and collect and preserve the specialized knowledge and experience of formulation experts. Numerous significant grants and financing initiatives for computational pharmaceuticals research have been announced globally in line with this trend. In a four year project, advanced digital design of pharmaceutical therapies aims to revolutionize the UK pharmaceutical business by enabling future digital design of woven pharmaceuticals tools OrBiTo, a 2012- launched consortium with 29 members from the academic and industrial worlds, intends to provide a framework for the logical use of predictive biopharmaceutics techniques for oral medication administration. In order to employ datasets effectively in the future, this study highlights PBPK and MD models as prediction tools and recommends using AI technology.

Since, this approach emphasizes the process understanding in product design, adhering to the regulatory authority's such as the FDA's should examine application of computational approaches to pharmaceuticals to promote the quality of the final

At a glance

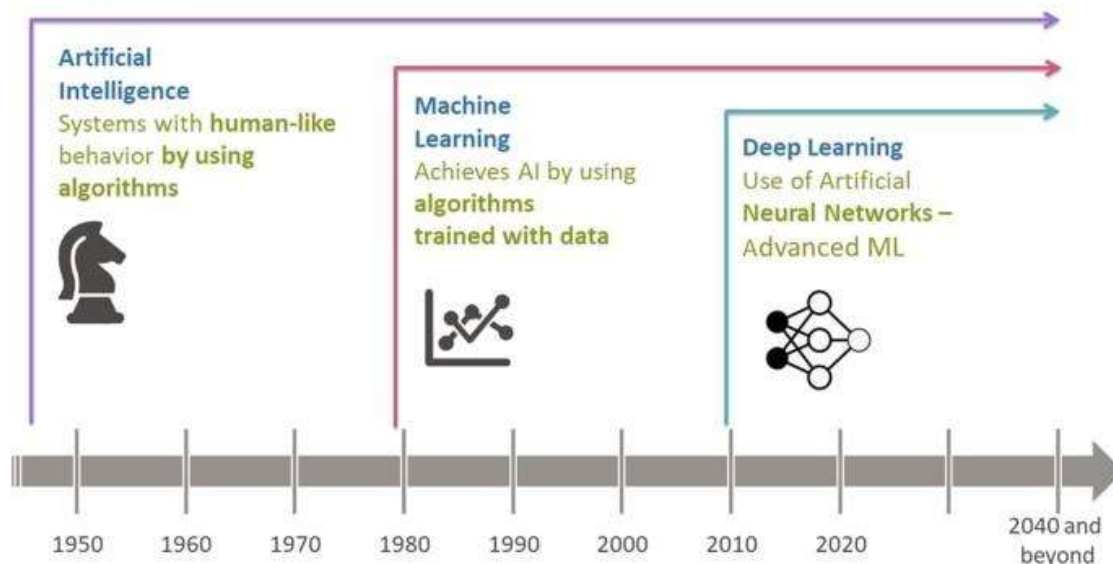


Figure num:1 At a glance

It is estimated that the size of the formulation space was around 10²⁵–10³⁰ (please refer to the Supplementary Information for calculation details). In such a high-dimensional space, it was hard to predict and optimize the formulation only by scientists' limited experience.

product. Model informed drug development or model informed drug discovery and development. The FDA's and EMA's favorable outlook in addition to the recently proposed methodologies. The Japanese pharmaceuticals and medical devices agency released a similar study in 2017. The centre for drug evaluation in china has been gathering recommendation for MIDD guidelines; these publications mostly emphasize the use of PK modeling in medication development reviewing the current uses of various silicon tools in the pharmaceutical field is necessary to understand where we need to go because computational approaches are altering the drug R/D paradigm and the way of think.

AI and Machine learning

The QbD strategy defined the design space as "the multidimensional combination and interaction of input variables and process parameters that have been demonstrated to provide assurance of quality". It was well recognized that pharmaceutical product development is a high dimensional optimization problem.

(AI), which can fit high-dimensional non-linear correlation based on big data and find the influence of minor variance of inputs on the difference of targeted labels. AI has attracted a lot of people's attentions and is increasingly becoming the core engine and driver of a new round of industrial change, constantly generating new technologies. Currently, AI has been applied to many fields, such as finance, retail, and medicine. AI is reported to be used in drug R&D at stages such as the development of active pharmaceutical ingredient (API), toxicology study, and clinical study, etc. Twenty-one leading pharmaceutical companies each have at least one application involving AI. This trend even has attracted tech giants like Google, Microsoft into medicine. Recently, the protein structure prediction tool AlphaFold2 from DeepMind shocked the world with its experiment-level precision, showing the potential of AI combined with biological science and pharmacy. The utilization of AI in this area has attracted attention from experts in pharmaceuticals. In fact, AI is not a new thing in pharmaceutical investigations. For example, in 1991, a study, which applied ANN to pharmaceutical formulation development, was published by Ajaz S. Hussain and co-workers. An ANN model was trained to predict the drug release parameter, the dissolution half-time. Compared with the traditional response surface methodology, it was shown that ANN had higher accuracy, probably due to the higher data fitting ability of ANN. Recently, with more cutting-edge algorithms occurring, such as deep neural networks (DNN), ensemble learning, transfer learning, and so on, AI has promoted the R&D of

numerous dosage forms, including but not limited to hydrophilic sustained-release matrix tablets, oral fast disintegrating film and tablets, cyclodextrin (CD) complex, amorphous solid dispersion (ASD), nanocrystals, and so on.

Machine learning in the creation of formulations

Currently, some efforts have been made to apply AI techniques to pharmaceutical product development, including pre-formulation physicochemical property and activity prediction, in vitro drug release, physical stability, in vivo pharmacokinetic (PK) parameters, drug distribution, in vivo-in vitro correlation (IVIVC) and so on. Machine learning attracted attention because of its powerful fitting and prediction ability. Machine learning algorithms were used to predict

the performance of various dosage forms, including ASD, CDs, nanoparticles, self-emulsifying DDS (SEDDS), and so on. Supplementary Table 1 summarized the progress. In addition, many machine learning techniques have been used to predict formulations or generate data, such as transfer learning, multitask learning, federated learning, generative adversarial networks, and interpretable machine learning methods. ASD dispersed the APIs uniformly in the carrier in amorphous, microcrystalline, or other highly dispersed states. Amorphous improved the solubility, dissolution rate, and bioavailability of poorly soluble drugs. Solid dispersion has two main problems, physical stability and dissolution behaviors. In 2019, Run Han and co-workers applied machine learning methods to the prediction of the 3-month and 6-month physical stability of solid dispersion. Eight learning algorithms were introduced to create models. 82.5% accuracy of the random forest model was further validated by experiments. Also, in 2021, in Hanlu Gao and co-workers'

work, the dissolution behaviors of solid dispersion were investigated by machine learning. The random forest algorithm was used to construct a classification model to distinguish two types of dissolution profiles of "spring-and-parachute" and "maintain super saturation" with 85% accuracy, 86% sensitivity, and 85% specificity in 5-fold cross-validation.

The random forest algorithm was used to construct a regression model to predict the time-dependent accumulative drug release with a mean absolute error of 7.78 in a 5-fold cross validation. CD complication enhanced the solubility of insoluble drugs and improved bioavailability and stability. CDs and guest drug molecules formed CD complication by the reversible binding. The binding free energy was a good indicator to estimate the binding strength. In 2019, the largest CD complication binding free energy dataset covering 3000 formulations were collected by Qianqian Zhao and co-workers. Eight types of CDs were included, and three machine learning algorithms were applied and compared. The results showed that the light GBM model demonstrated the best performance of 1.38 kJ/mol mean absolute error. The feature importance obtained from light GBM gained valuable insights that the minimum projection radius of APIs has a primary effect on the reversible binding. Nanoparticles were found to have advantages in delivering drugs to the target cells or tissues.

Various

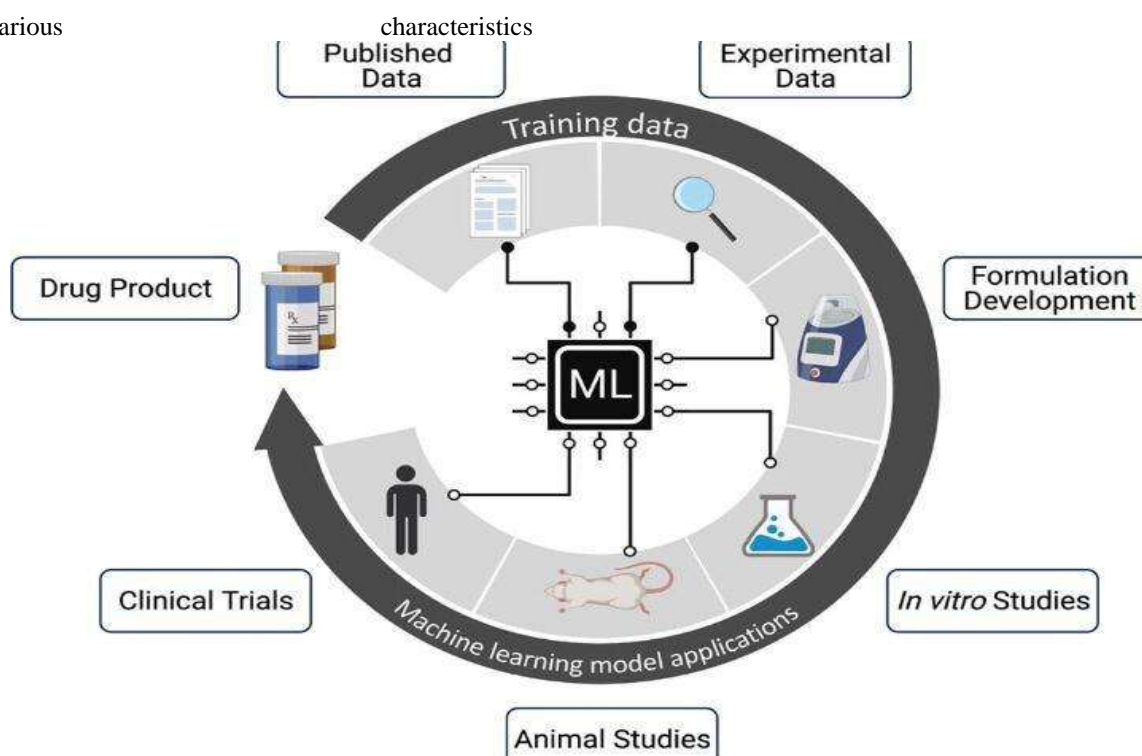


Figure num:2 Machine learning model applications

of nanoparticles account for the delivery, including the size, shape, chemical compositions, and surface chemistry of nanoparticles. However, designing the optimal nanoparticle DDS is challenging. There is an increasing number of experimental tests to probe the characteristics of nanoparticles in vitro, in vivo, and at the disease sites. In 2020, Yuan He and co-workers utilized machine learning techniques to predict nanocrystals. 910 particle size data and 310 PDI data covered ball wet milling, high pressure homogenization, and antisolvent precipitation methods. W. Wang et al. Journal of Controlled Release 338 (2021) 119–136. LightGBM models demonstrated good performance for the nanocrystals produced by ball wet milling and high-pressure homogenization methods. The SEDDS were composed of oil, surfactant, cosurfactant, and APIs. The selection of suitable emulsifying agents and stabilizers was a crucial step in the formulation development. In 2021, Haoshi Gao and co-workers collected a SEDDS dataset with 4495 formulation composition ratios. Seven machine learning algorithms were used to construct models to distinguish whether the oil, surfactant, and cosurfactant could form the SEDDS. Compared to other machine learning algorithms, random forest showed the best

accuracies of 91.3% accuracy, 92.0% sensitivity, and 90.7% specificity in a 5-fold cross-validation. ADOE method of central composite design (CCD) was used to further screen

the ratios. In pharmaceuticals, small data is a common problem in the machine learning modeling process. Transfer learning utilized the big data in the source domain and transferred the learned knowledge to the target domain with limited data to enhance the performance. Multitask learning predicted the multiple tasks simultaneously and used the data of multiple tasks to learn the common network weights and knowledge. In 2019, an integrated transfer learning and multitask learning approach was developed to construct quantitative structure-activity relationship (QSAR) models for the prediction of the four human PK parameters by Zhuyifan Ye and co-workers. Totally, the human PK data of 1104 listed small molecule drugs were collected, including oral bioavailability, plasma protein binding rate, apparent volume of distribution at steady-state, and elimination half-life. A pre-trained deep learning model was trained on bioactivity data with more than 30 million entries. The integrated transfer learning and multitask learning approach was used to fine-tune


the model on the PK dataset. The results showed that the integrated approach enhanced the model generalizability. Model interpretability was increasingly considered as important as model performance in formulation development. Though some post-hoc interpretable methods have been proposed, methods based on post-hoc analysis faced the concern of faithfulness. In 2021, attention-based DNNs were proposed for pharmaceutical formulation development by Zhuyifan Ye and co-workers. Attention-based DNNs distinguished inputs, leading to higher accuracies than plain DNNs and generated interpretable attention weights for DNNs. Compared with post-hoc interpretable methods, the proposed approach had the advantages of providing global and local (sample-level and feature-level) interpretations, self-interpretable models, and having high faithfulness. Besides in silico predicting pharmaceutical formulation performance, it was recognized that generating data using machine learning was of great significance, especially given some implicit parameters. Generative models estimated the joint probability distribution of data. For example, the description of nanoparticle distribution in targeted organisms was crucial for the R&D of

nanomedicine. In 2021, Yuxia Tang and co-workers used deep generative networks to describe the nanoparticle distribution within T1 breast cancer tumors. The conditional generative adversarial networks (cGAN) and pix-to-pix techniques were used to conditionally model the nanoparticle distributions. The generative network was trained on 27,775 breast cancer slide images

AI in precision medicine


Since precision medicine was announced in 2015, this new term was getting a lot of attention. Trace to its source, precision medicine is derived from personalized medicine. Personalized medicine has a long history, which had reflected the individualization of medical treatments since ancient times. From personalized medicine to precision medicine, it has many impacts on disease prevention, diagnosis, and treatment. As announced by the National Institute of Health (NIH), in precision medicine, the importance of factors of individual genes, environment and lifestyle is increasing. The role of AI in precision medicine is indispensable to predict which treatment is the best for a patient.

Artificial Intelligence


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Researchers have pursued different versions of AI based on


 - Fidelity to **human behavior**
 - **Rationality** ("doing the right thing")

in both **thought** and **action**
- 

Works **when**

 - Data are cheap
 - Success and failure are obvious
 - Rules are explicit
 - Tasks are repetitive
- 

Subfields can be

 - **General** (learning, reasoning, perception)
 - **Specific** (playing chess)
- 

Disciplines that contributed to AI include

 - Philosophy, Mathematics, Statistics, Economics, Neuroscience, Psychology, Computer Engineering, Control Theory & Linguistics

We focused on the impact of AI in precision medicine and drug delivery, taking theri

ght dose of insulin delivery for diabetes as an example. Patients with type 1 diabetes could be

treated with insulin. The insulin pump is a type of automatic drug delivery equipment. This automatic insulin components: AI control algorithm, continuous glucose monitoring sensor, drug delivery pump, and insulin. By closely monitoring the data of patients' meal time, types of food, and blood glucose, it delivers insulin at the right doses. It helps patients better control their blood glucose. This kind of healthcare achieved close monitoring, tailoring medical interventions, and dynamic modulation.

Application in lead optimization. It has been successful and adopted to select out the drug molecule. Current problems of AI in pharmaceuticals

The recent development of AI techniques has played an essential role in the rational design and development of pharmaceutical products. The successful application of many AI technologies has shortened the development time, ensured the quality of products, and promoted the successful R&D of pharmaceutical products. However, during applied machine learning algorithms, a common problem was lacking data. The high cost of pharmaceutical experiments

and lengthy research and optimization time caused this issue. Because big pharma companies usually strictly kept their data, the existing pharmaceutical data became isolated islands. In addition, people were no longer satisfied with only the good performance of machine learning models but hoped to understand the running mechanism behind the models. The interpretable machine learning methods could bring more deep insights for pharmaceutical formulation development. In the future, the further integration of the pharmaceutical industry and AI technologies will bring more opportunities for pharmaceutical research and development.

Molecular modeling

According to the timescale and length scale, molecular modeling mainly contains three different parts: quantum mechanics (QM), all-atom molecular dynamics (MD) simulation, and coarse-grained (CG) modeling. Their applications to pharmaceutical studies are listed in Supplementary.

QM and its applications in pharmaceuticals

Here, the QM refers primarily to quantum mechanical simulations and calculations using computer technology. Almost all properties of a molecule can be calculated by QM, such as structure, conformation, dipole moment, ionization potential, electron affinity, electron density,

transition states, and reaction pathways. Besides, they can provide fundamental data on interatomic interactions in molecular dynamics, such as bond length, bond angle, interatomic interactions, and energy. Hence, QM is applicable to study relatively small systems, including molecule-to-molecule interactions and reactions involving bond breakage and formation. In the development of PLGA contained drug delivery system, the QM method has been used to analyze the energy transition during the process of salted-out and PLGA cross linking, which involves the interaction between PLGA and N,N-dimethyl formamide (DMF) solvent, water, and hydrochloric acid (HCl). The simulation result for 26 formulations produces profiles of matrix resilience, energy absorbed, and mass deflection, which is consistent with the experimental value. These results are important to judge the formulation stability when immersed in the phosphate-buffered saline solution. QM also shows the one with the highest solubility from a series of similar compounds. The solubility of a molecule is correlated to the sum of the free energy change of crystal sublimation process and molecule hydration process, reflecting the molecule first overcome the lattice energy and then dissolves in water.

The energy change of sublimation is predicted by the QM method with the pPBE-vdW level of theory. This approach has been validated against derivatives of benzoylphenylurea and benzodiazepine. More importantly, this approach shows the source of the low solubility of the molecule. For both drugs, lead optimization targeting reduced energy change of sublimation is more efficient than reducing that of hydration

MD simulation and its application in pharmaceuticals

All-atom simulation is a traditional molecular dynamic (MD) simulation, wherein atoms are generally regarded as the smallest unit, which is based on the principles of Newtonian motion mechanics. The interaction between atoms is described by the empirical force field. According to the Boltzmann distribution law, the computer randomly assigns initial velocities to all atoms in the system, solves the equations of motion numerically to obtain the velocity and coordinate information at any moment, and then implements the simulation of macroscopic properties. Relative to QM calculations, the interactions of electrons within atoms are ignored in MD simulation, which largely decreases the degree of freedom of the system. Although all-atom simulation cannot obtain the

information about electronic interactions within atoms, this simplification can greatly increase the time and length scale of the simulated system, making MD simulation an effective method for calculating large system and macroscopic properties.

Recently, some studies investigated the preparation and dissolution process of solid dispersion formulations by MD simulation. According to the traditional theory, drug molecules randomly disperse in the cavity of the network structure formed by the polymer chains. Due to the high energy barrier of polymer network structures, amorphous drug molecules should be difficult to migrate and recrystallize, which is contrary to the aging phenomenon of a solid dispersion system. Those MD simulation results showed that the linear polymer formed irregular coils under heating conditions and drug molecules adhered to the surface of the polymer irregular coils. There were quite small voids in the coils of polymer, which was difficult to hold drug molecules. Drug molecules can easily move and aggregate to form crystals based on this theory, which better explains the physical instability of solid dispersion. Moreover, a study investigated the preparation and dissolution process of vemurafenib solid dispersion formulations by MD simulation. In the preparation process, two solid dispersion formulations were formed using the annealing method. And then, the dissolution results showed that more vemurafenib molecules were released from the HPMCAS carrier than the Eudragit carrier, which corresponds to the experimental results. This may be caused by the HPMCAS polymer containing more hydrophilic

group than the Eudragit polymer. The application of MD in CD inclusion technology is the fast-growing and the most effective field. The MD method is suitable to study the properties of the CD inclusion complex and provide a theoretical basis for stable structures [64,65], diffusion coefficient and chiral separation. In our previous study, the effects of different types of CD on the binding affinity of lutein were examined by Amber software. Simulation results found that lutein molecules cannot insert into the α -CD cavity, while it can maintain a stable binding pose in β -CD, hydroxypropyl (HP)- β -CD, and γ -CD with the 1:1 ratio. Through calculating the binding free energy by MM-PBSA, they found that the van der Waals force was the highest contribution to the binding of lutein-CDs complex. A similar method has also been applied to the study of

andrographolide CD formulation, comparing the binding free energy of drug molecules to different types of CDs. Another study combined the molecular docking and MD simulation method to determine the dominant conformation of the candesartan-HP- β -CD binding pose.

Besides,

MD has also been used in pharmaceutical studies of nucleic acid therapeutics. One early study investigated and compared the binding behavior of siRNA to polymers with four and eight positive charges. The 4+ polymer is preferentially bound to the major groove of siRNA, and this

system is easier to release siRNA since it has lower binding free energy. The following study further simulated the saturated binding of polymers to siRNA at a high charge ratio, showing the quantified evidence of the binding capacity of the siRNA. Uludag's group reported a lipid substituted polyethylenimine (PEI) for siRNA delivery. The simulation results showed that this delivery system did not affect the function of siRNA and the structure became more compact and stable. Moreover, the lipid was located on the periphery of siRNA, which can enhance cell permeability and protect the siRNA from nuclease degradation. Additionally, Jasmin used MD simulation and found that a cationic cholesterol derivative also was suitable to deliver DNA by ionic interactions. Another study investigated the dynamic process of the combination of dendrite's with DNA. This dendrite is mainly located at the grooves of DNA, stabilizing the DNA structure.

CG modeling and its application in pharmaceuticals

The all-atom to large systems due to the massive computational atom simulation is still limitedly applied calculation, and the time scale is only in the nanosecond range. For example, the shape transitions of micelles, the cell uptake process, as well as the interfacial diffusion behavior of surfactant molecule are difficult to simulate using the traditional MD simulation method. Therefore,

a CG model is designed to simplify the complex molecular interactions in a molecular system. The CG simulation is a further approximation to traditional all-atom MD simulation, greatly reducing the degrees of freedom of the system and improving the time scale of the simulated system to microsecond order of magnitude. A study has developed a CG model to study the interaction

between siRNA and cationic diblock copolymers, and the simulation results found that the length of the cationic block influenced the types of interaction. In the latest research, Marrink et al. observed the release process of short fragments of double-stranded DNA from nanoscale leptosomes using CG models. When lipids fuse with the endosomal membrane, they form a pore that connects water channels to the inside of the cell, allowing DNA to escape. A CG model has been established to study the penetration mechanism of peptides. When peptides were absorbed on the asymmetric membrane, it can cause the formation of hydrophilic pores in the membrane, thereby penetrating the cell membrane and reducing the membrane asymmetry.

Precipitation and crystallization of drugs

Basically, the crystallization process is suggested as two steps: nucleation and crystal growth. Nucleation is the birth of a crystal when several solute molecules aggregate to form a crystal nucleus. Then more molecules precipitate on the surface of the nucleus to enlarge their size. The mathematical model for depicting nucleation can be categorized as mechanical or empirical. The

mechanical model involves the computation of excess free energy of surface and volume between two

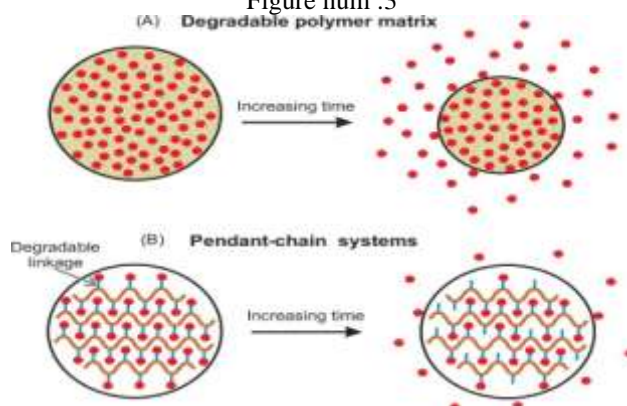
phases. The excess free energy of surface reflects the potential of the newly formed nucleus to rediscover, while excess free energy of volume indicates the tendency to condensation; their difference is a function of the nucleus's size, which determines a minimal radius necessary for nucleation where the propensity to rediscover and aggregate are equal. Energy combined with other properties like supersaturate solution activity and viscosity further defines the rate of nucleation. The empirical model

of nucleation rate is in the form of a power function, where the power index stands for the number of molecules needed to form a nucleus. For crystal growth, a classical explanation is the Gibbs-Volker absorption layer theory, which describes the formation of a two-dimensional nucleus layer absorbed onto the existing crystal surface in thermodynamic equilibrium. This process asks for a critical minimal radius of the initial crystal and can calculate the critical excess free energy and the consequent growth rate. Other remaining models include the Burton-Cabrera-Frank (BCF) equation and the "birth and spread (B+S)" model. Both of them provide models for the growth of the crystal layer on the surface. Proper choice of crystal growth

model usually depends on an alpha factor, which describes the crystal surface's roughness. BCF equation is suitable for a smooth surface, while the B + S model is applied to a rougher one. From the thermodynamic perspective, crystals tend to aggregate

to form larger particles to minimize the surface energy of the system. Thus, a crystal in a small size is prone to dissolve and re-crystallize on the surface of a bigger one. The Equation that depicts this transformation is called Ostwald ripening theory and has further been advanced by Lifshitz, Slyozof, and Wagner (LSW). Basic models contain one kinetic equation for the growth or reduction of an individual particle, one continuity equation for size distribution, and one mass conservation equation governing particle transformation. Besides the above crystal growth mechanism, two particles, especially nanoparticles, can directly attach to each other to form a bigger particle, named the oriented attachment (OA) process. OA is significant at the primary stage of crystal growth because small disorientation of OA contributes to the dissolution.

Figure num :3



Screw, and edges in crystals. Thus, many kinds of growth patterns, such as spiral growth, can occur. The kinetic model for OA has been previously summarized. Generally, equations for OA are similar to those for chemical reactions. Two small particles "react" at a rate constant to form bigger particles. What happens most frequently is the attachment of two primary particles to form a secondary particle. When a strong surface adsorbent is added into a system, particles at a higher level can integrate. The reaction rate constant for each level of reaction and particle concentration at each level can be computed by the Smoluchowski theory. Since crystallization to some degree can be seen as a process where the particles in the second phase aggregate and separate but the total size maintains unchanged, the population balance (PB) equation is a promising modeling tool. The PB model has undergone a large development form that only defines the particle as a sphere to consider three dimensional shape factors and growth rate variation on crystal faces [1].

Wang et al. [2] used PB equations as a basic theory to design a continuous crystallizer with the removal of fine crystals and conducted a detailed mathematical analysis. However, the limitation of the PB models may be its assumption that separates the nucleation process from Ostwald ripening. To handle this, Vetter et al. [3] have tested a hybrid kinetic reaction rate equation, including nucleation, crystal growth, and Ostwald ripening. A case study of the ADDopt project has tried to combine morphological PB with face specific growth rate data to predict the evolution of crystallization and further achieve the digital design of and control the manufacturing process. This model successively captures the evolution of the shape and size and the distribution of ibuprofen crystals in seeded batch crystallizers. The crystallization or precipitation can also be considered as the reverse of dissolution. Thus, the diffusion theory can also be used to simulate the precipitation. This method is popular and convenient, especially for biopharmaceutics investigations, where dissolution and following precipitation are usually modeled together if needed. One example is the spring-and-parachute-like dissolution profile, commonly seen in the solid dispersion formulation, which consists of a rapid dissolution and a slow precipitation process. This pattern of dissolution can be modeled by using an in-time-dependent solubility determined by the

maximal and eventual drug concentration and recrystallization rate constant. When the solubility gets less than the drug concentration at a certain time point, precipitation begins. This method has been proven to work well in amorphous temazepam formulation. Last, regarding the crystal surface as a sum of discrete points, departure or attachment of a single molecule off or to each point can be seen as a probability issue. Thus, the crystal growth process could be modeled by Monte Carlo simulation, similar to the dissolution process. A recent detailed review has introduced how to apply such a method to handle surface kinetic problems. The combination of Monte Carlo simulation and the first principle for electronic structure calculations seems to be a practical way to balance process modeling accuracy and efficiency.

Process simulation

The goal of the pharmaceutical industry is to produce stable and effective formulations. It is relatively easy to make a formulation with desired properties in the laboratory, but it will take more effort to manufacture qualified products on an industrial scale. The process simulation is a set of computational methods to control the quality of end products. So far, there are several good reviews about methodologies and applications of process simulation in the pharmaceutical industry. In the present review, these methods are introduced as process analytical technology (PAT), computational fluid dynamics (CFD) modeling, and the discrete element method (DEM). Some additional case studies using these methods are listed in Supplementary Table 4.

PAT and its application in pharmaceuticals

PAT strategy was early put forward in the FDA's guidance in 2004 to encourage pharmaceutical producers to utilize innovative technology to improve product quality. PAT strategy emphasizes the process understanding and integrates engineering principles, pharmaceutical science, and quality assurance in manufacturing processes design. A desired PAT system can monitor the critical quality attributes during the manufacturing process and manipulates the production lines to make sure the product quality. PAT should be a critical technique in the newly raised manufacturing strategy "continuous manufacturing" which highlights manufacturing from raw material to end product in a timely continuous manner. Currently, some measurement methods have been used in the PAT system. For

example, near-infrared spectroscopy (NIR) and focused beam reflectance measurement (FBRM) could be used to detect particle size, and Raman spectroscopy can measure the homogeneity in formulations. A PAT-based controlling system is introduced in the case study of crystallization to reduce the solvent content in crystals with bigger sizes. This system is named the automated direct nucleation control (ADNC) approach. When the solute completely dissolves, the ADNC is initialized and cool down the system until crystalline nucleation forms. The number of nucleation is counted by the system, and when nucleation achieves the upper limit number, ADNC automatically heats the system to dissolve nucleation shows the crystallization control route of the ADNC system. Cycles of heating and cooling facilitate nucleation at a smaller size to dissolve and precipitate on the crystals' surface with a bigger size, eliminating the solvent in crystals and enlarging their size, which benefits the downstream processing.

One tablet continuous manufacturing line involves a PAT system, which receives the NIR spectra from detectors attached after bender and tablet press and controls the material feeding. This system is developed basing on 460 spectra with various drug concentrations.

After validation, this PAT equipment can detect the error in feeding materials and stop the manufacturing process instantly. One 28-h manufacturing test with this system produced tablets 100.86% \pm 0.4% of label claim, showing the ability to control manufacturing accurate.

CFD modeling and its application in pharmaceuticals

Generally, there are two strategies to conduct a dynamic simulation. Suppose the number of particles contented in the considered system is large enough. In that case, usage of the average parameter value of these particles can precisely depict the disposition of the system, and there is no need to calculate the interactions between individual particles. In order to handle this situation, some model equations of the continuum approach can be used. The CFD is such a method, using numerical analysis and data structure to study the motion of flowing media, like fluid, gases, or powders. The basic theory of fluid dynamics includes conservation equations of mass, momentum, and energy, as well as state equations. These equations define the rules that substance mass and speed at every point in

the space of the system must conform to at any time.

In the pharmaceutical field, the CFD is often utilized in manufacturing process simulation to give understandings of underlying physical mechanics. First, CFD is usually used to investigate agitating processes, like mixing. A very recently published review. The typical route of ADNC for

controlling crystallization. (Redrawn from the article. W. Wangi Journal of Controlled Release 338 (2021) 119–136 128 discussed this topic in several aspects. The second situation involving CFD is granular material or powder flow. Models to handle this question were firstly referred to fluid or soil mechanics, and then combined kinetic theory of gas shows. CFD application in the granulation process has been introduced as one part of the review. Besides, two

other reviews have discussed CFD application to fluidized bed drying of wet porous granules and many other drying equipment types. Recently, there is an increasing interest in using CFD modeling to investigate the freeze-drying process. It can provide real-time information about the process where the flow visualization technique is difficult to apply in such low pressure. Alexeenko have used the CFD model to investigate the influence of the presence of clean in place (CIP)/sterilize in place (SIP) pipe

in connecting duct on the velocity of flow. This model is for a manufacturing scale where the Knudsen number is low. Thus, the gas flow is in agreement with continuum flow and could be solved by Navier-Stokes equation that depict the equilibrium in mass, momentum, and energy. The modeling result is that despite the section area of the CIP/SIP pipe only takes a 3% proportion of the whole connecting duct, it decreases the velocity of flow in the duct by 20%, consistent with 22% as the experimental value. Recently, Barresi and Rasetto and Marchisio introduced CFD modeling for lyophilization chamber, condenser duct, and valve. Authors have modeled multiple CFD results for freeze-drying equipment with different sizes, geometries, or configurations. Conclusions from these studies are profound because it gives clues about

how to optimize apparatus design. For example, the connecting duct is suggested to be deployed at the bottom of the chamber to make pressure on plates more uniform even though this is at the cost of increased pressure. Besides, similar operating conditions would possibly result in different pressure on plates of various sizes. Higher pressure is observed on plates with a larger size. Besides, CFD

is a helpful tool for the development of inhalation formulation.

An early review has simply introduced some flow parameters that impact the drug amount achieving alveoli part, such as tumor size in the airway, as well as the mechanics of particle growth of inhaled formulation. A later review specifically discussed how CFD is used to optimize the inhaler design. One recent study has used the CFD model to find a critical parameter utilized in children's inhalation design. The airway model is an idealized one that contains a mouth-throat and trachea-bronchial tree changing as a function of age. Drug

delivery systems of dry powder inhalers and nebulizer inhalers have been modeled. A dimensionless Stokes number has been used to characterize the disposition efficiency. The advantage of Stokes number is age independence. Stokes number at 0.06 and within the range of 0.03–0.04 indicates the dry powder inhaler and nebulizer inhaler achieve the highest disposition efficiency, respectively. This conclusion is useful for the development of inhalation for children. Besides, the commonly used human airway model for CFD does not consider the anonymous cartilage or ring-structure. However, this is improved in the newly developed Human Zygote5 model. Validation of CFD modeling with Zygote5 airway against observed dispositional data of Budesonide from dry powder inhalers shows a more consistent result than that from the traditional model. More dispositions of drugs are observed in the Zygote5 model.

If a flow cannot be considered a continuum flow, such as when the Knudsen number is large, CFD with Eulerian equations or Navier–Stokes equations will fail. In this case, DEM is more suitable. DEM is a Lagrangian model, which considers the interaction between elements by calculating the position, trajectory, and force burden of each unit and can address individual particle size distribution that cannot be processed in the continuum flow model. Thus, DEM is beneficial and commonly used in powder or granular pharmaceutical formulation. The basic concept or theory of DEM and its application has been comprehensively reviewed by Yeom. Recently Briefly, DEM is a process to calculate the force acting on each particle due to the collision, van der Waals interaction, liquid bridge, and electricity. Therefore, according to Newton's second law, update the position

information in each time step. So far, DEM has been used in many pharmaceutical processes, like milling, granulation, and coating, which have already been comprehensively reviewed. In another common situation where a liquid is co-existing with particles in a system either by happenstance or by design, the liquid's influence requires DEM modeling to handle more demanding conditions. Zhang and Wu recently have developed a DEM model for wet particles, and the simulated result is consistent with the elasto-hydrodynamic model. This study determines the Stokes number as a critical factor to influence rebound behavior. Further, an advanced CFD method, the lattice Boltzmann method, has been used with DEM to model the migration and aggregation of adhesive particles. Other applications of CFD-DEM modeling to the processes of separation, combination, filtration, and the processes in fluidized beds and bioreactors have also been very recently reviewed. Except for the applications reviewed above, other processes like freeze-drying also involves the usage of DEM modeling. The first step is randomly generating micro particles according to realistic particle size distribution. Then these micro particles are modeled to be thrown downwards and pile on the bottom of a vial. DEM models the collision between individual particles and calculates their motion. Following drying is modeled by the CFD model, and some packing properties like porosity, tortuosity, the average size of voids have been determined as related parameters to impact drying behavior.

PBPK Modeling & Simulation in Drug Development

What is PBPK Modeling & Simulation?

Physiological based pharmacokinetic modeling and simulation (PBPK) is a computer modeling approach that incorporates blood flow and tissue composition of organs to define the pharmacokinetics (PK) of drugs. The concept of PBPK was first described by Teorell in 1937. Simply put, PBPK is a tool to assess factors responsible for patient variability that impacts the PK of drugs. Alterations in PK properties, such as, absorption, distribution, metabolism, and excretion (ADME), can have a substantial impact on achieving the desired therapeutic concentration of a drug. Too low of a concentration results in ineffective therapy, and too high may result in side effects or even toxicity. PBPK is a powerful tool that requires modern computational power to handle the intense and complicated mathematical equations necessary

to make quantitative PK estimations and predictions. PBPK provides a mechanistic approach to study and predict the PK of drugs based on physiologic and anatomic characteristics, as well as the physical and chemical properties of a given drug. The goal of any drug or therapeutic intervention is to be effective without causing harm. Depending on the drug and the individual taking it, this can be a difficult task; nonetheless, this is an essential and actionable area for translational science. The utilization of intelligent PBPK models and simulations presents countless opportunities for improvements in drug development.

Methodology & Components of a PBPK Model

Non-compartmental analysis (NCA) is a standard PK modeling tool. NCA is an empirical model that lacks physiological meaning. NCA assumes that the dose administered is distributed uniformly throughout the body and that the elimination of the drug is defined through a rate constant that does not account for physiology. This modeling approach allows for rapid generation of PK parameter estimates but does not account for any physiological mechanisms or biological processes that drive or alter PK. Population pharmacokinetic analysis (PBPK) is another standard tool to describe the PK of a drug. Typically, population PK models are empirical as well but can also be semi-mechanistic. Alternatively, a PBPK model is based on physiology, biological processes, organ function, enzyme/transporter abundance and function, and blood flow, etc. PBPK modeling and simulation incorporates physiologically driven parameters that are responsible for PK variability among patients. The PBPK model allows us to include:

- Physico-chemical properties of the drug
- Specific physiological differences
- Trial design information. A population can be defined as nearly any group of people or clinical scenario such as:
 - Healthy patients
 - Patients with a tumor or disease that affects or alters organ function
 - Life event/stage (childhood, pregnancy, or post-surgery patients)

The patient's characteristics (age, sex, weight, body composition, organ function, genetics, etc.), can also be utilized and integrated in a PBPK model. The drug

properties used in PBPK models include molecular weight, log P, pKa, protein binding data, blood/plasma ratio, metabolism, permeability/solubility, transport mechanism, lipophilicity, etc. The model then can predict the PK of a drug before a study is conducted and the study can then be used to verify the prediction. Each cycle of prediction and verification from animal → healthy subjects' → to patient

*to special population - is accomplished by changing the physiological parameters within the model. Regulatory agencies have begun to accept PBPK modeling in place of many drug-drug interactions (DDI), pediatric, special population studies and more. PBPK modeling can also be referred to as bottom-up or mechanistic modeling and simulation.

Benefits and Applications of Using PBPK Models

The benefit of using PBPK modeling is that it is a cost-effective and robust predictive tool that is devoid of the ethical challenges associated with clinical trials in sensitive populations (e.g. cancer patients, pediatrics, pregnant women, etc.). The physiological effects that alter PK are vast and, in some cases, they are compounding. There is a critical need for PBPK investigation, especially for drugs with a narrow therapeutic window and sensitive patient populations. For example, applications can include pregnancy populations, organ transplant populations, and bariatric surgery patients

PBPK Limitations

PBPK models utilize assumptions about the rates of each individual process and sometimes these rates may be unknown. In these cases, sensitivity analyses can be undertaken to understand the consequences of uncertainty. Another limitation is that PBPK models tend to describe the average person with a disease of interest but does not describe inter-individual variability and unexplained variability (in contrast to population PK modeling). This limitation can be

overcome by sensitivity analyses with high and low values for important characteristics.

The future of computational pharmaceutics

Prospective contribution of computational pharmaceutics

“Today the computer is just as important a tool for chemists as the test tube.” (Karplus, Levitt and Warshel, Nobel Prize in Chemistry 2013) Analogous to the computer-aided method shifting the paradigm of drug design in the past three decades, computational methods also have great potential to change the approach of the pharmaceutical industry in the future. On the one hand, computational pharmaceuticals will promote the paradigm shift of drug delivery development. In the future, the QbD strategy should be the mainstream adopted for the formulation design to guarantee product quality. QbD stresses the integration of process understanding into the design, which is definitely benefited from modeling methods. The AI model gives suggestions based on the principle underlying the data, and molecular modeling, PBPK, and mathematical modeling simulate the formulation behavior from multiple scales, supplying mechanical explanation to *in vitro* and *in vivo*. Structure of newly developed PBPK model for cyclodextrin (CD) formulation (redrawn from the original article). W. Wan *et al.* *Journal of Controlled Release* 338 (2021) 119–136. On the other hand, computational pharmaceuticals will accelerate drug production. Future drug manufacturing should prefer the continuous manufacturing pipeline, which highlights the connection between producing units to avoid unnecessary exposure of the substance to the atmosphere and reduce the risk of error related to human manipulations. The continuous manufacturing relies on the PAT system, which can automatically supervise and control the production line during the process. Building a PAT system needs data science, requiring the AI method. The CFD and DEM method can simulate the manufacturing process, supplying process understanding about the PAT system. The era that pharmaceuticals is sufficiently supported by computational approach is expected as “Parma 4.0” where the drug and forms shall be in better design and the manufacturing process shall be digitized and automatically decided, performed, and controlled. As a result, the product with high quality shall be supplied to patients more efficiently.

Data challenges and opportunities with the increasingly complex learning task, sufficiently huge and diverse data were required for model training. In practice, we were rarely able to find enough training data in individual institutions. A practical way to access more data is to collaborate with others, like taking part in cooperative projects such as OrBiTo and ADD opt. However, data sharing

faces great challenges of privacy and data ownership. A federated learning strategy can promote multi-institutional collaboration without sharing data. Federated learning utilizes multi-institutional data by distributed model-training. A 10-institutional federated learning results in the model performance as good as 99% of the model that is trained on aggregated data, superior to other collaborative learning approaches. Another problem hindering data sharing is the heterogeneity in format or structure of different data sources [188, 194, 195]. A driving force from the regulatory agencies may promote the unification of data structure. KASA system, which is announced by FDA recently to assess the product risk and quality, is data and algorithm based. Submitters to KASA may make their data compatible with the system. High-throughput and automatic experimental method Computational pharmaceutical approaches also ask the way we

produce data and validate against models to speed up. A high throughput platform is one of the promising methods that perform a large number of experiments in a batch with high homogeneity. The results of this method are with high credit to validate against those predicted data newly developed tools. This validation also helps to determine the boundary conditions of these models. Besides, an automatic robot would further enhance the experiment efficiency. Linking the laboratory equipment and experimental results in one network can facilitate the process of data and reduce human error.

Talent training and maintaining

Computational pharmaceuticals counts on knowledge from both computational science and pharmaceuticals. However, there is a big gap between pharmaceutical scientists and computational scientists. Current computational tools are still loosely connected to each other and are hard to be used by pharmaceutical scientists. A serious problem is the lack of talent with both computational and pharmaceutical backgrounds and experiences. Initializing related education schemes covering undergraduate, postgraduate even Ph.D. periods is necessary to improve this situation. A new course, “Computational Pharmacy”, was developed for the postgraduate at the University of Macau in 2015 and has achieved good student feedbacks. Besides, some stimuli are needed to promote people becoming experts in multi-

discipline, such as funding and collaborative projects. However, this requires a change in culture in the pharmaceutical industry. A platform where researchers can communicate with each other can also promote the development of computational pharmaceuticals. Recently, the Computational Pharmacy Society was founded in November 2020. Furthermore, Computational Pharmaceuticals became the first theme of the Asian Pharmaceuticals Online Symposium. These actions mark that this new interdisciplinary field has attracted more attention from pharmaceutical scientists and practitioners.

Culture change in pharmaceuticals

It is no doubt that traditional pharmaceutical development is highly costly, which asks for modern pharmaceutical companies to take a more efficient way to develop competitive products. Some researchers combine computational techniques with pharmaceuticals and make progress. These investigations accelerate the development. Thus, the first understanding of computational pharmaceuticals is to realize the substantial benefit brought about by computational pharmaceuticals. Second, computational techniques bring is not only about the profit on time or economy but also reveals more knowledge about pharmaceuticals. Conventional pharmaceutical R&D is based on the trial-and error method, and the decision is made according to empirical knowledge, leaving some basic questions unresolved. However, we cannot solve problems “at the same level we created them”, and “a new type of thinking is essential if mankind is to survive and move to higher levels. Thus, we need computational methods in pharmaceuticals. In 1930, David Hilbert cited KANT's declaration in his famous speech, “I maintain that in each particular natural science there is only as much true science as there is mathematics.” Computational methods visualize the process, details how materials transfer and transform, and determine factors that significantly impact product quality. Knowing better about the process leads to safer and efficient formulations. Third, we should realize that the industry paradigm shift cannot be accomplished in a short period. Al has not shown market relevance for W. Wang et al. Journal of Controlled

Release 338 (2021) 119–136 132 the core strategies of most leading pharmaceutical companies that already have applied AI technology

at least until 2018. Therefore, it would be better to realize that involving computational techniques probably would cost considerable money and time but not produce a significantly observable profit in the near future. Historical materials typically tell that a successful revolution relies on long-term investment. During the First Industrial Revolution, the proportion of Britain's national income invested in purchasing long-lasting capital assets for future production was successively increasing for the whole period in that era. Moreover, electricity, which is the symbol of the second industrial revolution, did not result in considerable growth in productivity until 1914–1917, the last stage of the Second Industrial Revolution, after major investments were dedicated to large central power plants and large-scale power transmission grids. Therefore, there was a long delay in the profit resulted from industry electrification.

Interestingly, this similar delay could also be seen in the early stage of the Third Industrial Revolution, where the productivity did not increase in parallel with the development of information technology, which has even led to a novel concept of “productivity paradox” that has been debated until now. However, time has told how much the information revolution influences our modern life so far. The “productivity paradox” may be attributed to the difference in the financial nature between information and normal products or commodities, as early discussed by David. The traditional “market-oriented indicators of productivity” may not be suitable to account for the value of information and data. The “productivity paradox” vividly represents the relationship between economic development and industrial evolution, just like the indispensable significance of the Financial Revolution for the First Industrial Revolution. Therefore, from this perspective, a new quantitatively economic tool may be necessary to correctly describe the contribution of computational technology to the pharmaceutical industry. This development also helps to evaluate the work of multidisciplinary experts in companies and attract more talents into this area

CONCLUSION

Pharmaceuticals research has utilized a variety of computational pharmaceutical techniques in recent years. The application converted in this most recent assessment including A.I, PBPk molding, Mathematical molding, Process

simulation, Molecular modeling .By lowering the number of trial and error cycles and providing a better knowledge of formulations , computational approaches should lower the cost of pharmaceuticals R/D . But pharmaceutical's computational techniques are far from what is anticipated. For upcoming computational pharmaceuticals, an integrated approach is proffered. The many factors must be improved in order to achieve this modernization of experiment and production facilities, as well as data standardization and sharing are essentially technical components. The most crucial factor is to develop and preserve enough talent in this unique field. In order to successfully advance the paradigm shift and bring about pharma 4.0, we must currently appreciate the importance of computational pharmaceuticals, Maintain our trust ,and exercise patience.

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