Table 1. Cross track (CT) and along track (AT) errors for VSCS *Phailin* in the NCMRWF global models

Models	Day-0	Day-1	Day-2	Day-3
NGFS (CT)	6	–33	–24	45
NCUM (CT)	17	30	25	18
NGFS (AT)	–47	–89	–192	–219
NCUM (AT)	–20	–54	–85	–106

AT '–ve' (+ve) slow (fast) moving; CT '–ve' (+ve) left (right) of observed track.

Table 2. Forecast landfall position and time error for VSCS *Phailin* in the ESSO-NCMRWF global models

	NGFS		NCUM	
Initial condition	Position error (km)	Time error (h)	Position error (km)	Time error (h)
09102013	31	+15	47	+15
10102013	84	+15	11	+3
11102013	42	+9	39	+3
12102013	115	+15	69	+3

IMD reported landfall at 1500 UTC of 12 October at 19.1N 85.0E; time error '+' denotes delay and '–' denotes early.

Table 3. RMSE (mm/day) in the rainfall forecasts valid for 0000 UTC of 14 October 2013 based on NGFS and NCUM at different lead times over eastern India

	Day-1	Day-2	Day-3	Day-4	Day-5
NGFS	58.6	62.2	68.8	74.5	85.5
NCUM	47.4	50.9	52.5	55.5	76.9

NCUM. The panels show the 24 h accumulated rainfall from 13 October 2013 (mm) along with detailed summary statistics. Based on the contingency table in the figure, observed and forecast raining grids (>1 mm/day), various scores are computed. NCUM forecasts have higher (lower) correlation and equitable threat score (ETS) (RMSE, bias and false alarm). Table 3 shows RMSE at all lead times, to clearly suggest high RMSE in NGFS forecasts. Similar verification for NGFS (not shown) shows relatively poor performance compared to NCUM forecasts. Figure 2 *c* shows the skill of the rainfall forecast by both models at all lead times. ETS and correlation coefficient show that NCUM has higher skill in predicted rainfall after landfall up to four days in advance, after which skill is generally low in both models.

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Elucidation of drug–DNA intercalation binding mode

The interactive study of small molecules with double-stranded DNA has been a topic of research for a few decades to get control gene expression. A number of drugs, especially those with planar moiety, bind to DNA and help suppress or depress the replication and transcription processes. The binding via intercalation mode is reversible in nature which makes it advantageous over covalent binding, keeping drug metabolism and harmful side effects in view[1]. The Van der Waals, stacking and electrostatic forces are mainly responsible for the intercalation mode of binding. The drugs like proflavine, ethidium bromide and actinomycin D contain planar aromatic rings responsible for intercalation[2]. Many biophysical and computational techniques are used to illustrate the intercalation mode of binding. Generally small molecules (ligands) show an absorption peak in the visible region in UV–visible absorption spectrum. Hypochromic effect and bathochromic

shift (red shift) in UV–Vis spectrum are observed when a ligand binds to DNA via intercalating mode[3]. The intrinsic binding constant/association constant (K_b) can be calculated using Benesi–Hildebrand, double reciprocal curve and Scatchard plot. The fluorescence spectroscopy is a high sensitive technique to study the drug–DNA interactions. To study the mode of binding of a drug to DNA, the acridine orange (AO) displacement assay can be carried out. The intercalation binding mode is present if on the addition of ligand, the fluorescence of AO–DNA complex is effectively quenched[4]. Also, a decrease in K_{SV} (Stern–Volmer quenching constant) values is observed in intercalation binding mode. Cyclic voltammetry is also a good tool to study drug–DNA interactions, which gives weak absorption bands. This technique is mainly used for metal-based compounds due to their accessible redox state. The shift of peak potential to less negative values is reminiscent of intercalation of drug into DNA[5].

The thermal melting experiment can be used to study the interaction between ligands and DNA. The temperature at which half of the DNA strands are in the random coil state is known as melting temperature (T_M). When a ligand binds to DNA, a change in its melting temperature occurs depending on strength of interaction between them. The melting temperature of DNA generally increases on binding of a ligand in case of intercalation binding mode, as it shows the higher stability of its duplex structure on interaction with the ligands. The helix denaturation of DNA can be measured by the absorbance of DNA bases at 260 nm as a function of temperature. It is already reported that the intercalative binding increases T_M up to 3–8°C (ref. 6). Circular dichroism (CD) spectroscopy is a handy method to examine the optically active materials such as DNA. The CD spectrum of calf thymus DNA consists of a negative band at 245 nm due to helicity and positive band at 275 nm due to base stacking, which is typical of B form DNA, in the ultraviolet region[7]. On addition of ligand to DNA, the increase in the CD signal around 275 nm wavelength is an important affirmation of intercalation of the ligand into the double helix of DNA. Viscometry is also an important technique to find out the mechanism of drug–DNA complex. On intercalation of ligand into the double helix of DNA, the distance between base pairs is increased, due to which an increase in viscosity of DNA can be observed[8].

Molecular docking analysis can play an important role in drug design and correlate the experimental data with computational data. Docking analysis can be done by using AutoDock, PyMol, Spherical Polar Fourier (SPF), X3DNA, Discovery Studio and many other programs. With the help of docking analysis, we can calculate the binding and inhibition constant which give confirmation of interacalation of ligand if binding energy is found in –5 to –7 kcal/mol (refs 9, 10). The interaction study of drug–DNA can be done by many techniques, we have summarized a few of them briefly.

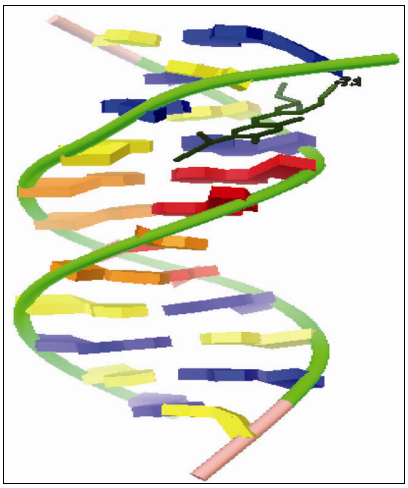

Figure 1. A pictorial representation of drug–DNA intercalation.

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